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OM protein - protein search, using sw model
 Run on: February 20, 2003, 10:05:32 ; Search time 30.834 seconds

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searches: 908470 seqs, 133250620 : residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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6: /SIDS2/gcgdata/geneseq/geneseq/geneseqp-emb1/AA1985.DAT:*

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23: /SIDS2/gcgdata/geneseq/geneseq/geneseqp-emb1/AA2002.DAT:*

Pred. NO. 18 the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query	Length	DB ID	Description
1	2218	100.0	425	16	AAR77338
2	2218	100.0	425	20	AAY05854
3	2218	100.0	425	20	AAY05510
4	2218	100.0	425	20	AAN97655
5	2218	100.0	425	20	AIW94488
6	2218	100.0	425	21	AAY95972
7	2218	100.0	425	21	AAY95281
8	2218	100.0	425	21	AAY96243
9	2218	100.0	425	21	AAY70576
10	2218	100.0	425	22	AKG65743

SUMMARIES

RESULT 1
 ID AAR77338 standard; Protein: 425 AA.
 AC AAR77338;
 DT 22-FEB-1996 (first entry)
 DE Chicken sonic hedgehog protein.
 KW Chicken; sonic hedgehog protein; stage 22/22 limb bud; probe;
 KW primer; diagnostic; nervous system disorder; gene therapy;
 KW antibody.
 XX OS Gallus domesticus.
 FH Key Location/Qualifiers
 FT Peptide 1..26 /note= "putative signal peptide"
 FT Peptide 27..32 /note= "conserved sequence (AAR77339)"
 FT Modified-site 282 /note= "N-linked glycosylation site"

(HARD) HARVARD COLLEGE.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
PA
XX Ingham PW, McMahon AP, Tabin CJ;
PI
XX DR WPI; 1995-255050/33.
DR N-PSDB; AAXQ91636.

PT Hedgehog-like protein(s) and nucleic acid(s) encoding them - useful
PT to treat degenerative nervous system disorder(s) and in gene
PT therapy.
XX
PS Claim 17; Page 133-35; 210pp; English.

Query Match 100 %; Score 2218; DB 16; Length 425;
Best Local Similarity 100 %; Pred. No. 1.7e-227; Mismatches 0; Indels 0; Gaps 0;
Matches 425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVEMILLTRILVERGICALIVSSGLTGGORGIGKRRRHKPLTPLAYKOPIPNVAEKTG 60
Db 1 MVEMILLTRILVERGICALIVSSGLTGGORGIGKRRRHKPLTPLAYKOPIPNVAEKTG 60
Qy 61 ASGRYEGKTRNRSERFKELTNPYNDIFKDEENTGADRMLTORCKDKUNALATSVMNOW 120
Db 61 ASGRYEGKTRNRSERFKELTNPYNDIFKDEENTGADRMLTORCKDKUNALATSVMNOW 120
Qy 121 PGVKLRLVTGEGWDEDGHHSSESLHYEGRAVDITTSRDRSKYGMARLAVEAGFDWVYES 180
Db 121 PGVKLRLVTGEGWDEDGHHSSESLHYEGRAVDITTSRDRSKYGMARLAVEAGFDWVYES 180
Qy 181 KAHHRCSVKALENSVAKSGCCFPSSATVHLEHGSKPLKLDSLSPDRVLAAADGRLLYSD 240
Db 181 KAHHRCSVKALENSVAKSGCCFPSSATVHLEHGSKPLKLDSLSPDRVLAAADGRLLYSD 240
Qy 241 FLTFEDRMDSSRKRYVIETQPRAHLTAHHLFVAPORNQSBATGSTSGQNLFSNV 300
Db 241 FLTFEDRMDSSRKRYVIETQPRAHLTAHHLFVAPORNQSBATGSTSGQNLFSNV 300
Qy 301 KPGQRVYVIGEGGQQLPASVHSYLRESEAAGAALPATAATTGTHWMSRLYLVIGSWLQDGDLHPIGM 360
Db 301 KPGQRVYVIGEGGQQLPASVHSYLRESEAAGAALPATAATTGTHWMSRLYLVIGSWLQDGDLHPIGM 360
Qy 361 WAHWAFAFPFLQAGLIAACPDGAALPTAAATTGTHWMSRLYLVIGSWLQDGDLHPIGM 420
Db 361 WAHWAFAFPFLQAGLIAACPDGAALPTAAATTGTHWMSRLYLVIGSWLQDGDLHPIGM 420
Qy 421 VAPAS 425
Db 421 VAPAS 425
SQ Sequence 425 AA;

Query Match 100 %; Score 2218; DB 20; Length 425;
Best Local Similarity 100 %; Pred. No. 1.7e-227; Mismatches 0; Indels 0; Gaps 0;
Matches 425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVEMILLTRILVERGICALIVSSGLTGGORGIGKRRRHKPLTPLAYKOPIPNVAEKTG 60
Db 1 MVEMILLTRILVERGICALIVSSGLTGGORGIGKRRRHKPLTPLAYKOPIPNVAEKTG 60
Qy 61 ASGRYEGKTRNRSERFKELTNPYNDIFKDEENTGADRMLTORCKDKUNALATSVMNOW 120
Db 61 ASGRYEGKTRNRSERFKELTNPYNDIFKDEENTGADRMLTORCKDKUNALATSVMNOW 120
Qy 121 PGVKLRLVTGEGWDEDGHHSSESLHYEGRAVDITTSRDRSKYGMARLAVEAGFDWVYES 180

KW cutaneous tissue; skin; hair; wound healing; vulvar; burn; skin grafting; pressure sore; ulcer; ulcerative colitis; alopecia; psoriasis; keratosis; acne; comedogenic lesions; folliculitis; pseudofolliculitis; keratoacanthoma; callosities; Darier's disease; scar; autoimmune disease; pemphigus; epidermolysis; lupus lesion; desquamative lesion; carcinoma; therapy; hedgehog therapeutic; ptc therapeutic; patched.

XX OS Gallus domesticus.

XX PN WO9920298-A1.

XX PD 29-ARR-1999.

XX PR 20-OCT-1998; 98WO-US22227.

XX PR 11-SEP-1998; 98US-0151999.

PR 20-OCT-1997; 97US-0955552.

XX PR (ONTO-) ONTOGENY INC.

XX PI Wang EA;

XX DR WPI; 1999-288170/24.

XX N-PSDB; AAX25617.

PT Use of hedgehog polypeptides on patched therapeutics

PS Claim 26; Page 119-120; 146pp; English.

XX The present sequence represents chicken Sonic hedgehog protein shh. The invention relates to a method for modulating the growth state an epithelial cell by ectopically contracting the epithelial cell, in vitro or in vivo, with a hedgehog therapeutic (i.e. a hedgehog polypeptide or gene therapy construct) or ptc therapeutic (i.e. a small organic molecule that mimics the effect of hedgehog proteins on patched signalling, or activates or potentiates patched signalling) in an amount effective to alter the rate of proliferation of the epithelial cell. The hedgehog therapeutic preferably comprises at least a biactive extracellular portion of a hedgehog protein (see AAY05854-62), encoded by a vertebrate hedgehog gene (see AAX2617-25), especially a human hedgehog gene. Promotion of proliferation of epithelial cells can be used to control a wound healing process in e.g. burn treatment, skin regeneration, skin grafting, pressure sore treatment, dermal ulcer treatment, post surgery scar reduction or treatment of ulcerative colitis (claimed). It can also be used to induce hair growth for the treatment of alopecia (claimed). Inhibition of the growth of epithelial tissue can be used to treat or prevent hyperplastic or neoplastic conditions, e.g. psoriasis, keratoses, acne, comedogenic lesions, folliculitis and pseudofolliculitis, keratoacanthoma, callosities, disorders, e.g. aphthous ulcers, pemphigus vulgaris, pemphigus foliaceus, pemphigus vegetans, pemphigus erythematosus, epidermolysis, lupus lesions, desquamative lesions or carcinomas. The methods can also be used to counteract the effects of ageing on skin.

XX SQ Sequence 425 AA;

Query Match 100 %; Score 2218; DB 20; Length 425;
Best Local Similarity 100 %; Pred. No. 1.7e-227; Mismatches 0; Indels 0; Gaps 0;
Matches 425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVEMILLTRILVERGICALIVSSGLTGGORGIGKRRRHKPLTPLAYKOPIPNVAEKTG 60
Db 1 MVEMILLTRILVERGICALIVSSGLTGGORGIGKRRRHKPLTPLAYKOPIPNVAEKTG 60
Qy 61 ASGRYEGKTRNRSERFKELTNPYNDIFKDEENTGADRMLTORCKDKUNALATSVMNOW 120
Db 61 ASGRYEGKTRNRSERFKELTNPYNDIFKDEENTGADRMLTORCKDKUNALATSVMNOW 120
Qy 121 PGVKLRLVTGEGWDEDGHHSSESLHYEGRAVDITTSRDRSKYGMARLAVEAGFDWVYES 180

Db	121 PGVLRVYEGWDEGGHSEESLHYEGRADITTSRDRSKYGMARLAVAGEFDWVYES 180	CC	(all claimed). The hedgehog polypeptide or ptc therapeutic can inhibit growth of myoblastic-derived tissue to provide treatment of hyperplastic or neoplastic growth of muscle tissue such as in myoblastic sarcoma (also claimed). The hedgehog therapeutic preferably comprises at least a bioactive extracellular portion of a hedgehog protein (see AAX25098-107), especially a human hedgehog gene.
Db	241 FLFELDRMDSRKFLFYVETRQPARLLTAHLFLVAPQHNSSEATGSTSGQALFASNV 300	CC	
Db	301 KPGQRVYVLGEQQQLPASVHSRBRASGAYAPLTAQPTGTLINRVASCYAVIEENS 360	CC	
Qy	361 WAHWAFAFLRAQGLLAALCPDGAIAPTAATTGIGHWYSRLYRIGSWVLGDGAHPLGM 420	CC	
Db	361 WAHWAFAFLRAQGLLAALCPDGAIAPTAATTGIGHWYSRLYRIGSWVLGDGAHPLGM 420	CC	
Qy	421 VAPAS 425	CC	
Db	421 VAPAS 425	CC	
RESULT 3		XX	Sequence 425 AA;
AAY05510		XX	
ID AAY05510 standard; Protein: 425 AA.		XX	
AC AAY05510;		XX	
DT 05-JUL-1999 (first entry)		XX	
DE Chicken Sonic hedgehog protein Shh.		XX	
KW Sonic hedgehog; Shh protein; chicken; hedgehog therapeutic; Ptc therapeutic; patched; signal transduction; muscle atrophy; cachexia; muscular myopathy; myoblastic sarcoma; therapy.		XX	
KW Gallus sp.		XX	
OS Gallus sp.		XX	
PN WO9910004-A2.		XX	
PD 04-MAR-1999.		XX	
PF 28-AUG-1998;	98WO-US17922.	XX	
PR 29-AUG-1997;	97US-0057394.	XX	
PA (ONTO-) ONTOGENY INC.		XX	
PT Bladgen CS, Currie PD, Hughes SM, Ingham PW;		XX	
XX WPT; 1999-243557/20.		XX	
DR N-PSSB; AAX25098.		XX	
PT A new method to regulate muscle growth		XX	
PS Disclosure; Page 111-112; 13pp; English.		XX	
CC The present sequence is chicken sonic hedgehog protein Shh. The invention relates to a method for modulating the formation and/or maintenance of muscle tissue by ectopically contacting muscle cells, especially muscle stem/progenitor cells, in vitro or in vivo, with a hedgehog therapeutic (i.e. hedgehog polypeptides and gene therapy constructs) or ptc therapeutic (i.e. a small organic molecule that mimics the effect of hedgehog proteins on patched signalling, or activates or potentiates patched signalling) in an amount effective to alter the growth state of the treated cells. Also claimed is a method for treatment or prevention of disorders of, or surgical or cosmetic repair of, such muscle tissues, by administering a hedgehog polypeptide or ptc therapeutic. The disorder may be muscle atrophy, in particular skeletal muscle atrophy or cardiac muscle atrophy, cachexia, or muscular myopathy.			
Db	121 PGVLRVYEGWDEGGHSEESLHYEGRADITTSRDRSKYGMARLAVAGEFDWVYES 180	CC	
Db	241 FLFELDRMDSRKFLFYVETRQPARLLTAHLFLVAPQHNSSEATGSTSGQALFASNV 300	CC	
Qy	301 KPGQRVYVLGEQQQLPASVHSRBRASGAYAPLTAQPTGTLINRVASCYAVIEENS 360	CC	
Db	361 WAHWAFAFLRAQGLLAALCPDGAIAPTAATTGIGHWYSRLYRIGSWVLGDGAHPLGM 420	CC	
Qy	421 VAPAS 425	CC	
Db	421 VAPAS 425	CC	
RESULT 4		XX	Sequence 425 AA;
AAY97765		XX	
ID AAY97765 standard; Protein: 425 AA.		XX	
AC AAY97765;		XX	
DT 21-MAY-1999 (first entry)		XX	
DE Chicken Sonic hedgehog (shh) protein.		XX	
KW Sonic hedgehog; Shh protein; chicken; dopaminergic; GABA-nergic; Ptc therapeutic; patched; signal transduction; Parkinson's disease; Huntington's disease; amyotrophic lateral sclerosis; cerebral ischaemia; hypoxia; neuroprotective; therapy.		XX	
KW Gallus domesticus.		XX	
OS WO9904775-A2.		XX	
PD 04-FEB-1999.		XX	
PF 24-JUL-1998;	98WO-US15419.	XX	
PR 24-JUL-1997;	97US-0900220.	XX	
PA (ONTO-) ONTOGENY INC.		XX	

RESULT 5									
PI	AAW94468	ID	AAW94468						
XX	XX	XX	XX						
PT	AAW94468;	AC	AAW94468;						
DR	XX	XX	XX						
XX	XX	XX	XX						
PT	29-APR-1999 (first entry)	DT	29-APR-1999 (first entry)						
PT	Chicken Shh hedgehog protein sequence.	DE	Chicken Shh hedgehog protein sequence.						
XX	KW	KW	KW						
XX	Patched; hedgehog; ptc therapeutic; neuroprotective; neuronal cell; brain infarction; cerebral infarction; transient ischaemic attack; stroke; cerebral infarct volume; spinal cord oedema; trauma; haemorrhage; encephalomyelitis; coronary bypass; cerebral hypoxia.	KW	KW						
XX	Gallus sp.	OS	Gallus sp.						
XX	PN09900117-A2.	PN	PN09900117-A2.						
XX	PD07-JAN-1999.	PD	PD07-JAN-1999.						
XX	PR26-JUN-1998;	PR	PR26-JUN-1998;						
XX	98WO-US13387.	XX	98WO-US13387.						
XX	27-JUN-1997;	XX	27-JUN-1997;						
XX	97US-0883656.	PA	97US-0883656.						
XX	(ONTO-) ONTOGENY INC.	XX	(ONTO-) ONTOGENY INC.						
XX	Mahanthappa NK;	PT	Mahanthappa NK;						
XX	DRWPI: 1999-095158/08.	DR	DRWPI: 1999-095158/08.						
XX	N-PSDB; AX16182.	XX	N-PSDB; AX16182.						
PT	Method for limiting damage to neurons caused by ischaemic or epoxic conditions - is used for the treatment and prevention of e.g. cerebral infarction, stroke and transient ischaemic attacks	PT	Method for limiting damage to neurons caused by ischaemic or epoxic conditions - is used for the treatment and prevention of e.g. cerebral infarction, stroke and transient ischaemic attacks						
XX	Disclosure: Page 63-64; 104pp; English.	XX	Disclosure: Page 63-64; 104pp; English.						
CC	A method has been developed for limiting the damage to neuronal cells by ischaemic or epoxic conditions by administering a ptc (patched) therapeutic agent to reduce cerebral infarct volume (CIV). Damage to neuronal cells can also be limited by administering a gene activation construct which recombines with the genomic hedgehog gene to provide a heterologous transcription regulator linked to the coding region of this gene. Administration of the ptc therapeutic agent is used to protect cerebral tissues against ischaemic injury, to treat cerebral infarct or ischaemia, stroke (thrombotic or embolic), and transient ischaemic attacks. It may also be used as a prophylactic in many other cases of injury to the brain or spinal cord, oedema caused by trauma, haemorrhage and encephalomyelitis, or in conjunction with (coronary bypass) surgery. Treatment (which may be prophylactic) is used where ischaemic/epoxic conditions may cause cerebral hypoxia, or progressive loss of neurons due to oxygen depletion, including in patients with hypotension. The treatment reduces CIV by at least 25, particularly at least 70%. The present sequence represents a hedgehog sequence given in the present invention.	CC	A method has been developed for limiting the damage to neuronal cells by ischaemic or epoxic conditions by administering a ptc (patched) therapeutic agent to reduce cerebral infarct volume (CIV). Damage to neuronal cells can also be limited by administering a gene activation construct which recombines with the genomic hedgehog gene to provide a heterologous transcription regulator linked to the coding region of this gene. Administration of the ptc therapeutic agent is used to protect cerebral tissues against ischaemic injury, to treat cerebral infarct or ischaemia, stroke (thrombotic or embolic), and transient ischaemic attacks. It may also be used as a prophylactic in many other cases of injury to the brain or spinal cord, oedema caused by trauma, haemorrhage and encephalomyelitis, or in conjunction with (coronary bypass) surgery. Treatment (which may be prophylactic) is used where ischaemic/epoxic conditions may cause cerebral hypoxia, or progressive loss of neurons due to oxygen depletion, including in patients with hypotension. The present sequence represents a hedgehog sequence given in the present invention.						
SQ	Sequence 425 AA;	SQ	Sequence 425 AA;						
Query	Match 100.0%; Score 2218; DB 20; Length 425;	Query	Match 100.0%; Score 2218; DB 20; Length 425;						
Best Local Similarity 100.0%; Pred. No. 1.7e-227; Matches 425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Best Local Similarity 100.0%; Pred. No. 1.7e-227; Matches 425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
CC	1 MVEMMLTRILLVFGFICALIVSSGLTCTGPGRGIGKRRHKKLPLAKOIFPNAEKTLG 60	CC	1 MVEMMLTRILLVFGFICALIVSSGLTCTGPGRGIGKRRHKKLPLAKOIFPNAEKTLG 60						
Db	1 MVEMMLTRILLVFGFICALIVSSGLTCTGPGRGIGKRRHKKLPLAKOIFPNAEKTLG 60	Db	1 MVEMMLTRILLVFGFICALIVSSGLTCTGPGRGIGKRRHKKLPLAKOIFPNAEKTLG 60						
QY	61 ASGRYEGKTRNSRKFELTPNNDIIFKDEENITGADRMLTQCKDKNLATISVMNOW 120	QY	61 ASGRYEGKTRNSRKFELTPNNDIIFKDEENITGADRMLTQCKDKNLATISVMNOW 120						
Db	61 ASGRYEGKTRNSRKFELTPNNDIIFKDEENITGADRMLTQCKDKNLATISVMNOW 120	Db	61 ASGRYEGKTRNSRKFELTPNNDIIFKDEENITGADRMLTQCKDKNLATISVMNOW 120						
QY	121 PGVKLRVTEGGDGHHSBESLHYEGRAVDITTSDRDRSKYGMARLAVEAGEDWVYES 180	QY	121 PGVKLRVTEGGDGHHSBESLHYEGRAVDITTSDRDRSKYGMARLAVEAGEDWVYES 180						
Db	121 PGVKLRVTEGGDGHHSBESLHYEGRAVDITTSDRDRSKYGMARLAVEAGEDWVYES 180	Db	121 PGVKLRVTEGGDGHHSBESLHYEGRAVDITTSDRDRSKYGMARLAVEAGEDWVYES 180						
QY	181 KAHHCWSVKAESTAAKGCFPSATVHLEHGKTKLVLDSRCPDRVLAAADGRLYSD 240	QY	181 KAHHCWSVKAESTAAKGCFPSATVHLEHGKTKLVLDSRCPDRVLAAADGRLYSD 240						
Db	181 KAHHCWSVKAESTAAKGCFPSATVHLEHGKTKLVLDSRCPDRVLAAADGRLYSD 240	Db	181 KAHHCWSVKAESTAAKGCFPSATVHLEHGKTKLVLDSRCPDRVLAAADGRLYSD 240						
QY	241 PLTFIDRMDSRSKRFYVETRQPRAILTAHHLFVARQHNSSEATGSTSGOFLASNV 300	QY	241 PLTFIDRMDSRSKRFYVETRQPRAILTAHHLFVARQHNSSEATGSTSGOFLASNV 300						
Db	241 PLTFIDRMDSRSKRFYVETRQPRAILTAHHLFVARQHNSSEATGSTSGOFLASNV 300	Db	241 PLTFIDRMDSRSKRFYVETRQPRAILTAHHLFVARQHNSSEATGSTSGOFLASNV 300						
QY	301 KPGGRVYVIGEGQQLPASVHSLSREASAGAAMPLAQTTINRYASCYVIEEHS 360	QY	301 KPGGRVYVIGEGQQLPASVHSLSREASAGAAMPLAQTTINRYASCYVIEEHS 360						
Db	301 KPGGRVYVIGEGQQLPASVHSLSREASAGAAMPLAQTTINRYASCYVIEEHS 360	Db	301 KPGGRVYVIGEGQQLPASVHSLSREASAGAAMPLAQTTINRYASCYVIEEHS 360						
QY	361 WAHHAFAPERLAQDLAALCPCGPIPTATTGIIHWYSLRLYRIGSWLGDGLAHPLGM 420	QY	361 WAHHAFAPERLAQDLAALCPCGPIPTATTGIIHWYSLRLYRIGSWLGDGLAHPLGM 420						
Db	361 WAHHAFAPERLAQDLAALCPCGPIPTATTGIIHWYSLRLYRIGSWLGDGLAHPLGM 420	Db	361 WAHHAFAPERLAQDLAALCPCGPIPTATTGIIHWYSLRLYRIGSWLGDGLAHPLGM 420						
QY	421 VAPAS 425	QY	421 VAPAS 425						
Db	421 VAPAS 425	Db	421 VAPAS 425						
QY	121 PGVKLRVTEGGDGHHSBESLHYEGRAVDITTSDRDRSKYGMARLAVEAGEDWVYES 180	QY	121 PGVKLRVTEGGDGHHSBESLHYEGRAVDITTSDRDRSKYGMARLAVEAGEDWVYES 180						

Db 121 PGVKLAVTEGWDDEGHSEESLHYGRAVDITTSQRDRSKYGMARLAVEGFDWVYES 180
 CC |||||||
 CC especially a human) by administering a lipid modulator selected
 CC from a hedgehog antagonist or hedgehog agonist. In particular, the
 CC lipid metabolism disorder is a lipid storage disorder, a lipid
 CC transport disorder, a triglyceride metabolism disorder, a triglyceride
 CC disorder, e.g. a triglyceride storage disorder; a
 CC transport disorder or a triglyceride storage disorder; a
 CC diet-induced hypercholesterolemia, hypercholesterolemia,
 CC abetalipoproteinemia, hypobetalipoproteinemia;^a
 CC chylomicron-retention disorder. Anderson's disease, a fat
 CC absorption disorder, e.g. obesity or associated with weight loss,
 CC normotriglyceridemic abetalipoproteinemia, an apolipoprotein-B100
 deficiency, a fat soluble vitamin disorder, where the fat soluble
 CC vitamin is vitamin A or E, or atherosclerosis (all claimed). The
 CC hedgehog antagonist binds to the hedgehog receptor, but does not
 CC elicit a response. It is preferably a hedgehog mimetic, a modified
 CC hedgehog protein, e.g. an inactive hedgehog variant, or an
 CC anti-hedgehog homologue, especially a human, chimeric or humanized
 CC antibody. The methods are useful in preventing these disorders or
 CC protecting a subject from these disorders. The hedgehog antagonist
 CC and agonist are also useful in diagnosis and research associated
 CC with these disorders. The lipid modulators may also be used as a
 CC part of a gene therapy protocol to deliver polynucleotides encoding
 CC these lipid modulators.

RESULT 6

AY95972
 ID AAY95972 standard; Protein; 425 AA.
 XX
 AC AAY95972;
 XX
 DT 05-DEC-2000 (first entry)

XX Chicken Sonic hedgehog Shh protein.

XX Sonic hedgehog; Shh; chicken; agonist; antagonist;
 KW lipid modulator; vacuole; cholesterol disorder; lipid disorder;
 KW lipid metabolism; lipid storage; lipid transport; apolipoprotein;
 KW triglyceride; hypercholesterolemia; abetalipoproteinemia;
 KW hypobeta lipoproteinemia; chylomicron retention; Anderson's disease;
 KW fat absorption; atherosclerosis; obesity; weight loss;
 KW vitamin A disorder; vitamin E disorder; antilipemia; anorectic;
 KW antiarteriosclerotic; gene therapy; diagnosis.
 XX OS Gallus sp.
 XX WO200051628-A2.
 XX PD 08-SEP-2000.
 XX 03-MAR-2000; 2000WO-US05662.
 XX PR 03-MAR-1999; 99US-012640.
 PR 15-MAR-1999; 99US-012446.
 XX PA (BIO) BIOPAC INC.
 XX PI Burkly L, Wang LC;
 XX DR WPI: 2000-611340/5B.
 DR P-PSDB; AA50446.

PT Use of lipid modulators (e.g. hedgehog agonists or antagonists) for
 PT modulating lipid metabolism and storage, especially useful for treating
 PT lipid metabolism or cholesterol disorders, e.g. obesity or
 PT hypercholesterolemia -

XX Disclosure; Page 107-109; 136pp; English.

CC The present sequence of that of chicken Sonic hedgehog (Shh)
 CC protein. The invention provides claimed methods for modulating
 CC lipid metabolism, for modulating vacuole formation in intestinal
 CC epithelial cells, for modulating the accumulation of fat in
 CC intestinal epithelial cells, for treating a cholesterol disorder

CC and for treating a lipid metabolism disorder in an animal
 CC (especially a human) by administering a lipid modulator selected
 CC from a hedgehog antagonist or hedgehog agonist. In particular, the
 CC lipid metabolism disorder is a lipid storage disorder, a lipid
 CC transport disorder, a triglyceride metabolism disorder, a triglyceride
 CC disorder, e.g. a triglyceride storage disorder; a
 CC transport disorder or a triglyceride storage disorder; a
 CC diet-induced hypercholesterolemia, hypercholesterolemia,
 CC abetalipoproteinemia, hypobetalipoproteinemia;^a
 CC chylomicron-retention disorder. Anderson's disease, a fat
 CC absorption disorder, e.g. obesity or associated with weight loss,
 CC normotriglyceridemic abetalipoproteinemia, an apolipoprotein-B100
 deficiency, a fat soluble vitamin disorder, where the fat soluble
 CC vitamin is vitamin A or E, or atherosclerosis (all claimed). The
 CC hedgehog antagonist binds to the hedgehog receptor, but does not
 CC elicit a response. It is preferably a hedgehog mimetic, a modified
 CC hedgehog protein, e.g. an inactive hedgehog variant, or an
 CC anti-hedgehog homologue, especially a human, chimeric or humanized
 CC antibody. The methods are useful in preventing these disorders or
 CC protecting a subject from these disorders. The hedgehog antagonist
 CC and agonist are also useful in diagnosis and research associated
 CC with these disorders. The lipid modulators may also be used as a
 CC part of a gene therapy protocol to deliver polynucleotides encoding
 CC these lipid modulators.

XX SQ Sequence 425 AA:

Query	Match	Score	Length
Best Local Similarity	100 %	2218	DB 21;
Matches	425;	Pred. No. 1.7e-227;	Indels 0;
Db	1	MVEMILLTRILVGICALVSSGLTCGPRGIGRRRHPKLTPLAYKOPTIPNVAEKTG 60	Gaps 0;
Qy	1	MVEMILLTRILVGICALVSSGLTCGPRGIGRRRHPKLTPLAYKOPTIPNVAEKTG 60	
Db	61	ASGRYEGKIRTRNSERKEFLPNYNDDIFKDEENTGADRMTQRCDKKLNAISVMNQ 120	
Qy	61	ASGRYEGKIRTRNSERKEFLPNYNDDIFKDEENTGADRMTQRCDKKLNAISVMNQ 120	
Db	121	PGVKLAVTEGWDDEGHSEESLHYGRAVDITTSQRDRSKYGMARLAVEGFDWVYES 180	
Qy	121	PGVKLAVTEGWDDEGHSEESLHYGRAVDITTSQRDRSKYGMARLAVEGFDWVYES 180	
Db	181	KAHHSVKAENSAVAKSGCFPSATVHLEGGTKLVKDLSPGDVRVLADADGRLLSD 240	
Qy	181	KAHHSVKAENSAVAKSGCFPSATVHLEGGTKLVKDLSPGDVRVLADADGRLLSD 240	
Db	241	FITFELDRMDSSRKRFLFYVIETRQPARLLTAHLIFVAPOHNOSEATGSTSGQALFASN 300	
Qy	241	FITFELDRMDSSRKRFLFYVIETRQPARLLTAHLIFVAPOHNOSEATGSTSGQALFASN 300	
Db	301	KPGQRYVVLGEQGQQLPASVHSVLSREESAGAYPLTAGTILNRVLASCYVIEENS 360	
Qy	301	KPGQRYVVLGEQGQQLPASVHSVLSREESAGAYPLTAGTILNRVLASCYVIEENS 360	
Db	361	WAHHAFAPERLAQGLAALCPDGAIPTAATTGTHWYSRLLYRIGSWVLDGDAHLHPLGM 420	
Qy	361	WAHHAFAPERLAQGLAALCPDGAIPTAATTGTHWYSRLLYRIGSWVLDGDAHLHPLGM 420	
Db	421	VAPAS 425	
Qy	421	VAPAS 425	

RESULT 7

AY95281
 ID AAY95281 standard; Protein; 425 AA.
 XX
 AC AAY95281;
 XX DT 12-SEP-2000 (first entry)

XX DE Chicken Sonic hedgehog Shh protein.

XX	KW	Sonic hedgehog; Shh; chicken; excitotoxicity; Parkinson's disease;	OY	241 FFLFLRMDSSRKLFVVIETOPRARLPLRAHLLFVAPOHNOSETRTGSTSGQALFASNV 300
XX	KW	Huntington's disease; neuronal degeneration; neuroprotective; dopaminergic; GABAergic; substantia nigra; therapy.	Db	241 FFLFLRMDSSRKLFVVIETOPRARLPLRAHLLFVAPOHNOSETRTGSTSGQALFASNV 300
OS	XX	Gallus sp.	OY	301 KPGQRYVYLGGGQQLPASPHVSREESAGAYPLTAGTILINVLASCYAVIEHS 360
PN	XX	WO200035948-A1.	Db	301 KPGQRYVYLGGGQQLPASPHVSREESAGAYPLTAGTILINVLASCYAVIEHS 360
XX	XX	22-JUN-2000.	OY	361 WAHWAFAFPFLAQGLIALCPDGATPAATTGIGIHWYSLYRIGSWLGDALHPLGM 420
PD	XX	03-DEC-1999; 99WO-US28721.	Db	361 WAHWAFAFPFLAQGLIALCPDGATPAATTGIGIHWYSLYRIGSWLGDALHPLGM 420
PF	XX	03-DEC-1999; 99WO-US28721.	OY	361 WAHWAFAFPFLAQGLIALCPDGATPAATTGIGIHWYSLYRIGSWLGDALHPLGM 420
PR	XX	03-DEC-1999; 99US-023843.	Db	361 WAHWAFAFPFLAQGLIALCPDGATPAATTGIGIHWYSLYRIGSWLGDALHPLGM 420
PR	XX	03-JUN-1999; 99US-032502.	OY	421 VAPAS 425
PR	XX	(BIOJ) BIOTEC INC.	Db	421 VAPAS 425
PA	PA	(ONTO-) ONTOGENY INC.	OY	421 VAPAS 425
PA	XX	Galdes A, Mahanthappa N;	PT	421 VAPAS 425
PI	XX	WPI; 2000-43150/37.	PR	421 VAPAS 425
PT	XX	N-PSDB; AAA27876.	DR	421 VAPAS 425
PS	XX	Treating disorders involving exotoxicity, e.g. trauma, hypoglycemia, senile dementia and Korsakoff's disease, by using lipophilic modified hedgehog polypeptide -	PT	RESULT 8
XX	XX	Disclosure: Page 149-151; 174pp; English.	AY96243	AY96243 standard; Protein; 425 AA.
CC	CC	The present sequence of that of chicken Sonic hedgehog (Shh) protein. The invention relates to a method for promoting the survival and/or functional performance of neuronal cells, especially substantia nigra, dopamimetic or GABAergic neurons that are susceptible to exotoxicity, by contacting the cells, in vitro or in vivo, with a lipophilic (e.g. cholesterol) modified hedgehog polypeptide. The method is used to treat or prevent Parkinson's disease, Huntington's disease, domic acid poisoning, spinal cord trauma, hypoglycemia, mechanical trauma to the nervous system, senile dementia, Korsakoff's disease, schizophrenia, AIDS dementia, multiple-infarct dementia, mood disorders, depression, chemical toxicity, neuronal damage associated with uncontrolled seizures such as epileptic seizures, neuronal injury associated with HIV and AIDS, neurodegeneration associated with Down's syndrome, neuropathic pain syndrome, olivopontocerebral atrophy, amyotrophic lateral sclerosis, mitochondrial abnormalities, Alzheimer's disease, hepatic encephalopathy, Tourette's syndrome and drug addiction (all claimed). The lipophilic modified hedgehog polypeptide is also useful for promoting survival and/or functional performance of neuronal cells susceptible to exotoxicity.	XX	AY96243
CC	CC	XX	AC	AY96243;
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC	CC	XX	DR	11-SEP-2000 (first entry)
CC	CC	XX	DE	Partial chicken Shh.
CC	CC	XX	PT	421 VAPAS 425
CC	CC	XX	PR	421 VAPAS 425
CC				

Db 361 |||||||WAHAFAPERLAQDQLLAALCPDGAIPTAATTGIHWSRLYRIGSMWLDGDALHPLGM 420
 Qy 421 VAPAS 425
 Db 421 VAPAS 425

RESULT 10

ID AAGG5743 standard; Protein; 425 AA.
 XX
 AC AAGG5743;
 XX
 DT 07-JAN-2002 (first entry)
 DE Chicken sonic hedgehog (Shh) polypeptide.
 XX
 KW Adipocyte; hedgehog polypeptide; desert hedgehog; Indian hedgehog; Dh; Ih; sonic hedgehog; Shh; therapeutic; cytostatic; tumor.
 XX
 OS Gallus sp.
 XX
 PN WO200164738-A2.

XX
 PD 07-SEP-2001.
 XX
 PF 28-FEB-2001; 2001WO-US06450.
 XX
 PR 29-FEB-2000; 2000US-186058P.
 XX
 PA (CURT-) CURIS INC.
 XX
 PI Zehentner B, Leder-Reiff U, Burtscher H;
 XX
 DR N-PDB; AA16671.
 XX
 PT Method for regulating formation and/or maintenance of adipocyte tissue by contacting pre-adipocyte or adipocyte cells with a hedgehog polypeptide or ptc therapeutic
 XX
 Disclosure; Page 90-92; 132pp; English.
 XX
 CC The invention provides a method for regulating formation and/or maintenance of adipocyte tissue that comprises contacting pre adipocyte or adipocyte cells with a hedgehog polypeptide or ptc therapeutic. The method is used for regulating the growth state of an adipocyte stem/ progenitor cell, and treating or preventing disorders of, or surgical or cosmetic repair of, adipocyte tissues, e.g. for treating or preventing hyperplastic or neoplastic conditions affecting adipocyte tissue, such as soft tissue tumors, especially adipose cell tumors, e.g. lipomas, fibrolipomas, lipoblastomas, lipomatosis, hibernomas, hemangiomas and/or liposarcomas. Hedgehog polypeptides can be used in combination with other therapeutic agents. The present sequence represents a chicken sonic hedgehog (Shh) polypeptide.
 XX
 SQ Sequence 425 AA;

Query Match 100.0%; Score 2218; DB 22; Length 425;
 Best Local Similarity 100.0%; Pred. No. 1; 7e-227;
 Matches 425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX
 PT Novel nucleic acid encoding a hedgehog polypeptide, used to produce the polypeptide, which is used to promote proliferation, survival, and/or differentiation of neuronal and mesodermal tissue -
 XX
 PS Claim 1; Column 117-120; 118pp; English.

XX
 CC The invention relates to nucleic acids encoding hedgehog proteins selected from sonic hedgehog (Shh), Indian hedgehog (Ihh), desert hedgehog (Dhh) polypeptides. The hedgehog genes are involved in the formation of ordered spatial arrangements of differentiated tissue in vertebrates. The nucleic acid sequences are useful for producing hedgehog proteins, used for promoting differentiation of, or survival of differentiated, neuronal cells, and for promoting proliferation, survival or differentiation of mesenchymal, endodermal or ectodermal tissue, particularly chondrocytes, or testicular germ line cells. The present sequence represents a chicken Shh polypeptide.

Db 121 PGVKLRLVTECWDDECHHSSEBSLHYEGRAVDITTSDRDRSKYGLARLAVEAGEDFWVYSES 180
 Qy 181 KAHIFCSVKAENSAAKSGCCFGPSATVIELEGGTKLVKVLDSPGDRVIAADAGRLLYSD 240
 Db 181 KAHIFCSVKAENSAAKSGCCFGPSATVIELEGGTKLVKVLDSPGDRVIAADAGRLLYSD 240

RESULT 11

ID AAB85733 standard; Protein; 425 AA.
 XX
 AC AAB85733;
 XX
 DT 29-OCT-2001 (first entry)
 DE Chicken sonic hedgehog (Shh) polypeptide.
 XX
 KW Hedgehog protein; sonic hedgehog; Shh; Indian hedgehog; Ih; Dh; desert hedgehog; cell differentiation; chicken.
 XX
 OS Gallus sp.
 XX
 PN US6271363-B1.
 XX
 PD 07-AUG-2001.
 XX
 PR 20-OCT-1997; 97US-0954698.
 XX
 PR 05-JUN-1995; 95US-0463386.
 PR 30-DEC-1993; 93US-0176427.
 PR 14-DEC-1994; 94US-0336060.
 PR 04-MAY-1995; 95US-045093.
 XX
 PA (HARD) HARVARD COLLEGE.
 PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
 XX
 PI Ingham PW, McMahon AP, Tabin CJ;
 XX
 DR WPI; 2001-456723/49.
 DR N-PSDB; AAH76107.

XX
 PT Novel nucleic acid encoding a hedgehog polypeptide, used to produce the polypeptide, which is used to promote proliferation, survival, and/or differentiation of neuronal and mesodermal tissue -
 XX
 PS Claim 1; Column 117-120; 118pp; English.

XX
 CC The invention relates to nucleic acids encoding hedgehog proteins selected from sonic hedgehog (Shh), Indian hedgehog (Ihh), desert hedgehog (Dhh) polypeptides. The hedgehog genes are involved in the formation of ordered spatial arrangements of differentiated tissue in vertebrates. The nucleic acid sequences are useful for producing hedgehog proteins, used for promoting differentiation of, or survival of differentiated, neuronal cells, and for promoting proliferation, survival or differentiation of mesenchymal, endodermal or ectodermal tissue, particularly chondrocytes, or testicular germ line cells. The present sequence represents a chicken Shh polypeptide.

Qy 1 MVENLLTRILVYFCIALVSSSLTCGPGRCGKRRHPKLTPLAYKOFIPNVAEKTLG 60
 Db 1 MVENLLTRILVYFCIALVSSSLTCGPGRCGKRRHPKLTPLAYKOFIPNVAEKTLG 60

Qy 61 ASGYEGKTRNSRKEELTPNTNPDIKFDEENTGADRMLQTCKDKNLALASVMQW 120
 61 ASGYEGKTRNSRKEELTPNTNPDIKFDEENTGADRMLQTCKDKNLALASVMQW 120

Qy 121 PGVLRVTEGWDERGHHSSEBSLHYEGRAVDITTSDRDRSKYGLARLAVEAGEDFWVYSES 180

XX	Sequence	425 AA;	SQ	
Query Match	100.0%	Score 2218; DB 22; Length 425;	PT	Modulating immune function comprises administration of a hedgehog or
Best Local Similarity	100.0%	Pred. No. 1.7e-227; Mismatches 0;	PT	ptc agent, for treating e.g. diabetes, eczematous dermatitis, urticaria
Matches	425;	Conservative	PT	or vasculitis.
QY	1	MVEMLLITRLVFGIFCALLVSSGLTGGPGRIGKRRHKKLTPLAYQFIPNVAEKTG 60	XX	claim 4: Page 77-78: 105pp: English.
Db	1	MVEMLLITRLVFGIFCALLVSSGLTGGPGRIGKRRHKKLTPLAYQFIPNVAEKTG 60	CC	The present sequence represents a hedgehog (Shh) polypeptide. Hedgehog
QY	61	ASGRYECKITRNSEREFELTPNYPDTIKDENTGADRIMTORCKOKNLALISTMNQW 120	CC	gene products and signal transduction pathways involving hedgehog are
Db	61	ASGRYECKITRNSEREFELTPNYPDTIKDENTGADRIMTORCKOKNLALISTMNQW 120	CC	involved in the maturation of T lymphocytes. The specification describes
QY	121	PGVKLRYTEGMDEDGHISEESHLHYEGRAVDITSDRDRSKYGMMLARAVEAGFDWVYES 180	CC	a method for modulating immune function, by administration of a hedgehog
Db	121	PGVKLRYTEGMDEDGHISEESHLHYEGRAVDITSDRDRSKYGMMLARAVEAGFDWVYES 180	CC	or patched (ptc) polypeptide, agonists or antagonists. The method is
QY	181	KAIHCSVKAENSAAKSGGCFFPSATVHLEGGTKLVKDLSPGDRVLADADGRILYSD 240	CC	used to treat disorders affecting the regulation of lymphocytes, is used
Db	181	KAIHCSVKAENSAAKSGGCFFPSATVHLEGGTKLVKDLSPGDRVLADADGRILYSD 240	CC	particularly maturation and/or activation of T lymphocytes. It is used
QY	241	FILFLDRDSSRKLYFEVETROPRARILTTAHLLFVAPQHNOSEATGSTSGQALFASNV 300	CC	to treat bacterial or viral infection, diabetes, nutritional
Db	241	FILFLDRDSSRKLYFEVETROPRARILTTAHLLFVAPQHNOSEATGSTSGQALFASNV 300	CC	deficiencies, graft rejection or other hyperacute response such as
QY	301	KPGQRYVVLGEGGQQLPPASVHSVSLREEEASGAYPLTAQTLINRVLASCYAVIEHS 360	CC	kidney, heart, lung, bone marrow spleen skin or cornea transplant or
Db	301	KPGQRYVVLGEGGQQLPPASVHSVSLREEEASGAYPLTAQTLINRVLASCYAVIEHS 360	CC	autoimmune disorders such as multiple sclerosis, psoriasis or atopic
QY	361	WAHWAFAFPRLAQGLLALCPDGAIPTAATTGIGIHWYSRLYLIRGSWVLDGDLAHLPLGM 420	CC	dermatitis. The method is used to treat inflammatory, proliferative and
Db	361	WAHWAFAFPRLAQGLLALCPDGAIPTAATTGIGIHWYSRLYLIRGSWVLDGDLAHLPLGM 420	CC	hyperproliferative diseases, as well as cutaneous manifestations of
QY	421	VAPAS 425	CC	immunological disorders such as eczematous dermatitis, urticaria,
Db	421	VAPAS 425	CC	vasculitis and scleroderma.
XX	Sequence	425 AA;	SQ	
Query Match	100.0%	Score 2218; DB 22; Length 425;	PT	
Best Local Similarity	100.0%	Pred. No. 1.7e-227; Mismatches 0;	PT	
Matches	425;	Conservative	PT	
QY	1	MVEMLLITRLVFGIFCALLVSSGLTGGPGRIGKRRHKKLTPLAYQFIPNVAEKTG 60	XX	
Db	1	MVEMLLITRLVFGIFCALLVSSGLTGGPGRIGKRRHKKLTPLAYQFIPNVAEKTG 60	CC	
QY	61	ASGRYECKITRNSEREFELTPNYPDTIKDENTGADRIMTORCKOKNLALISTMNQW 120	CC	
Db	61	ASGRYECKITRNSEREFELTPNYPDTIKDENTGADRIMTORCKOKNLALISTMNQW 120	CC	
QY	121	PGVKLRYTEGMDEDGHISEESHLHYEGRAVDITSDRDRSKYGMMLARAVEAGFDWVYES 180	CC	
Db	121	PGVKLRYTEGMDEDGHISEESHLHYEGRAVDITSDRDRSKYGMMLARAVEAGFDWVYES 180	CC	
QY	181	KAIHCSVKAENSAAKSGGCFFPSATVHLEGGTKLVKDLSPGDRVLADADGRILYSD 240	CC	
Db	181	KAIHCSVKAENSAAKSGGCFFPSATVHLEGGTKLVKDLSPGDRVLADADGRILYSD 240	CC	
QY	241	FILFLDRDSSRKLYFEVETROPRARILTTAHLLFVAPQHNOSEATGSTSGQALFASNV 300	CC	
Db	241	FILFLDRDSSRKLYFEVETROPRARILTTAHLLFVAPQHNOSEATGSTSGQALFASNV 300	CC	
DE	Amino acid sequence of a chicken hedgehog (Shh) polypeptide.			
XX	Shh gene; hedgehog gene; T lymphocyte; patched gene; infection; diabetes; nutritional deficiency; graft rejection; hyperacute response; cornea transplant; autoimmune disorder; multiple sclerosis; psoriasis; atopic dermatitis; inflammatory disease; proliferative disease; hyperproliferative disease; eczematous dermatitis; urticaria; vasculitis; scleroderma.			
XX	Galus sp.			
XX	W0200140438-A2.			
PD	07-JUN-2001.			
XX	30-NOV-2000; 2000WO-US32590.			
PF	30-NOV-1999; 99US-0168112.			
PR	(CURI-) CURIS INC.			
PA	Crompton T;			
PI	WPI: 2001-441484/47.			
XX	N-PSDB; RAH28446.			
RESULT 13				
AAE04682	AAE04682 standard; Protein; 425 AA.			
XX				
AAE04682;				
XX	04-SEP-2001 (first entry)			
XX	Chicken sonic hedgehog (Shh) protein.			
DE	Chicken; hedgehog protein; nootropic; neuroprotective; anticonvulsant;			

KW cytostatic; therapy; Alzheimer's disease; Parkinson's disease; injury;
 KW Huntington's chorea; amyotrophic lateral sclerosis; multiple sclerosis;
 KW nervous system aging; neurodegenerative disease; immunological disease;
 KW malignant glioma; medulloblastoma; neuroectodermal tumour; cancer;
 KW extracellular signalling protein.

XX OS Gallus sp.
 XX PN WO200134654-A1.
 XX PD 17-MAY-2001.
 XX PP 02-NOV-2000; 2000WO-US30405.
 XX PR 05-NOV-1999; 99US-0164025.
 XX PA (BIOJ) BIOPRO INC.
 XX PI Strauch K;
 XX DR N-PSDB; RAD0929.
 XX PT Novel isolated hedgehog fusion polypeptide useful for treating
 PT neurological conditions such as Alzheimer's disease, Parkinson's
 disease, Huntington's chorea, amyotrophic lateral sclerosis, and
 PT multiple sclerosis.
 XX PS Disclosure; Page 111-112; 17pp; English.

XX CC The present invention relates to hedgehog fusion proteins. Hedgehog
 proteins are a family of extracellular signalling proteins that regulate
 various aspects of embryonic development both in vertebrates and in
 invertebrates. Hedgehog fusion protein is useful for the prophylaxis or
 treatment of any condition or disease state for which a hedgehog or
 patched protein constituent is efficacious and in the diagnosis of
 constituents or conditions of disease states in biological system or
 specimens and for diagnostic purposes in non-physiological systems.
 CC Hedgehog fusion protein is useful for treating neurological conditions
 due to injury, aging of nervous system, including Alzheimer's disease,
 chronic neurodegenerative diseases of the nervous system, including
 Parkinson's disease, Huntington's chorea, amyotrophic lateral sclerosis
 and chronic immunological diseases of nervous system including multiple
 CC sclerosis and malignant gliomas, medulloblastomas, neuroectodermal
 tumours and to specifically target medical therapies against cancers and
 CC tumours which express the receptor for the protein. The present sequence
 CC is chicken sonic hedgehog (Shh) protein.

XX SQ Sequence 425 AA:

Query Match 100.0%; Score 2218; DB 22; Length 425;
 Best Local Similarity 100.0%; Pred. No. 1.7e-227; Mismatches 425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVEMILLILVLLVCPICALVSSGCGPQSATWHLEHGKTKLWDLSGDRVIAADAGRLIS 60
 QY 1 MVEMLULTRILVGGPICALVSSGCGPQSATWHLEHGKTKLWDLSGDRVIAADAGRLIS 60

QY 61 ASGRVEGKTTRNSRKEKTPNYPDIFKDEEITGADRMLTQRCKDKUNALASVMNW 120
 QY 61 ASGRVEGKTTRNSRKEKTPNYPDIFKDEEITGADRMLTQRCKDKUNALASVMNW 120

Db 121 PGVILRVTVGWDGCHHSESLHVEGRADITTSDRSKYMLARLAVEAGDWYVES 180
 Db 121 PGVILRVTVGWDGCHHSESLHVEGRADITTSDRSKYMLARLAVEAGDWYVES 180

Qy 181 KAHHCSVAENSAAKSGCGPQSATWHLEHGKTKLWDLSGDRVIAADAGRLIS 240
 Qy 181 KAHHCSVAENSAAKSGCGPQSATWHLEHGKTKLWDLSGDRVIAADAGRLIS 240

Qy 241 FLTTIDRMDSSRKLYVITRQPRLTAHHFLVAOHNGSEATGSTSGQLAFASNV 300
 Qy 241 FLTTIDRMDSSRKLYVITRQPRLTAHHFLVAOHNGSEATGSTSGQLAFASNV 300

Db 241 FFLTLDRMOSSRKLYVITRQPRLTAHHFLVAOHNGSEATGSTSGQLAFASNV 300

XX Result 14
 AAE03372 standard; Protein; 425 AA.
 XX ID AAE03372
 XX AC AAE03372;
 XX DT 12-SEP-2001 (first entry)
 XX DE Chicken Sonic hedgehog protein.
 XX OS Chicken; sonic hedgehog; Shh; morphogenic signal; neuron;
 KW embryonic patterning; cell culture; cell differentiation; ischaemia;
 KW cell proliferation; disorder; intracerebral grafting; Huntington's chorea;
 KW neurological disorder; Alzheimer's disease; Parkinson's disease;
 KW amyotrophic lateral sclerosis; ALS; multiple sclerosis.
 XX Gallus sp.
 XX Key Location/Qualifiers
 FT 1..26
 FT /label= Signal_peptide
 FT 27..425
 FT Protein /label= Mature_Shh_protein
 PN US6261786-B1.
 XX PD 02-JUL-1996; 96US-0674509.
 XX PR 30-DEC-1993; 93US-0176427.
 PR 14-DEC-1994; 94US-035060.
 PR 04-MAY-1995; 95US-0435093.
 PR 05-JUN-1995; 95US-0469900.
 PR 05-JUN-1995; 95US-0462386.
 XX PA (IMR) IMPERIAL CANCER RES TECHNOLOGY LTD.
 PA (HARD) HARVARD COLLEGE.
 XX PI Mario V. Tabin CJ, Ingham PW, McMahon AP;
 XX DR WPI; 2001-440859/47.
 XX N-PSDB; RAD10146.

PT Screening compounds that potentiate or inhibit binding of hedgehog
 PT polypeptide to naturally occurring patched receptor, comprises
 PT contacting polypeptide with receptor and test compound, and detecting
 PT change in binding
 Claim 2; Fig 5A; 127pp; English.

CC The present invention relates to assay for screening compounds that
 CC potentiate or inhibit binding of hedgehog polypeptide to naturally
 CC occurring patched receptor. The hedgehog proteins comprise morphogenic
 CC signals produced by embryonic patterning centres, and are involved in the
 CC formation and maintenance of ordered spatial arrangements of
 CC differentiated tissues in vertebrates, both adult and embryonic. The
 CC proteins can be used to generate and/or maintain an array of different
 vertebrate tissues both in vitro and in vivo. The invention also relates

CC	to a method for modulating growth, differentiation or survival of a mammalian cell (e.g., neuron, testicular cell) responsive to hedgehog induction. Hedgehog agonists and antagonists can be used in cell culture techniques to enhance survival and maintenance of neurons and various vertebrate organogenic pathways. The hedgehog gene is useful in determining whether a patient is at the risk of disorder characterised by hedgehog proteins or mimetics can be used to induce foetal neurons especially neuronal stem cells in intracerebral grafting. The protein or its mimetic can be used in the treatment of neurological conditions e.g. injury to nervous system, ischaemia resulting from stroke, Alzheimer's disease, Parkinson's disease, Huntington's chorea, amyotrophic lateral sclerosis (ALS) and multiple sclerosis. The present sequence is chicken sonic hedgehog (Shh) protein.	XX	US6165747-A.
CC	Sequence 425 AA;	XX	
CC	Query Match 100.0%; Score 2218; DB 22; Length 425; Best Local Similarity 100.0%; Pred. No. 1.7e-227; Mismatches 0; Indels 0; Gaps 0;	PR 30-DEC-1993; 93US-0176427. PR 14-DEC-1994; 94US-0356060. PR 04-MAY-1995; 95US-0435093.	PR 05-JUN-1995; 95US-0460900.
CC	Matches 425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DR (HARD) HARVARD COLLEGE RES TECHNOLOGY LTD.	DR (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
CC	Db 1 MVENMLLIRILLYGFGICALLVSSGLTGPGRGIGKRRRKKLTPLAYQFIPNVAEKTG 60 1 MVENMLLIRILLYGFGICALLVSSGLTGPGRGIGKRRRKKLTPLAYQFIPNVAEKTG 60	N-PSDB; AAC87074.	PI Ingham PW, McMahon AP, Tabin CJ, Marti-gorostiza E, Bumcrot DA;
CC	Qy 61 ASGRYEKGITRNSERKELTNPYNDIFKDEENTGADRMLTORCKDKLNALAISVNQW 120 61 ASGRYEKGITRNSERKELTNPYNDIFKDEENTGADRMLTORCKDKLNALAISVNQW 120	XX WPI: 2001-019847/09.	XX DR
CC	Qy 121 PGVKLRVTEGWDGDGHSEESLHYEGRAVDIT'SDRDRSKYGMALARLAVEAGFDWVYES 180 121 PGVKLRVTEGWDGDGHSEESLHYEGRAVDIT'SDRDRSKYGMALARLAVEAGFDWVYES 180	PT Polynucleotides encoding hedgehog proteins, useful for treating diseases of nervous system such as Alzheimer's disease, Parkinson's disease, Huntington's chorea, amyotrophic lateral sclerosis, multiple sclerosis -	PT PT
CC	Db 121 PGVKLRVTEGWDGDGHSEESLHYEGRAVDIT'SDRDRSKYGMALARLAVEAGFDWVYES 180 121 KAHICCSYKAENSAKGGCFPGSATVHLEGGTKLVKLSLSPGDRVLADADGRLLSD 240 181 KAHICCSYKAENSAKGGCFPGSATVHLEGGTKLVKLSLSPGDRVLADADGRLLSD 240	PS Claim 10: Columns 135-138; 119PP: English.	PS XX
CC	Qy 241 FLFLDRDMDSSRLKFVYETROPRARULLTAHLFLVAPOHNOSEATGSTSQALFASNV 300 241 FLFLDRDMDSSRLKFVYETROPRARULLTAHLFLVAPOHNOSEATGSTSQALFASNV 300	The present sequence represents a hedgehog related-protein. The specification describes a sonic hedgehog protein (Shh), a desert hedgehog protein (Dhh), and an Indian hedgehog protein (Ihh). The hedgehog polynucleotides are useful in diagnostic, in antisense therapy and in therapeutic assays for detecting and treating disorders involving, e.g., aberrant expression of vertebrate hedgehog homologue. Hedgehog polypeptides are useful therapeutically to enhance survival of neurons and other neuron cells and in treating neurological conditions deriving from acute, subacute, or chronic injury to the nervous system, including traumatic injury, chemical injury, vasal injury and deficits (such as the ischaemia resulting from stroke), together with infectious/inflammatory and induced-induced injury, ageing of the nervous system including Alzheimer's disease, chronic neurodegenerative diseases of the nervous system, including Huntington's disease, Huntington's chorea, amyotrophic lateral sclerosis, spinocerebellar degenerations, and chronic immunological diseases of the nervous system or affecting the nervous system, including multiple sclerosis.	CC CC CC CC
CC	Db 301 KPGQRVYLGEGQQQLLPASVHSVSLREASGAYAPLTAQGTLINRLASCYAVIEBHS 360 301 KPGQRVYLGEGQQQLLPASVHSVSLREASGAYAPLTAQGTLINRLASCYAVIEBHS 360	CC CC CC CC	CC
CC	Qy 361 WAHWAFAFPRLAQGLLAMCPDGAIPTAATTGTHIHWYSLRYRIGSWLDSDALHPLGM 420 421 WAHWAFAFPRLAQGLLAMCPDGAIPTAATTGTHIHWYSLRYRIGSWLDSDALHPLGM 420	CC CC CC CC	CC
CC	Db 361 WAHWAFAFPRLAQGLLAMCPDGAIPTAATTGTHIHWYSLRYRIGSWLDSDALHPLGM 420 421 WAHWAFAFPRLAQGLLAMCPDGAIPTAATTGTHIHWYSLRYRIGSWLDSDALHPLGM 420	CC CC CC CC	CC
CC	Qy 421 VARAS 425 421 VARAS 425	Sequence 425 AA;	Sequence 425 AA;
CC	Qy 421 VARAS 425 421 VARAS 425	Query Match 100.0%; Score 2218; DB 22; Length 425; Best Local Similarity 100.0%; Pred. No. 1.7e-227; Mismatches 0; Indels 0; Gaps 0;	Query Match 100.0%; Score 2218; DB 22; Length 425; Best Local Similarity 100.0%; Pred. No. 1.7e-227; Mismatches 0; Indels 0; Gaps 0;
CC	Db 1 MVENMLLIRILLYGFGICALLVSSGLTGPGRGIGKRRRKKLTPLAYQFIPNVAEKTG 60 1 MVENMLLIRILLYGFGICALLVSSGLTGPGRGIGKRRRKKLTPLAYQFIPNVAEKTG 60	PR 181 KAHICCSYKAENSAKGGCFPGSATVHLEGGTKLVKLSLSPGDRVLADADGRLLSD 240 181 KAHICCSYKAENSAKGGCFPGSATVHLEGGTKLVKLSLSPGDRVLADADGRLLSD 240	PR 121 PGVKLRVTEGWDGDGHSEESLHYEGRAVDIT'SDRDRSKYGMALARLAVEAGFDWVYES 180 121 PGVKLRVTEGWDGDGHSEESLHYEGRAVDIT'SDRDRSKYGMALARLAVEAGFDWVYES 180
CC	AC AAB31217;	Db 61 ASGRYEKGITRNSERKELTNPYNDIFKDEENTGADRMLTORCKDKLNALAISVNQW 120 61 ASGRYEKGITRNSERKELTNPYNDIFKDEENTGADRMLTORCKDKLNALAISVNQW 120	Db 61 ASGRYEKGITRNSERKELTNPYNDIFKDEENTGADRMLTORCKDKLNALAISVNQW 120
CC	AC AAB31217;	Qy 121 PGVKLRVTEGWDGDGHSEESLHYEGRAVDIT'SDRDRSKYGMALARLAVEAGFDWVYES 180 121 PGVKLRVTEGWDGDGHSEESLHYEGRAVDIT'SDRDRSKYGMALARLAVEAGFDWVYES 180	Qy 121 PGVKLRVTEGWDGDGHSEESLHYEGRAVDIT'SDRDRSKYGMALARLAVEAGFDWVYES 180
CC	AC AAB31217;	Db 241 FLFLDRDMDSSRLKFVYETROPRARULLTAHLFLVAPOHNOSEATGSTSQALFASNV 300 241 FLFLDRDMDSSRLKFVYETROPRARULLTAHLFLVAPOHNOSEATGSTSQALFASNV 300	Db 241 FLFLDRDMDSSRLKFVYETROPRARULLTAHLFLVAPOHNOSEATGSTSQALFASNV 300
CC	AC AAB31217;	Qy 301 KPGQRVYLGEGQQQLLPASVHSVSLREASGAYAPLTAQGTLINRLASCYAVIEBHS 360 301 KPGQRVYLGEGQQQLLPASVHSVSLREASGAYAPLTAQGTLINRLASCYAVIEBHS 360	Qy 301 KPGQRVYLGEGQQQLLPASVHSVSLREASGAYAPLTAQGTLINRLASCYAVIEBHS 360
OS	Galus sp.		

Db	KPGQRVYVLGEQQQLPASVHSNSLREESGAVAPLTAQTLINRVLASCYVIEEHS	360
Qy	361 WAHHWFAPERLAQGLIAALCPDGAIPTAATTTGTHWYSRLYIGSWLTDGDAHLHPLGM	420
Db	361 WAHHWFAPERLAQGLIAALCPDGAIPTAATTTGTHWYSRLYIGSWLTDGDAHLHPLGM	420
Qy	421 VAPAS 425 	
Db	421 VAPAS 425	

Search completed: February 20, 2003, 10:10:17
Job time : 32.834 secs

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GenCore version 5.1.3

Run on: February 20, 2003, 10:08:38 ; Search time 11.1257 Seconds
(without alignments)
1123.955 Million cell updates/sec

Title: US-09-827-110A-10
Perfect score: 2218

Sequence: 1 MYEMLLTRILLVGFICALL.....GSWVLGDGDLHPLGMAPAS 425

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs., 23422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:
1: /cgn2_6/ptodata/1/iaa/5A_COMB_pep:
2: /cgn2_6/ptodata/1/iaa/5B_COMB_pep:
3: /cgn2_6/ptodata/1/iaa/6A_COMB_pep:
4: /cgn2_6/ptodata/1/iaa/6B_COMB_pep:
5: /cgn2_6/ptodata/1/iaa/PCUTS_COMB_pep:
6: /cgn2_6/ptodata/1/iaa/backfilesl_pep:

Pred. No. 1s is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2218	100.0	425	1 US-08-176-427B-2
2	2218	100.0	425	2 US-08-356-060A-8
3	2218	100.0	425	4 US-08-450-900C-8
4	2218	100.0	425	4 US-08-674-505B-8
5	2218	100.0	425	4 US-08-954-698-B
6	2218	100.0	425	4 US-08-957-871-B
7	2218	100.0	425	4 US-09-352-230A-9
8	2085	94.0	425	3 US-08-946-329R-18
9	2085	94.0	425	4 US-08-946-329R-18
10	2085	94.0	425	4 US-08-946-329R-18
11	2085	94.0	425	4 US-08-946-329R-18
12	2085	94.0	425	5 PCT-US95-15463-19
13	2085	94.0	425	5 PCT-US95-15463-19
14	1807	81.5	462	1 US-08-718-591-4
15	1807	81.5	462	1 US-08-718-591-4
16	1807	81.5	462	1 US-08-718-591-4
17	1807	81.5	475	4 US-08-916-320A-13
18	1807	81.5	475	4 US-08-916-320A-13
19	1807	81.5	475	4 US-08-674-505B-13
20	1807	81.5	475	4 US-08-957-871-B
21	1807	81.5	475	4 US-08-957-871-B
22	1791	80.7	437	4 US-08-916-320A-13
23	1791	80.7	437	4 US-08-567-357A-20
24	1791	80.7	437	4 US-08-726-743A-20
25	1791	80.7	437	4 US-09-057-860B-6
26	1791	80.7	437	4 US-08-349-499-20
27	1791	80.7	437	4 US-09-293-505-14

ALIGNMENTS

28	1791	80.7	437	5 PCT-US95-15463-20	Sequence 20, Appl
29	1791	80.7	437	5 PCT-US95-15463-20	Sequence 20, Appl
30	1788	80.6	437	4 US-08-356-060A-11	Sequence 8, Appl
31	1788	80.6	437	2 US-08-460-900C-11	Sequence 11, Appl
32	1788	80.6	437	4 US-08-460-900C-11	Sequence 11, Appl
33	1788	80.6	437	4 US-08-674-505B-11	Sequence 11, Appl
34	1788	80.6	437	4 US-08-954-698-11	Sequence 11, Appl
35	1788	80.6	437	4 US-08-957-871-B	Sequence 11, Appl
36	1780	80.3	437	4 US-08-757-230A-2	Sequence 2, Appl
37	1780	80.3	437	4 US-08-757-230A-2	Sequence 2, Appl
38	1780	80.3	437	4 US-08-757-230A-9	Sequence 9, Appl
39	1780	80.3	437	5 PCT-US95-02315-2	Sequence 18, Appl
40	1494	67.4	418	3 US-08-946-329R-18	Sequence 18, Appl
41	1494	67.4	418	4 US-08-567-357A-18	Sequence 18, Appl
42	1494	67.4	418	4 US-08-729-743A-18	Sequence 18, Appl
43	1494	67.4	418	4 US-08-757-20A-18	Sequence 7, Appl
44	1494	67.4	418	4 US-08-319-498-18	Sequence 18, Appl
45	1494	67.4	418	5 PCT-US95-15453-18	Sequence 18, Appl

RESULT 1

US-08-176-427B-2
Sequence 2, Application US/08176427B
; Patent No. 5785543
GENERAL INFORMATION:
APPLICANT: Ingham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: LALIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:

MEDIA TYPE: FLOPPY disk
COMPILER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,427B
FILING DATE: 30-DEC-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-006

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 425 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-176-427B-2
Query Match Best Local Similarity 100.0%; Pred. No. 1.5e-241;
Matches 425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MYEMLLTRILLVGFICALL.....GSWVLGDGDLHPLGMAPAS 60
Db 1 MYEMLLTRILLVGFICALLSSGLTGGPGRIGKRRHKPLPLAYQFPVNAEKTG 60

Query Match 100 %; Score 2218; DB 2; Length 425;
 Best Local Similarity 100 %; Pred. No. 1.5e-241;
 Matches 425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVEMLILTRITLVGPGICALLYVSSGLTCGPRGIGCKRRHPPKKLPLAYQFIPNVAEKTIG 60
 1 PGVKLKVTEGWDDEGHHSSESLHREGRAVITSDRDRSKYGMARLAVEAGEDWVYES 180
 121 PGVKLKVTEGWDDEGHHSSESLHREGRAVITSDRDRSKYGMARLAVEAGEDWVYES 180
 121 PGVKLKVTEGWDDEGHHSSESLHREGRAVITSDRDRSKYGMARLAVEAGEDWVYES 180
 QY 181 KAHICSVKAENSAKSGGCFPSATVILEHGCKLVLSPDRLAADDAGRLLYSD 240
 181 KAHICSVKAENSAKSGGCFPSATVILEHGCKLVLSPDRLAADDAGRLLYSD 240
 Db 181 KAHICSVKAENSAKSGGCFPSATVILEHGCKLVLSPDRLAADDAGRLLYSD 240
 QY 241 FLTFIDRMDSSRSKLFYVIMTQPRLLTAAHILFVAPQHNOSEATGSTSGQALFASV 300
 241 FLTFIDRMDSSRSKLFYVIMTQPRLLTAAHILFVAPQHNOSEATGSTSGQALFASV 300
 Qy 301 KPGQRYVYLGEGQOLLPAVHSVSREASGAVAPLTAQGTLINRVASCYVIEHS 360
 361 WAHMFAPEPLAQGLAAALCPDGAIPTAATTTCIHWMSRLYRIGSWVLDGALHPGM 420
 361 WAHMFAPEPLAQGLAAALCPDGAIPTAATTTCIHWMSRLYRIGSWVLDGALHPGM 420
 Qy 421 VAPAS 425
 Db 421 VAPAS 425

RESULT 2
 US-08-356-060A-8
 Sequence 8 Application US/08356060A
 ; Patent No. 6844079
 ; GENERAL INFORMATION:
 ; APPLICANT: Ingham, Phillip W.
 ; APPLICANT: McMahon, Andrew P.
 ; APPLICANT: Tabin, Clifford J.
 ; TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
 ; NUMBER OF SEQUENCES: 47
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD
 ; STREET: 60 State Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: ASCII;text)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/356, 060A
 ; FILING DATE: 14-DEC-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/176, 427
 ; FILING DATE: 30-DEC-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Vincent, Matthew P.
 ; REGISTRATION NUMBER: 36,709
 ; REFERENCE/DOCKET NUMBER: HMI-005CP
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 227-7400
 ; TELEFAX: (617) 227-941
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 425 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-356-060A-8

RESULT 3
 US-08-460-900C-8
 Sequence 8 Application US/08460900C
 ; Patent No. 6165747
 ; GENERAL INFORMATION:
 ; APPLICANT: Ingham, Phillip W.
 ; APPLICANT: McMahon, Andrew P.
 ; APPLICANT: Tabin, Clifford J.
 ; APPLICANT: Blumrot, David A.
 ; APPLICANT: Marti-Gorostiza, Elisa
 ; TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
 ; NUMBER OF SEQUENCES: 62
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: FOLEY, HONG & ELLIOT LLP
 ; STREET: One Post Office Square
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/460, 900C
 ; FILING DATE: 5-JUNE-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/435, 093
 ; FILING DATE: 4-MAY-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/08/460, 900C
 ; FILING DATE: 14-DEC-1994
 ; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/176,427
 FILING DATE: 30-DEC-1993
 ATTORNEY / AGENT INFORMATION:
 NAME: Vincent, Matthew P.
 REGISTRATION NUMBER: 36,709
 REFERENCE/DOCKET NUMBER: HMV-006-05
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 832-7000
 TELEFAX: (617) 832-7000
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 425 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-460-900C-B

Query Match 100.0%; Score 2218; DB 4; Length 425;
 Best Local Similarity 100.0%; Pred. No. 1.5e-241;
 Matches 425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVEMLLURTRILVGFTCALYSSGLTGGPGRGIGKRRHKPKLTPLAYKOFIPNVAEKTG 60
 Db 1 MVEMLLURTRILVGFTCALYSSGLTGGPGRGIGKRRHKPKLTPLAYKOFIPNVAEKTG 60

Qy 61 ASGRYEGKTRNSERFEKLTPNYNPDIFKDEENTGADRMLTORCKDKLNALAI SVNQW 120
 Db 61 ASGRYEGKTRNSERFEKLTPNYNPDIFKDEENTGADRMLTORCKDKLNALAI SVNQW 120

Qy 121 PGVKLRVTEGWDGDGHSEESLHVEGRADITTSDRDRSKYGMARLAVAEAGFDWVYES 180
 Db 121 PGVKLRVTEGWDGDGHSEESLHVEGRADITTSDRDRSKYGMARLAVAEAGFDWVYES 180

Qy 181 KAHICSVKAENSAVAKSGGCFFPSATVHLEHGKTLYKDLSPGDRVLADADGRLLYS 240
 Db 181 KAHICSVKAENSAVAKSGGCFFPSATVHLEHGKTLYKDLSPGDRVLADADGRLLYS 240

Qy 241 FLTFFLDRMDSRKLFLFYIETROPARLLTAHLFVAPRHOSEATGSTSGQALFASNV 300
 Db 241 FLTFFLDRMDSRKLFLFYIETROPARLLTAHLFVAPRHOSEATGSTSGQALFASNV 300

Qy 301 KPGQRVYVLGEGQQQLPASVHSVLREASAYAQPPLAQTLTINRLASCYAVIEHS 360
 Db 301 KPGQRVYVLGEGQQQLPASVHSVLREASAYAQPPLAQTLTINRLASCYAVIEHS 360

Qy 361 WAHWAFAFPRLAQGLAALCPDGAIPMTATTGIHWSRLYRIGSWVLDDALHPLGM 420
 Db 361 WAHWAFAFPRLAQGLAALCPDGAIPMTATTGIHWSRLYRIGSWVLDDALHPLGM 420

Qy 421 VAFAS 425
 Db 421 VAFAS 425

RESULT 4
 US-08-4509B-B

Sequence 8, Application US/08674509B
 Patent No. 6261786
 GENERAL INFORMATION:

APPLICANT: Ingham, Phillip W.
 APPLICANT: McMahon, Andrew P.
 APPLICANT: Tabin, Clifford J.
 APPLICANT: McMahon, Andrew P.
 APPLICANT: Tabin, Clifford J.
 APPLICANT: Ma'go, Valeia
 TITLE OF INVENTION: SCREENING ASSAYS FOR HEDGESEG AGONISTS
 NUMBER OF SEQUENCES: 48
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FOLEY, HOAG & ELIOT LLP
 STREET: One Post Office Square
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109-2170

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/674,509B
 FILING DATE: 02-JUL-1996
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/460,900
 FILING DATE: 05-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Vincent, Matthew P.
 REGISTRATION NUMBER: 36,709
 REFERENCE/DOCKET NUMBER: HMV-006-06
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-832-1000
 TELEFAX: 617-832-7000

INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 425 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-674-509B-8
 Query Match 100.0%; Score 2218; DB 4; Length 425;
 Best Local Similarity 100.0%; Pred. No. 1.5e-241;
 Matches 425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVEMLLURTRILVGFTCALYSSGLTGGPGRGIGKRRHKPKLTPLAYKOFIPNVAEKTG 60
 Db 1 MVEMLLURTRILVGFTCALYSSGLTGGPGRGIGKRRHKPKLTPLAYKOFIPNVAEKTG 60

Qy 61 ASGRYEGKTRNSERFEKLTPNYNPDIFKDEENTGADRMLTORCKDKLNALAI SVNQW 120
 Db 61 ASGRYEGKTRNSERFEKLTPNYNPDIFKDEENTGADRMLTORCKDKLNALAI SVNQW 120

Qy 121 PGVKLRVTEGWDGDGHSEESLHVEGRADITTSDRDRSKYGMARLAVAEAGFDWVYES 180
 Db 121 PGVKLRVTEGWDGDGHSEESLHVEGRADITTSDRDRSKYGMARLAVAEAGFDWVYES 180

Qy 181 KAHICSVKAENSAVAKSGGCFFPSATVHLEHGKTLYKDLSPGDRVLADADGRLLYS 240
 Db 181 KAHICSVKAENSAVAKSGGCFFPSATVHLEHGKTLYKDLSPGDRVLADADGRLLYS 240

Qy 241 FLTFFLDRMDSRKLFLFYIETROPARLLTAHLFVAPRHOSEATGSTSGQALFASNV 300
 Db 241 FLTFFLDRMDSRKLFLFYIETROPARLLTAHLFVAPRHOSEATGSTSGQALFASNV 300

Qy 301 KPGQRVYVLGEGQQQLPASVHSVLREASAYAQPPLAQTLTINRLASCYAVIEHS 360
 Db 301 KPGQRVYVLGEGQQQLPASVHSVLREASAYAQPPLAQTLTINRLASCYAVIEHS 360

Qy 361 WAHWAFAFPRLAQGLAALCPDGAIPMTATTGIHWSRLYRIGSWVLDDALHPLGM 420
 Db 361 WAHWAFAFPRLAQGLAALCPDGAIPMTATTGIHWSRLYRIGSWVLDDALHPLGM 420

Qy 421 VAFAS 425
 Db 421 VAFAS 425

RESULT 5
 US-08-934-698-B
 Sequence 8, Application US/08954698
 Patent No. 6271363
 GENERAL INFORMATION:

APPLICANT: Ingham, Phillip W.
 APPLICANT: McMahon, Andrew P.
 APPLICANT: Tabin, Clifford J.
 TITLE OF INVENTION: vertebrate Embryonic Pattern-Inducing

TITLE OF INVENTION: Proteins and Uses Related Thereto
 NUMBER OF SEQUENCES: 48
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FOLEY, HOAG & ELLIOT LLP
 STREET: One Post Office Square
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109-2170
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/954,698
 FILING DATE: 20-OCT-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/462,386
 FILING DATE: 05-DEC-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/435,093
 FILING DATE: 04-MAY-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/356,060
 FILING DATE: 14-DEC-1994
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/176,427
 FILING DATE: 30-DEC-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Vincent, Matthew P.
 REGISTRATION NUMBER: 36,709
 REFERENCE/DOCKET NUMBER: HMV-006.10
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-832-7000
 TELEFAX: 617-832-7000
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 425 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-954,698-8

Query Match 100.0%; Score 2218; DB 4; Length 425;
 Best Local Similarity 100.0%; Pred. No. 1.5e-241; Mismatches 425; Conservative 0; Indels 0; Gaps 0;

Qy 1 MVEMMLTRILLVGGTICLVSSGLTGGCGRGIGKRRHKPLKPLAYKQFPINVAEKTIG 60
 Db 1 MVEMLLRLTRILLVGGTICLVSSGLTGGCGRGIGKRRHKPLKPLAYKQFPINVAEKTIG 60

Qy 61 ASGRYEGKTRNRSERKELPNPYNDIIFDEENIGADRMLTORCKDKNLALISVMNOW 120
 Db 61 ASGRYEGKTRNRSERKELPNPYNDIIFDEENIGADRMLTORCKDKNLALISVMNOW 120

Qy 121 PGVKLRVTEGWDCHHSEESLHYEGRAVDTTSQRDRSKYGMARLAVENGFWVYES 180
 Db 121 PGVKLRVTEGWDCHHSEESLHYEGRAVDTTSQRDRSKYGMARLAVENGFWVYES 180

Qy 181 KAHTICSVKAENSAKSGCFPSSATVHLHGKGKLVLSPDRVLAADAGRLYSD 240
 Db 181 KAHTICSVKAENSAKSGCFPSSATVHLHGKGKLVLSPDRVLAADAGRLYSD 240

Qy 241 FLTFLDRMDSRSRKRKYVTEROPRRLTAAHLFVAPQHNOSEATGSTSGQALFASNV 300
 Db 241 FLTFLDRMDSRSRKRKYVTEROPRRLTAAHLFVAPQHNOSEATGSTSGQALFASNV 300

Qy 301 KPGQRYVVGEGGQQLPASHVSLSREASAGAALPQGQTILINRVLASCVIEEHS 360
 Db 301 KPGQRYVVGEGGQQLPASHVSLSREASAGAALPQGQTILINRVLASCVIEEHS 360

Qy 361 WAHWAFAFPFLAQLAALCPDGAIPTAFTTGTGHWYSRLYRIGSWLUDGDAHLHPLGN 420
 Db 361 WAHWAFAFPFLAQLAALCPDGAIPTAFTTGTGHWYSRLYRIGSWLUDGDAHLHPLGN 420

RESULT 6
 US-08-957-874-8
 ; Sequence 8, Application US/08957874
 ; Patent No. 6384192
 GENERAL INFORMATION:
 APPLICANT: Ingham, Phillip W.
 APPLICANT: McMahon, Andrew P.
 APPLICANT: Tabin, Clifford J.
 TITLE OF INVENTION: Verefrade Embryonic Pattern-Inducing
 NUMBER OF SEQUENCES: 47
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FOLEY, HOAG & ELLIOT LLP
 STREET: One Post Office Square
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII(text)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/957,874
 FILING DATE: 20-OCT-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/462,386
 FILING DATE: 14-DEC-1994
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/435,093
 FILING DATE: 04-MAY-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/356,060
 FILING DATE: 14-DEC-1994
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/176,427
 FILING DATE: 30-DEC-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Vincent, Matthew P.
 REGISTRATION NUMBER: 36,709
 REFERENCE/DOCKET NUMBER: HMV-006.09
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 832-1000
 TELEFAX: (617) 832-7000
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 425 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-957-874-8

Query Match 100.0%; Score 2218; DB 4; Length 425;
 Best Local Similarity 100.0%; Pred. No. 1.5e-241; Mismatches 425; Conservative 0; Indels 0; Gaps 0;

Qy 1 MVEMMLTRILLVGGTICLVSSGLTGGCGRGIGKRRHKPLKPLAYKQFPINVAEKTIG 60
 Db 1 MVEMLLRLTRILLVGGTICLVSSGLTGGCGRGIGKRRHKPLKPLAYKQFPINVAEKTIG 60

Qy 61 ASGRYEGKTRNRSERKELPNPYNDIIFDEENIGADRMLTORCKDKNLALISVMNOW 120
 Db 61 ASGRYEGKTRNRSERKELPNPYNDIIFDEENIGADRMLTORCKDKNLALISVMNOW 120

Qy 301 KPGQRYVVGEGGQQLPASHVSLSREASAGAALPQGQTILINRVLASCVIEEHS 360
 Db 301 KPGQRYVVGEGGQQLPASHVSLSREASAGAALPQGQTILINRVLASCVIEEHS 360

Qy 361 WAHWAFAFPFLAQLAALCPDGAIPTAFTTGTGHWYSRLYRIGSWLUDGDAHLHPLGN 420
 Db 361 WAHWAFAFPFLAQLAALCPDGAIPTAFTTGTGHWYSRLYRIGSWLUDGDAHLHPLGN 420

RESULT 7
US 09-325-256-17
; Sequence 17, Application US/09325256
; Patent No. 644793
GENERAL INFORMATION:
APPLICANT: PERNISKY, R. BLAKE
APPLICANT: BAKER, DARREN P.
APPLICANT: WEN, DINGYI
APPLICANT: WILLIAMS, KEVIN P.
APPLICANT: GANGER, ELLEN A.
APPLICANT: TAYLOR, FREDERICK R.
APPLICANT: GALDES, ALPHONSE
APPLICANT: PORTER, JEFFREY
TITLE OF INVENTION: HYDROPHOBICALLY-MODIFIED PROTEIN COMPOSITIONS AND
METHODS
FILE REFERENCE: BIW-067_01
CURRENT APPLICATION NUMBER: US/09/325, 256
CURRENT FILING DATE: 1999-06-03
PRIOR APPLICATION NUMBER: 60/099, 800
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/078, 935
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/089, 685
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/067, 423
PRIOR FILING DATE: 1997-12-03
PRIOR APPLICATION NUMBER: PCT/US98/25676
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 17
LENGTH: 425
TYPE: PRTR
ORGANISM: Gallus sp.
US-09-325-256-17

Query Match 100.0%; Score 2218; DB 4; Length 425;
Best Local Similarity 100.0%; Pred. No. 1.5e+21; Mismatches 425; Conservative 0; Indels 0; Gaps 0;

QY 1 MVMMLLTRLIGFICALLYSSGLITCPGRGKGRRPKKLTPLAKQFIPWAETLG 60
1 MVMLLTRLIGFICALLYSSGLITCPGRGKGRRPKKLTPLAKQFIPWAETLG 60

Db 61 ASRYEGKTRNSERFKEFLPNNPDIKFDEENTGADRMLTQRCKOKLNALAVMNQW 120
61 ASRYEGKTRNSERFKEFLPNNPDIKFDEENTGADRMLTQRCKOKLNALAVMNQW 120

QY 121 PGVLRVTEGGWDGDGHSEESLHYEGRAVDTTSDRRSKGMLARAVEAGFDWVYES 180
121 PGVLRVTEGGWDGDGHSEESLHYEGRAVDTTSDRRSKGMLARAVEAGFDWVYES 180

Db 121 PGVLRVTEGGWDGDGHSEESLHYEGRAVDTTSDRRSKGMLARAVEAGFDWVYES 180
121 PGVLRVTEGGWDGDGHSEESLHYEGRAVDTTSDRRSKGMLARAVEAGFDWVYES 180

QY 181 KAHICSYKAENSAAKSGCCPGSATVHLENGTKLVKDLSPGDRVLAAADGRLLYS 240
181 KAHICSYKAENSAAKSGCCPGSATVHLENGTKLVKDLSPGDRVLAAADGRLLYS 240

Db 240 KAHICSYKAENSAAKSGCCPGSATVHLENGTKLVKDLSPGDRVLAAADGRLLYS 240
241 FLTFLDRMDSRKLFFYIETRQPRARLLTA AHLLFVAPQHNOSEATGSTSQALFASNV 300
301 KPQORVYVIGEGQQLIPASVHSVSLREASGAYAPLTAQGTLLINRVLASCVAVIEHS 360

QY 360 KPQORVYVIGEGQQLIPASVHSVSLREASGAYAPLTAQGTLLINRVLASCVAVIEHS 360
361 WAHWAFAFPRLAQGLLAACPDGAIPTRAATTGIHWSRLYRIGSWLQDGDALHPLGM 420
361 WAHWAFAFPRLAQGLLAACPDGAIPTRAATTGIHWSRLYRIGSWLQDGDALHPLGM 420

Db 420 WAHWAFAFPRLAQGLLAACPDGAIPTRAATTGIHWSRLYRIGSWLQDGDALHPLGM 420
421 VAPAS 425
Db 425 VAPAS 425

RESULT 8
US-08-946-329A-19
; Sequence 19, Application US/08946329A
; Patent No. 605791
GENERAL INFORMATION:
APPLICANT: Beachy, Philip A.
APPLICANT: Porter, Jeffrey A.
TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES
NUMBER OF SEQUENCES: 109
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/946, 3 29A
FILING DATE: 07-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/061, 323
FILING DATE: 07-OCT-1996
APPLICATION NUMBER: 08/729, 743
FILING DATE: 10-JUL-1996
APPLICATION NUMBER: 08/667, 357
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/349, 498
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hallie, Lisa A.
REGISTRATION NUMBER: 38, 347
REFERENCE/DOCKET NUMBER: 07265/140001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 425 amino acids
TYPE: amino acid
TOPOLOGY: both
MOLECULE TYPE: protein
US-08-946-329A-19

Query Match 94.0%; Score 2085; DB 3; Length 425;
best Local Similarity 96.2%; Pred. No. 1. 5e-226; Mismatches 13; Indels 2; Gaps 2;

b 1 MYEMLLITRILVGFICALLVSSGLTCGGRGIGKRRHPPKKLPLAYKQFIPNVAEKTG 60
b 1 MYEMLLITRILVGFICALLVSSGLTCGGRGIGKRRHPPKKLPLAYKQFIPNVAEKTG 60

b 61 ASGRYEKTRNSERFELTPNYNPDIKFDEENTGADRMLTCRKDKLNALASVMNCW 120
b 61 ASGRYEKTRNSERFELTPNYNPDIKFDEENTGADRMLTCRKDKLNALASVMNCW 120

b 121 PGVLRLRTEGWDGHHSKESLHYEGRAVDTTSDRSKYGMALARAVEAGFDWVYES 180
b 121 PGVLRLRTEGWDGHHSKESLHYEGRAVDTTSDRSKYGMALARAVEAGFDWVYES 180

b 181 KAHHCYCSKAENSAAKSGCCFPSSATVHLIEHGGTKLVQDLSPGDRVLAADGRILYSD 240
b 181 KAHHCYCSKAENSAAKSGCCFPSSATVHLIEHGGTKLVQDLSPGDRVLAADGRILYSD 240

b 181 KAH-CSYKAENSAAKSGCCFPSSATVHLIEHGGTKLVQDLSPGDRVLAADGRILYSD 239
b 181 KAH-CSYKAENSAAKSGCCFPSSATVHLIEHGGTKLVQDLSPGDRVLAADGRILYSD 239

b 241 F-LTFFLDRMDSSRKLFLVYETROPRARLLTAHHLFVAPQHNOSEATGSTSQALFASN 299
b 240 FILTFLDRMDSSRKLFLVYETROPRARLLTAHHLFVAPQHNOSEATGSTSQALFASN 299

b 300 VKGQPYVVLGEQGQQLPASVHSYSLREASGRAYAPITTAATTGIGHWSRSLRIGSWLGDALHPLG 419
b 300 VKGQPYVVLGEQGQQLPASVHSYSLREASGRAYAPITTAATTGIGHWSRSLRIGSWLGDALHPLG 419

b 360 SWAHAFAPHRLAQGLLAAICPDGAIPAATTGIGHWSRSLRIGSWLGDALHPLG 419
b 360 SWAHAFAPHRLAQGLLAAICPDGAIPAATTGIGHWSRSLRIGSWLGDALHPLG 419

b 420 MYAPAS 425
b 420 MYAPAS 425

RESULT 9
S-08-567-357A-19

Sequence 19 Application US/08567357A
Patient No. 6132728
GENERAL INFORMATION:
APPLICANT: Beachy, Philip A.
APPLICANT: Moon, Randall T.
APPLICANT: Porter, Jeffrey A.
TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/567,357A
FILING DATE: 04-DEC-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/349,498
FILING DATE: 02-DEC-1994

ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/080001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 19:

Query Match 94.0%; Score 2085; DB 4; Length 425;
best Local Similarity 96.2%; Pred. No. 1. 5e-226; Mismatches 13; Indels 2; Gaps 2;

Qy 1 MYEMLLITRILVGFICALLVSSGLTCGGRGIGKRRHPPKKLPLAYKQFIPNVAEKTG 60
Qy 1 MYEMLLITRILVGFICALLVSSGLTCGGRGIGKRRHPPKKLPLAYKQFIPNVAEKTG 60

Db 61 ASGRYEKTRNSERFELTPNYNPDIKFDEENTGADRMLTCRKDKLNALASVMNCW 120
Db 61 ASGRYEKTRNSERFELTPNYNPDIKFDEENTGADRMLTCRKDKLNALASVMNCW 120

Db 121 PGVLRLRTEGWDGHHSKESLHYEGRAVDTTSDRSKYGMALARAVEAGFDWVYES 180
Db 121 PGVLRLRTEGWDGHHSKESLHYEGRAVDTTSDRSKYGMALARAVEAGFDWVYES 180

Db 181 KAHHCYCSKAENSAAKSGCCFPSSATVHLIEHGGTKLVQDLSPGDRVLAADGRILYSD 240
Db 181 KAH-CSYKAENSAAKSGCCFPSSATVHLIEHGGTKLVQDLSPGDRVLAADGRILYSD 239

Db 241 F-LTFFLDRMDSSRKLFLVYETROPRARLLTAHHLFVAPQHNOSEATGSTSQALFASN 299
Db 240 FILTFLDRMDSSRKLFLVYETROPRARLLTAHHLFVAPQHNOSEATGSTSQALFASN 299

Db 300 VKGQPYVVLGEQGQQLPASVHSYSLREASGRAYAPITTAATTGIGHWSRSLRIGSWLGDALHPLG 419
Db 300 VKGQPYVVLGEQGQQLPASVHSYSLREASGRAYAPITTAATTGIGHWSRSLRIGSWLGDALHPLG 419

Db 360 SWAHAFAPHRLAQGLLAAICPDGAIPAATTGIGHWSRSLRIGSWLGDALHPLG 419
Db 360 SWAHAFAPHRLAQGLLAAICPDGAIPAATTGIGHWSRSLRIGSWLGDALHPLG 419

Db 420 MYAPAS 425
Db 420 MYAPAS 425

RESULT 10
US-08-729-743A-19

Sequence 19 Application US/08729743A
Patient No. 621794
GENERAL INFORMATION:
APPLICANT: Beachy, Philip A.
APPLICANT: Moon, Randall T.
APPLICANT: Porter, Jeffrey A.
TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,743A
FILING DATE: 07-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/567,357
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/349,498

SEQUENCE CHARACTERISTICS:
LENGTH: 425 amino acids
TYPE: amino acid
TOPOLOGY: both
MOLECULE TYPE: protein
US-08-567-357A-19

FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/099001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5099
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 425 amino acids
TYPE: amino acid
TOPOLGY: both
MOLECULE TYPE: protein
US-08-729-743A-19

Query Match 94.0%; Score 2085; DB 4; Length 425;
Best Local Similarity 96.2%; Pred. No. 1.6e-226; Matches 410; Conservative 1; Mismatches 13; Indels 2; Gaps 2;

QY 1 MVEMLLTRILVGIFCALLVSSGLTGGPGRGIGKRRRKKLPLAKQFIPNVAEKTIG 60
Db 1 MVEMLLTRILVGIFCALLVSSGLTGGPGRGIGKRRRKKLPLAKQFIPNVAEKTIG 60

QY 61 ASRYEGKTRNTERFERKELTPNPDTIKDEENTGADRMLTQRCOKNLALASVNCW 120
Db 61 ASRYEGKTRNTERFERKELTPNPDTIKDEENTGADRMLTQRCOKNLALASVNCW 120

Qy 121 PGYKLRYTEGWDGDGHSEESLHVEGRADITTSDRRSKGMLARAVEAGFDWVYES 180
Db 121 PGYKLRYTEGWDGDGHSEESLHVEGRADITTSDRRSKGMLARAVEAGFDWVYES 180

Qy 181 KAHICSYKAENSAKSGGCFFPSATVHLENGTKLYDKISFGDRVLAAADGRLLYS 240
Db 181 KAHICSYKAENSAKSGGCFFPSATVHLENGTKLYDKISFGDRVLAAADGRLLYS 240

Qy 181 KAHICSYKAENSAKSGGCFFPSATVHLENGTKLYDKISFGDRVLAAADGRLLVS 239
Db 181 KAHICSYKAENSAKSGGCFFPSATVHLENGTKLYDKISFGDRVLAAADGRLLVS 239

Qy 241 F-LTFLDRMDSRKLFVETROPRARLLTAHLTVAPQHNOSEATGSTSGQALFASN 299
Db 240 F-LTFLDRMDSRKLFVETROPRARLLTAHLTVAPQHNOSEATGSTSGQALFASN 299

Qy 300 VKPGQPVVGLGEQQQLIPASVHSVSLREASGAYAPTAAGTILINRVASCYAYIEEH 359
Db 300 VKPGQPVVGLGEQQQLIPASVHSVSLREASGAYAPTAAGTILINRVASCYAYIEEH 359

Qy 360 SWAHAAFPRLAQGLLAALCPDGAIPATAATTGIGHWSRLYLIGSWLVDGDLHPLG 419
Db 360 SWAHAAFPRLAQGLLAALCPDGAIPATAATTGIGHWSRLYLIGSWLVDGDLHPLG 419

Qy 420 MVAPAS 425
Db 420 MVAPAS 425

RESULT 11
US-08-349-498-19
Sequence 19, Application US/08349498
Patent No. 6281332
GENERAL INFORMATION:
APPLICANT: Beachy, Phillip A.
TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: U.S.A.
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

RESULT 12
PCT-US95-15463-19
Sequence 19, Application PC/TUS9515463
GENERAL INFORMATION:
APPLICANT: The Johns Hopkins University School of Medicine
TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: U.S.A.
ZIP: 92037
COMPUTER READABLE FORM:

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/349,498
FILING DATE: 02-DEC-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/043001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5070
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 425 amino acids
TOPOLGY: both
MOLECULE TYPE: protein
STRANDEDNESS: not relevant
TYPE: amino acid
TOPOLGY: both
MOLECULE TYPE: protein
US-08-349-498-19

Query Match 94.0%; Score 2085; DB 4; Length 425;
Best Local Similarity 96.2%; Pred. No. 1.6e-226; Matches 410; Conservative 1; Mismatches 13; Indels 2; Gaps 2;

QY 1 MVEMLLTRILVGIFCALLVSSGLTGGPGRGIGKRRRKKLPLAKQFIPNVAEKTIG 60
Db 1 MVEMLLTRILVGIFCALLVSSGLTGGPGRGIGKRRRKKLPLAKQFIPNVAEKTIG 60

QY 61 ASRYEGKTRNTERFERKELTPNPDTIKDEENTGADRMLTQRCOKNLALASVNCW 120
Db 61 ASRYEGKTRNTERFERKELTPNPDTIKDEENTGADRMLTQRCOKNLALASVNCW 120

Qy 121 PGYKLRYTEGWDGDGHSEESLHVEGRADITTSDRRSKGMLARAVEAGFDWVYES 180
Db 121 PGYKLRYTEGWDGDGHSEESLHVEGRADITTSDRRSKGMLARAVEAGFDWVYES 180

Qy 181 KAHICSYKAENSAKSGGCFFPSATVHLENGTKLYDKISFGDRVLAAADGRLLYS 240
Db 181 KAHICSYKAENSAKSGGCFFPSATVHLENGTKLYDKISFGDRVLAAADGRLLYS 240

Qy 181 KAHICSYKAENSAKSGGCFFPSATVHLENGTKLYDKISFGDRVLAAADGRLLVS 239
Db 181 KAHICSYKAENSAKSGGCFFPSATVHLENGTKLYDKISFGDRVLAAADGRLLVS 239

Qy 241 F-LTFLDRMDSRKLFVETROPRARLLTAHLTVAPQHNOSEATGSTSGQALFASN 299
Db 240 F-LTFLDRMDSRKLFVETROPRARLLTAHLTVAPQHNOSEATGSTSGQALFASN 299

Qy 300 VKPGQPVVGLGEQQQLIPASVHSVSLREASGAYAPTAAGTILINRVASCYAYIEEH 359
Db 300 VKPGQPVVGLGEQQQLIPASVHSVSLREASGAYAPTAAGTILINRVASCYAYIEEH 359

Qy 360 SWAHAAFPRLAQGLLAALCPDGAIPATAATTGIGHWSRLYLIGSWLVDGDLHPLG 419
Db 360 SWAHAAFPRLAQGLLAALCPDGAIPATAATTGIGHWSRLYLIGSWLVDGDLHPLG 419

Qy 420 MVAPAS 425
Db 420 MVAPAS 425

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.30
 CURRENT APPLICATION DATA:
 APPLICANT NUMBER: PCT-US95/15463
 FILING DATE: 01-DEC-1995
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Haile, Lisa A.
 REGISTRATION NUMBER: 38,347
 REFERENCE/DOCKET NUMBER: 07265/080W01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619/678-5070
 TELEFAX: 619/678-5099
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 425 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: both
 MOLECULE TYPE: protein
 PCT-US95-15463-19

Query Match 94.0%; Score 2085; DB 5; Length 425;
 Best Local Similarity 96.2%; Pred. No. 1.6e-226; Gaps 2;
 Matches 410; Conservative 1; Mismatches 13; Indels 2;

Oy 1 MVEMLLITRLVGLFGICLAVLSSGLTGCGRGIGRRHPKLTPLAYKQIPNVAEKTIG 60
 Db 1 MVEMLLITRLVGLFGICLAVLSSGLTGCGRGIGRRHPKLTPLAYKQIPNVAEKTIG 60
 Qy 61 ASGRVEGKTRNRSERKEELTPNYNPDIKDEENTGADRIMTORCKDKLNALATSVMNQW 120
 Db 61 ASGRVEGKTRNRSERKEELTPNYNPDIKDEENTGADRIMTORCKDKLNALATSVMNQW 120
 Qy 121 PGVKLKVTEGDEGHSESLHYSGRAVDTTSDRDSRKYGMALARLAVEAGDWYYES 180
 Db 121 PGVLMLVTEGDEGHSESLHYSGRAVDTTSDRDSRKYGMALARLAVEAGDWYYES 180
 Qy 181 KAHTHCSVKAKNSVAAKSGCCFPGSATVHLHGRKLVLKDLSPGIVLAADADGRLLSD 240
 Db 181 KAHTHCSVKAKNSVAAKSGCCFPGSATVHLHGRKLVLKDLSPGIVLAADADGRLLSD 240
 Qy 241 F-LTFLDRMDSRKRKFYVIEETRQPRAILITAHLFLVAPQHNOSEATGSTSGQALFASN 299
 Db 240 F-LTFLDRMDSRKRKFYVIEETRQPRAILITAHLFLVAPQHNOSEATGSTSGQALFASN 299
 Qy 300 VKPGQRVYVIGEGGQQLPASVHSLSREERASGAYAPTAATTGTTGHWYSRLYRIGGSWLDGALHPLG 419
 Db 300 VKPGQRVYVIGEGGQQLPASVHSLSREERASGAYAPTAATTGTTGHWYSRLYRIGGSWLDGALHPLG 419
 Qy 360 SWAHAFAPFLAQLAALCPDGAIPTAATTGTTGHWYSRLYRIGGSWLDGALHPLG 419
 Db 360 SWAHAFAPFLAQLAALCPDGAIPTAATTGTTGHWYSRLYRIGGSWLDGALHPLG 419
 Qy 420 MVAPAS 425
 Db 420 MVAPAS 425

RESULT 13
 PCT-US95-1593-19

; Sequence 19, Application PC/TUS951593

; GENERAL INFORMATION:

; APPLICANT: The Johns Hopkins University School of Medicine, et al.
 ; TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES
 ; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.
 ; STREET: 4225 Executive Square, Suite 1400
 ; CITY: La Jolla
 ; STATE: CA

COUNTRY: U.S.A.
 ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

SOFTWARE: PatentIn Release #1.0, version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT-US95/15923

FILING DATE: 04-DEC-1995

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Haile, Lisa A.

REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: 07265/043W01

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619/678-5070

TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 425 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: both

MOLECULE TYPE: protein

PCT-US95-15923-19

Query Match 94.0%; Score 2085; DB 5; Length 425;
 Best Local Similarity 96.2%; Pred. No. 1.6e-226; Gaps 2;
 Matches 410; Conservative 1; Mismatches 13; Indels 2;

Oy 1 MVEMLLITRLVGLFGICLAVLSSGLTGCGRGIGRRHPKLTPLAYKQIPNVAEKTIG 60
 Db 1 MVEMLLITRLVGLFGICLAVLSSGLTGCGRGIGRRHPKLTPLAYKQIPNVAEKTIG 60
 Qy 61 ASGRVEGKTRNRSERKEELTPNYNPDIKDEENTGADRIMTORCKDKLNALATSVMNQW 120
 Db 61 ASGRVEGKTRNRSERKEELTPNYNPDIKDEENTGADRIMTORCKDKLNALATSVMNQW 120
 Qy 121 PGVKLKVTEGDEGHSESLHYSGRAVDTTSDRDSRKYGMALARLAVEAGDWYYES 180
 Db 121 PGVLMLVTEGDEGHSESLHYSGRAVDTTSDRDSRKYGMALARLAVEAGDWYYES 180
 Qy 181 KAHTHCSVKAKNSVAAKSGCCFPGSATVHLHGRKLVLKDLSPGIVLAADADGRLLSD 240
 Db 181 KAHTHCSVKAKNSVAAKSGCCFPGSATVHLHGRKLVLKDLSPGIVLAADADGRLLSD 240
 Qy 241 F-LTFLDRMDSRKRKFYVIEETRQPRAILITAHLFLVAPQHNOSEATGSTSGQALFASN 299
 Db 240 F-LTFLDRMDSRKRKFYVIEETRQPRAILITAHLFLVAPQHNOSEATGSTSGQALFASN 299
 Qy 300 VKPGQRVYVIGEGGQQLPASVHSLSREERASGAYAPTAATTGTTGHWYSRLYRIGGSWLDGALHPLG 419
 Db 300 VKPGQRVYVIGEGGQQLPASVHSLSREERASGAYAPTAATTGTTGHWYSRLYRIGGSWLDGALHPLG 419
 Qy 360 SWAHAFAPFLAQLAALCPDGAIPTAATTGTTGHWYSRLYRIGGSWLDGALHPLG 419
 Db 360 SWAHAFAPFLAQLAALCPDGAIPTAATTGTTGHWYSRLYRIGGSWLDGALHPLG 419
 Qy 420 MVAPAS 425
 Db 420 MVAPAS 425

RESULT 14
 US-08-748-591-4

; Sequence 4, Application US/08748591

; General Information:
 ; Patient No. 5759811

; APPLICANT: Epstein, Ervin
 ; APPLICANT: Hu, Zhiyan
 ; APPLICANT: Bonifas, Jeanette

; TITLE OF INVENTION: Mutant Human Hedgehog Gene

Patent No. 5759811
 GENERAL INFORMATION:
 APPLICANT: Epstein, Ervin
 APPLICANT: Hu, Zhilan
 APPLICANT: Bonifas, Jeanette
 TITLE OF INVENTION: Mutant Human Hedgehog Gene

NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish and Richardson
 STREET: 2200 Sand Hill Road
 CITY: Menlo Park
 STATE: CA
 COUNTRY: USA
 ZIP: 94025

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/748,591

FILING DATE:
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: Sherwood, Pamela J
 REGISTRATION NUMBER: 36,677
 REFERENCE/DOCKET NUMBER: 06510/067001

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 322-5070
 TELEFAX: (415) 854-0875

INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 462 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

US-08-748-591-4

Query Match 81.5%; Score 1807; DB 1; Length 462;
 Best Local Similarity 77.8%; Pred. No. 4.7e-159;
 Matches 361; Conservative 22; Mismatches 37; Indels 44; Gaps 6;

Qy 4 MLLTRILVGFCALVSSGLTCTGPGRGIGKRRHPKLTPLAYKQFIPNVAEKTIGASG 63
 ||||| | : ; ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 1 MLLARCLLVLVSSLVCSLGACCPGPGRGFKRHPKLTPLAYKQFIPNVAEKTIGASG 60

Qy 64 RVEGKTRNSERKELEPNYNIDIFKDEENTGADRMTQRCKDLNALATSVMNQPGV 123
 ||||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 61 RVEGKTRNSERKELEPNYNIDIFKDEENTGADRMTQRCKDLNALATSVMNQPGV 120

Qy 124 KLRVTEGDEDGHHSERSELSHYSGRAVDTTSRDRSKYGMALARLAVAGFDWVYSEKAH 183
 ||||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 121 KLRVTEGDEDGHHSERSELSHYSGRAVDTTSRDRSKYGMALARLAVAGFDWVYSEKAH 180

Qy 184 IHCSVKAENSAVAKSGCCFGPSATVHLBHGPKLKVDLSPGDRVLAAADAGRLLSDFLT 243
 ||||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 181 IHCSVKAENSAVAKSGCCFGPSATVHLBQGGTKLVKDLSPGDRVLAAADQGRLLSDFLT 240

Qy 244 FLDRMDSSRLKFVITERQPRARLLTAHLFVAPOHNOSEATG ----STSG---- 292
 ||||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 241 FLDRDGAKKVYVITERPREBLLAHLFVAPOHNOSEATG ----STSG---- 298

Qy 293 ---QALFASNVKGQRYVVLGE--GGQQLPASVHSVSLREESAGAYAPLTAQGTILNR 347
 ||||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 299 LGPRALFAASRVQGRQVYWAERDGRRLPLPAVHSVTSEERAGAYAPLTAQGTILNR 358

Qy 348 VLASCYAVIEEWSWAHWAFAPELQLAQLA-----CP 381
 ||||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 359 VLASCYAVIEEWSWAHRAFAPELQLAALAPARTDRGGDGGDRGGGGGRVALTAP 418

Qy 382 DGAIIPTAATTGCIHWYSRRLYRIGSWLGDGLALHPIGMVAPAS 425
 ||||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 419 GADAPGAGATAGIHWYSOLQYQIGTWLILDSEALHPIGMVAPAS 462
 ; Sequence 9, Application US/08/48591
 RESULT 15
 US-08-48-591-9

Thu Feb 20 10:43:48 2003

Db 419 GAAADAPGAGATAGIHWYSQLYQICGTMWLDSSEALHPLGMAVKS 462

Search completed: February 20, 2003, 10:14:10
Job time : 13.1257 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on:

February 20, 2003, 10:10:28 ; Search time 7.62902 Seconds

(without alignments)

1423.285 Million cell updates/sec

Title: US-09-827-110A-10

Perfect score: 2218

1 MVEMLLTRILLVFFICALL.....GSWVLGDAHLHPLGMVAPAS 425

Sequence: Sequence 1, Appl

Scoring table: BLOSUM62 Sequence 2, Appl

Gapop 10.0 , Gapext 0.5 Sequence 3, Appl

Searched: 140259 seqs, 25548876 residues Sequence 4, Appl

Total number of hits satisfying chosen parameters: 140259 Sequence 5, Appl

Minimum DB seq length: 0 Sequence 6, Appl

Maximum DB seq length: 200000000 Sequence 7, Appl

Post-processing: Minimum Match 0% Sequence 8, Appl

Maximum Match 100% Sequence 9, Appl

Listing first 45 summaries Sequence 10, Appl

Database : Published Applications AA: *

1: /cgn2_6/ptodata/1/pubpa/us08 NEW PUB, pep: *

2: /cgn2_6/ptodata/1/pubpa/pct_NEW_PUB, pep: *

3: /cgn2_6/ptodata/1/pubpa/us06 NEW_PUB, pep: *

4: /cgn2_6/ptodata/1/pubpa/us07_NEW_PUB, pep: *

5: /cgn2_6/ptodata/1/pubpa/us07_PUBCOMB, pep: *

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7: /cgn2_6/ptodata/1/pubpa/pctPubpa/PUBCOMB, pep: *

8: /cgn2_6/ptodata/1/pubpa/us08_PUBCOMB, pep: *

9: /cgn2_6/ptodata/1/pubpa/us09_NEW_PUB, pep: *

10: /cgn2_6/ptodata/1/pubpa/us10_NEW_PUB, pep: *

11: /cgn2_6/ptodata/1/pubpa/us10_PUBCOMB, pep: *

12: /cgn2_6/ptodata/1/pubpa/us10_PUBCOMB, pep: *

13: /cgn2_6/ptodata/1/pubpa/us60_NEW_PUB, pep: *

14: /cgn2_6/ptodata/1/pubpa/us60_PUBCOMB, pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	2218	100.0	425	8 US-09-900-220C-10 Sequence 10, Appl
2	2218	100.0	425	9 US-09-883-848A-10 Sequence 11, Appl
3	2218	100.0	425	10 US-09-021-660A-34 Sequence 12, Appl
4	2218	100.0	425	10 US-09-031-9910-10 Sequence 13, Appl
5	1807	81.5	462	9 US-09-733-634-14 Sequence 14, Appl
6	1807	81.5	475	8 US-08-900-220C-15 Sequence 15, Appl
7	1807	81.5	475	9 US-09-883-848A-15 Sequence 16, Appl
8	1807	81.5	475	10 US-09-021-660A-39 Sequence 17, Appl
9	1807	81.5	475	10 US-09-151-9915-15 Sequence 18, Appl
10	1791	80.7	437	9 US-09-990-046-14 Sequence 19, Appl
11	1791	80.7	437	9 US-09-965-520A-1 Sequence 20, Appl
12	1791	80.7	437	9 US-10-013-310-1 Sequence 21, Appl
13	1791	80.7	437	9 US-09-733-634-16 Sequence 22, Appl
14	1791	80.7	437	10 US-09-021-660A-37 Sequence 23, Appl
15	1788	80.6	437	8 US-08-900-220C-13 Sequence 24, Appl
16	1788	80.6	437	9 US-09-883-848A-13 Sequence 25, Appl
17	1788	80.6	437	10 US-09-151-9913-13 Sequence 26, Appl
18	1785	80.5	437	9 US-09-969-520A-3 Sequence 27, Appl
19	1782	80.3	437	9 US-09-969-520A-11 Sequence 28, Appl

Post-processing: Minimum Match 0% Sequence 29, Appl

Maximum Match 100% Sequence 30, Appl

Listing first 45 summaries Sequence 31, Appl

SUMMARIES

ALIGNMENTS

RESULT 1

US-08-900-220C-10

; Sequence 10, Application US/08900220C

; Patent No. US20020045206A1

; GENERAL INFORMATION:

; APPLICANT: Miao, Ningning

; Wang, Monica

; Mahanthappa, Nagesh K.

; Pang, Kevin

; Jin, Pang

; TITLE OF INVENTION: Method of Treating Dopaminergic and

; GABA-nergic Disorders

; NUMBER OF SEQUENCES: 32

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FOLEY, HOAG & ELIOT LLP

; STREET: ONE POST OFFICE SQUARE

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII (text)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/900, 220C

; FILING DATE: 24-Jul-1997

; CLASSIFICATION: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Vincent, Matthew P.

; REGISTRATION NUMBER: 36,709

; REFERENCE/DOCKET NUMBER: ONY-044.01

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 832-1000

; INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 425 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-900-220C-10
SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Query Match 100 %; Score 2218; DB 8; Length 425;
Best Local Similarity 100.0%; Pred. No. 7. 8e-196; Mismatches 425; Conservative 0; Indels 0; Gaps 0;

Qy 1 MVEMLLTRILVGRLGICALLYSSGLTCCGCGRGKRRHKPLPLAYQFIPNVAEKTG 60
Db 1 MVEMLLTRILVGRLGICALLYSSGLTCCGCGRGKRRHKPLPLAYQFIPNVAEKTG 60
Qy 61 ASGRYEGKTRNSERFKELTIPNYNDIFKDEENGADRMLTQCKDKLNALATSVMNW 120
Db 61 ASGRYEGKTRNSERFKELTIPNYNDIFKDEENGADRMLTQCKDKLNALATSVMNW 120
Qy 121 PGVKLKVTEGWDCHHSEESLHVEGRAVDTTSDRSKYGMARLAVEAGDWYES 180
Db 121 PGVKLKVTEGWDCHHSEESLHVEGRAVDTTSDRSKYGMARLAVEAGDWYES 180
Qy 181 KAHICSVKAENSAAKSGCCFPSSATVHLEHGSKLVLKDLSPODRLAADDGRLLSD 240
Db 181 KAHICSVKAENSAAKSGCCFPSSATVHLEHGSKLVLKDLSPODRLAADDGRLLSD 240

Qy 121 PGVKLKVTEGWDCHHSEESLHVEGRAVDTTSDRSKYGMARLAVEAGDWYES 180
Db 121 PGVKLKVTEGWDCHHSEESLHVEGRAVDTTSDRSKYGMARLAVEAGDWYES 180
Qy 241 FLTFLDRMDSSRKLFYVIETRQPRARLLTAHLFLVAPOHNOSEATGSTSGOFLASNV 300
Db 241 FLTFLDRMDSSRKLFYVIETRQPRARLLTAHLFLVAPOHNOSEATGSTSGOFLASNV 300
Qy 301 KPGQRYVYLGEGQQLPAPSHVSLSREESAGAYAPLTAQGTILINRVASCYVIEHS 360
Db 301 KPGQRYVYLGEGQQLPAPSHVSLSREESAGAYAPLTAQGTILINRVASCYVIEHS 360
Qy 361 WAHWAFAPELAQGULLAACPDGAIPATAATTTCGHWSRRLYRIGSWLGDALHPGM 420
Db 361 WAHWAFAPELAQGULLAACPDGAIPATAATTTCGHWSRRLYRIGSWLGDALHPGM 420
Qy 421 VAPAS 425
Db 421 VAPAS 425

Qy 121 PGVKLKVTEGWDCHHSEESLHVEGRAVDTTSDRSKYGMARLAVEAGDWYES 180
Db 121 PGVKLKVTEGWDCHHSEESLHVEGRAVDTTSDRSKYGMARLAVEAGDWYES 180
Qy 181 KAHICSVKAENSAAKSGCCFPSSATVHLEHGSKLVLKDLSPODRLAADDGRLLSD 240
Db 181 KAHICSVKAENSAAKSGCCFPSSATVHLEHGSKLVLKDLSPODRLAADDGRLLSD 240

RESULT 3
US-02-021-660A-34
; Sequence 34, Application US/09021660A
; Patent No. US20010041668A1
; GENERAL INFORMATION:
; APPLICANT: Baron, M.
; APPLICANT: Farrington, S.
; APPLICANT: Belausoft, M.
; TITLE OF INVENTION: METHODS FOR MODULATING HEMATOPOIESIS AND VASCULAR
FILE REFERENCE: HU1P-P01-060
CURRENT APPLICATION NUMBER: US/09/0211, 660A
CURRENT FILING DATE: 2001-08-27
PRIOR APPLICATION NUMBER: 60/037, 513
PRIOR FILING DATE: 1997-02-10
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 34
LENGTH: 425
TYPE: PRT
ORGANISM: Gallus gallus

US-09-883-848A-10
Query Match 100.0%; Score 2218; DB 9; Length 425;
Best Local Similarity 100.0%; Pred. No. 7. 8e-196; Mismatches 425; Conservative 0; Indels 0; Gaps 0;

Qy 1 MVEMLLTRILVGRLGICALLYSSGLTCCGCGRGKRRHKPLPLAYQFIPNVAEKTG 60
Db 1 MVEMLLTRILVGRLGICALLYSSGLTCCGCGRGKRRHKPLPLAYQFIPNVAEKTG 60
Qy 61 ASGRYEGKTRNSERFKELTIPNYNDIFKDEENGADRMLTQCKDKLNALATSVMNW 120
Db 61 ASGRYEGKTRNSERFKELTIPNYNDIFKDEENGADRMLTQCKDKLNALATSVMNW 120
Qy 121 PGVKLKVTEGWDCHHSEESLHVEGRAVDTTSDRSKYGMARLAVEAGDWYES 180
Db 121 PGVKLKVTEGWDCHHSEESLHVEGRAVDTTSDRSKYGMARLAVEAGDWYES 180
Qy 181 KAHICSVKAENSAAKSGCCFPSSATVHLEHGSKLVLKDLSPODRLAADDGRLLSD 240
Db 181 KAHICSVKAENSAAKSGCCFPSSATVHLEHGSKLVLKDLSPODRLAADDGRLLSD 240
Qy 241 FLTFLDRMDSSRKLFYVIETRQPRARLLTAHLFLVAPOHNOSEATGSTSGOFLASNV 300
Db 241 FLTFLDRMDSSRKLFYVIETRQPRARLLTAHLFLVAPOHNOSEATGSTSGOFLASNV 300
Qy 301 KPGQRYVYLGEGQQLPAPSHVSLSREESAGAYAPLTAQGTILINRVASCYVIEHS 360
Db 301 KPGQRYVYLGEGQQLPAPSHVSLSREESAGAYAPLTAQGTILINRVASCYVIEHS 360
Qy 361 WAHWAFAPELAQGULLAACPDGAIPATAATTTCGHWSRRLYRIGSWLGDALHPGM 420
Db 361 WAHWAFAPELAQGULLAACPDGAIPATAATTTCGHWSRRLYRIGSWLGDALHPGM 420
Qy 421 VAPAS 425
Db 421 VAPAS 425

RESULT 2
US-09-883-848A-10
; Sequence 10, Application US/09083848A
; Publication No. US200302281A1
; GENERAL INFORMATION:
; APPLICANT: Ling, L.
; APPLICANT: Sanicola-Nadel, M.
; TITLE OF INVENTION: ANGIOGENESIS-MODULATING COMPOSITIONS AND USES
FILE REFERENCE: CIBT-P01-119
CURRENT APPLICATION NUMBER: US/09/883, 848A
CURRENT FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 60/211, 919
NUMBER OF SEQ ID NOS: 48
; FILE REFERENCE: PatentIn Ver. 2.1
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/049, 763
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-021-660A-34
Query Match 100.0%; Score 2218; DB 10; Length 425;
Best Local Similarity 100.0%; Pred. No. 7. 8e-196; Mismatches 425; Conservative 0; Indels 0; Gaps 0;

Qy 1 MVEMLLTRILVGRLGICALLYSSGLTCCGCGRGKRRHKPLPLAYQFIPNVAEKTG 60
Db 1 MVEMLLTRILVGRLGICALLYSSGLTCCGCGRGKRRHKPLPLAYQFIPNVAEKTG 60
Qy 61 ASGRYEGKTRNSERFKELTIPNYNDIFKDEENGADRMLTQCKDKLNALATSVMNW 120
Db 61 ASGRYEGKTRNSERFKELTIPNYNDIFKDEENGADRMLTQCKDKLNALATSVMNW 120
Qy 121 PGVKLKVTEGWDCHHSEESLHVEGRAVDTTSDRSKYGMARLAVEAGDWYES 180
Db 121 PGVKLKVTEGWDCHHSEESLHVEGRAVDTTSDRSKYGMARLAVEAGDWYES 180
Qy 181 KAHICSVKAENSAAKSGCCFPSSATVHLEHGSKLVLKDLSPODRLAADDGRLLSD 240
Db 181 KAHICSVKAENSAAKSGCCFPSSATVHLEHGSKLVLKDLSPODRLAADDGRLLSD 240
Qy 241 FLTFLDRMDSSRKLFYVIETRQPRARLLTAHLFLVAPOHNOSEATGSTSGOFLASNV 300
Db 241 FLTFLDRMDSSRKLFYVIETRQPRARLLTAHLFLVAPOHNOSEATGSTSGOFLASNV 300

QY 301 KPGORVYVLGECCQQLPAPSHVSLSREASGAYAPLTAQGTILINRVLASCYAVIEHS 360

; Sequence 14, Application US/09733634

Db 301 KPGORVYVLGECCQQLPAPSHVSLSREASGAYAPLTAQGTILINRVLASCYAVIEHS 360

; Publication No. US20030013664A1

QY 361 WAWHAFAPFLAOGLLAALCPDGAIPTAATTTGIGHWSRLYLIGSGWLDGALHPLGM 420

; GENERAL INFORMATION:

; APPLICANT: Massachusetts General Hospital

; TITLE OF INVENTION: Method to stimulate insulin production by pancreatic b-cells

; FILE REFERENCE: 17633/1240

; CURRENT APPLICATION NUMBER: US/09/733, 634

; CURRENT FILING DATE: 2000-11-08

; PRIORITY APPLICATION NUMBER: US 60/170, 282

; PRIORITY FILING DATE: 1999-12-10

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: Patentin version 3.0

; SEQ ID NO 14

; LENGTH: 462

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-151-999-10

; Query Match Best Local Similarity 100.0%; Score 2218; DB 10; Length 425;

; Best Local Similarity 100.0%; Pred. No. 7; 8e-156; Mismatches 0; Indels 0; Gaps 0;

; Matches 425; Conservative 0; Organism: chicken Shh

; CURRENT FILING DATE: 1998-08-11

; EARLIER FILING DATE: 1997-10-20

; NUMBER OF SEQ ID NOS: 28

; SEQ ID NO 10

; LENGTH: 425

; TYPE: PRT

; ORGANISM: chicken Shh

; US-09-151-999-10

; Query Match Best Local Similarity 100.0%; Score 2218; DB 10; Length 425;

; Best Local Similarity 100.0%; Pred. No. 7; 8e-156; Mismatches 0; Indels 0; Gaps 0;

; Matches 425; Conservative 0; Organism: chicken Shh

; CURRENT FILING DATE: 1998-08-11

; EARLIER FILING DATE: 1997-10-20

; NUMBER OF SEQ ID NOS: 28

; SEQ ID NO 10

; LENGTH: 425

; TYPE: PRT

; ORGANISM: chicken Shh

; US-09-151-999-10

; Query Match Best Local Similarity 100.0%; Score 2218; DB 10; Length 425;

; Best Local Similarity 100.0%; Pred. No. 7; 8e-156; Mismatches 0; Indels 0; Gaps 0;

; Matches 425; Conservative 0; Organism: chicken Shh

; CURRENT FILING DATE: 1998-08-11

; EARLIER FILING DATE: 1997-10-20

; NUMBER OF SEQ ID NOS: 28

; SEQ ID NO 10

; LENGTH: 425

; TYPE: PRT

; ORGANISM: chicken Shh

; US-09-151-999-10

US-09-733-634-14
; Sequence 14, Application US/09733634
; Publication No. US20030013664A1
; GENERAL INFORMATION:
; APPLICANT: Massachusetts General Hospital
; TITLE OF INVENTION: Method to stimulate insulin production by pancreatic b-cells
; FILE REFERENCE: 17633/1240
; CURRENT APPLICATION NUMBER: US/09/733, 634
; CURRENT FILING DATE: 2000-11-08
; PRIORITY APPLICATION NUMBER: US 60/170, 282
; PRIORITY FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 32

RESUL 4
; Sequence 10, Application US/09151999
; Patent No. US2002015460A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Elizabeth
; TITLE OF INVENTION: REGULATION OF EPITHELIAL TISSUE BY HEDGEHOG-LIKE
; POLYPEPTIDES, AND FORMULATIONS AND USES RELATED THERETO
; FILE REFERENCE: ONV-031-02
; CURRENT APPLICATION NUMBER: US/09/151, 999
; CURRENT FILING DATE: 1998-08-11
; EARLIER FILING DATE: 1997-09/555, 552
; NUMBER OF SEQ ID NOS: 28
; SEQ ID NO 10
; LENGTH: 425
; TYPE: PRT
; ORGANISM: chicken Shh

RESUL 5
; Sequence 15, Application US/08900220C
; Patent No. US2002004206A1
; GENERAL INFORMATION:
; APPLICANT: Miao, Ningning
; Wang, Monica
; Mahanthappa, Nagesh K.
; Pang, Kevin
; Jin, Ping
; TITLE OF INVENTION: Method of Treating Dopaminergic and
; GABA-nergic Disorders
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: ONE POST OFFICE SQUARE
; CITY: Boston

FILE REFERENCE: CIBT-P01-119
 CURRENT APPLICATION NUMBER: US/09/883,849A
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII (text)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/900,220C
 FILING DATE: 24 Jul-1997
 CLASSIFICATION: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Vincent, Matthew P.
 REGISTRATION NUMBER: 36,709
 REFERENCE/DOCKET NUMBER: ONY-044.01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 832-1000
 TELEX/FAX: (617) 832-7000
 INFORMATION FOR SEQ ID NO: 15:
 LENGTH: 475 amino acids
 SEQUENCE CHARACTERISTICS:
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 15:
 ;US-08-900-220C-15
 Query Match 81.5%; Score 1807; DB 8; Length 475;
 Best Local Similarity 77.8%; Pred. No. 5.3e-158;
 Matches 361; Conservative 22; Mismatches 37; Indels 44; Gaps 6;
 QY 4 MLLTRILLYGFTICALLYVSSGLTCGGPGRGKGKRRHPPKKLTPPLAYQFIPNVAEKTIGASG 63
 ||||| | : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 1 MLLARCLLVLVLLVSSLLVCSGLACGGPGRGKGKRRHPPKKLTPPLAYQFIPNVAEKTIGASG 60
 QY 64 RYEKIKTRNRSERFKELTPNNPDLFKEDENTGADPLMTQCKDKNLAISVMNQPGV 123
 ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 61 RYEKIKTRNRSERFKELTPNNPDLFKEDENTGADPLMTQCKDKNLAISVMNQPGV 120
 QY 124 KLRVTEGWDGHHSRSELSHYEGRAVDTTSDRSKYGMJLARLAVEAGFDWVYESKAH 183
 ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 121 KLRVTEGWDGHHSRSELSHYEGRAVDTTSDRSKYGMJLARLAVEAGFDWVYESKAH 180
 QY 184 IHCSVKAENSAVAKSGCCPGSATVHLERGGTKVLDLSPGRDVLIAADAGRLLSDFLT 243
 ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 181 IHCSVKAENSAVAKSGCCPGSATVHLERGGTKVLDLSPGRDVLIAADAGRLLSDFLT 240
 QY 244 FLDRMDSRKLFYVETRQPRLLTAHLLFVAPQHNOSEATG---STSG----- 292
 ||||| | : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 241 FLDRDGAKKVYVYETRPREPRLLTAAHLLFVAP-HNDS-ATGEPERASSGSPGSGA 298
 QY 293 --QALFASNVKPGQRYVYGE-GGQQLIPASVHSVSLREASGAYAATLQGTILINR 347
 ||||| | : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 299 LGPRALFAASRVPGQRVYVAERDGDRRLPAAVSHTVLSBEEAGAYAATLQGTILINR 358
 QY 348 VLASCYAVIEEHSHWAFAFPRLAQGLAAL-----CP 381
 ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 359 VLASCYAVIEEHSHWAFAFPRLAHALLALAPARTDRGGDGGDRGGGRVALTAP 418
 QY 382 DGAIPATTGIIHWYSRLIXRIGSWLGDALHLGLMAPAS 425
 ||||| | : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 419 GAADAPGAGATAGIHWSOLYQIGTWLIDSEALHPLGMVKSS 462
 RESULT 8
 US-09-021-660A-39
 Sequence 39, Application US/09021660A
 Patent No. US2001041668A1
 GENERAL INFORMATION:
 APPLICANT: Baron, M.
 APPLICANT: Farrington, S.
 APPLICANT: Belauoff, M.
 APPLICANT: Belauoff, M.
 TITLE OF INVENTION: METHODS FOR MODULATING HEMATOPOIESIS AND VASCULAR
 TITLE OF INVENTION: GROWTH
 FILE REFERENCE: HU1P-P01-060
 CURRENT APPLICATION NUMBER: US/09/021,660A
 CURRENT FILING DATE: 2001-08-27
 PRIOR APPLICATION NUMBER: 60/037,513
 PRIOR FILING DATE: 1997-02-10
 PRIOR APPLICATION NUMBER: 60/049,763
 PRIOR FILING DATE: 1997-06-16
 NUMBER OF SEQ ID NOS: 42
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 15
 LENGTH: 475
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: SITE
 LOCATION: (463)
 OTHER INFORMATION: Xaa=unknown amino acid residue
 US-09-803-848A-15
 Query Match 81.5%; Score 1807; DB 9; Length 475;
 Best Local Similarity 77.8%; Pred. No. 5.3e-158;
 Matches 361; Conservative 22; Mismatches 37; Indels 44; Gaps 6;
 QY 4 MLLTRILLYGFTICALLYVSSGLTCGGPGRGKGKRRHPPKKLTPPLAYQFIPNVAEKTIGASG 63
 ||||| | : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 1 MLLARCLLVLVLLVSSLLVCSGLACGGPGRGKGKRRHPPKKLTPPLAYQFIPNVAEKTIGASG 60
 QY 64 RYEKIKTRNRSERFKELTPNNPDLFKEDENTGADPLMTQCKDKNLAISVMNQPGV 123
 ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 61 RYEKIKTRNRSERFKELTPNNPDLFKEDENTGADPLMTQCKDKNLAISVMNQPGV 120
 QY 124 KLRVTEGWDGHHSRSELSHYEGRAVDTTSDRSKYGMJLARLAVEAGFDWVYESKAH 183
 ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 121 KLRVTEGWDGHHSRSELSHYEGRAVDTTSDRSKYGMJLARLAVEAGFDWVYESKAH 180
 QY 184 IHCSVKAENSAVAKSGCCPGSATVHLERGGTKVLDLSPGRDVLIAADAGRLLSDFLT 243
 ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 181 IHCSVKAENSAVAKSGCCPGSATVHLERGGTKVLDLSPGRDVLIAADAGRLLSDFLT 240
 QY 244 FLDRMDSRKLFYVETRQPRLLTAHLLFVAPQHNOSEATG---STSG----- 292
 ||||| | : : ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 241 FLDRDGAKKVYVYETRPREPRLLTAAHLLFVAP-HNDS-ATGEPERASSGSPGSGA 298
 QY 293 --QALFASNVKPGQRYVYGE-GGQQLIPASVHSVSLREASGAYAATLQGTILINR 347
 ||||| | : : ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 299 LGPRALFAASRVPGQRVYVAERDGDRRLPAAVSHTVLSBEEAGAYAATLQGTILINR 358
 QY 348 VLASCYAVIEEHSHWAFAFPRLAQGLAAL-----CP 381
 ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 359 VLASCYAVIEEHSHWAFAFPRLAHALLALAPARTDRGGDGGDRGGGRVALTAP 418
 QY 382 DGAIPATTGIIHWYSRLIXRIGSWLGDALHLGLMAPAS 425
 ||||| | : : ||| ||| ||| ||| ||| ||| ||| ||| |||
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 419 GAADAPGAGATAGIHWSOLYQIGTWLIDSEALHPLGMVKSS 462
 RESULT 8
 US-09-021-660A-39
 Sequence 39, Application US/09021660A
 Patent No. US2001041668A1
 GENERAL INFORMATION:
 APPLICANT: Baron, M.
 APPLICANT: Farrington, S.
 APPLICANT: Belauoff, M.
 TITLE OF INVENTION: METHODS FOR MODULATING HEMATOPOIESIS AND VASCULAR
 TITLE OF INVENTION: GROWTH
 FILE REFERENCE: HU1P-P01-060
 CURRENT APPLICATION NUMBER: US/09/021,660A
 CURRENT FILING DATE: 2001-08-27
 PRIOR APPLICATION NUMBER: 60/037,513
 PRIOR FILING DATE: 1997-02-10
 PRIOR APPLICATION NUMBER: 60/049,763
 PRIOR FILING DATE: 1997-06-16
 NUMBER OF SEQ ID NOS: 42
 SOFTWARE: PatentIn Ver. 2.1

;

SEQ ID NO 39
LENGTH: 475
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (463)
OTHER INFORMATION: Xaa=unknown amino acid
US-09-021-660A-39

Query Match 81.5%; Score 1807; DB 10; Length 475;
Best Local Similarity 77.8%; Pred. No. 5; 3e-18;
Matches 361; Conservative 22; Mismatches 37; Indels 44; Gaps 6;

QY 4 MLLTRILNGFICALLYVSSGLTCGPGRGIGKRRHPPKKLTPLAYKOFIPNVAEKTIGAS 63
Db 1 MLLARCLLVLLVSLVSGLACPGPGRGFGRRHPPKKLTPLAYKOFIPNVAEKTIGAS 60

QY 64 RYEGKTRNSERKEELTPNNPDIFKDEENTGADRMLTQRCKDLNALATSVMNOPGV 123
Db 61 RYEGKTRNSERKEELTPNNPDIFKDEENTGADRMLTQRCKDLNALATSVMNOPGV 120

QY 124 KLRVTEGDEDGHSEESLHYSGRAVDTTSRDRSKYGMALARLAVAGFDWVYESKAH 183
Db 121 KLRVTEGDEDGHSEESLHYSGRAVDTTSRDRSKYGMALARLAVAGFDWVYESKAH 180

QY 184 IHCSVKAENSAVAKSGCCPGSATVHLERGGTKLVKOLSPGDRVLADADGRLLYSDFLT 243
Db 181 IHCSVKAENSAVAKSGCCPGSATVHLERGGTKLVKOLSPGDRVLADADGRLLYSDFLT 240

QY 244 FLDRMDSSRKLFVYIETHQPRARLLTAHLLEVAPVAPQINOSERTG----STSG---- 292
Db 241 FLDRDGAKKVVFVIEPREPRLLTAAHLLEVAPVAPDNOHNS-ATGEPEASSSGGPPSGGA 298

QY 293 --QALFASNVKGQRYVVLGE--GGQOLLPSVHSVSLREBASGAYAPLQGTLINR 347
Db 299 LGPRALFASVRGVQRYVVLGE--GGQOLLPSVHSVSLREBASGAYAPLQGTLINR 347

QY 348 VLASCYAVIEEHSAWAHMAPFLAQLLAL-----CP 381
Db 359 VLASCYAVIEEHSAWAHMAPFLAQLLALAPARTDRGGDGGDGRGGGRVALTAP 418

QY 382 DGAITPTAMTTGIGHWSRLLYRIGSWLGDALHPLGMWAPAS 425
Db 419 GAADAPGAGATAGIHWSQLLQIGTWILDSEALHPLGMAVKS 462

RESULT 9
US-09-151-999-15
Sequence 15, Application US/09151999
; Patent No. US2002015460A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Elizabeth
; TITLE OF INVENTION: REGULATION OF EPITHELIAL TISSUE BY HEDGEHOG-LIKE
; FILE REFERENCE: P1405R1
; CURRENT APPLICATION NUMBER: US/09/990,046
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/293,505
; PRIORITY FILING DATE: EARLIER FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 32

SEQ ID NO 14
LENGTH: 437
TYPE: PRT
ORGANISM: Mus musculus
US-09-990-046-14

Query Match 80.7%; Score 1791; DB 9; Length 437;
Best Local Similarity 80.5%; Pred. No. 1.4e-156;
Matches 354; Conservative 21; Mismatches 43; Indels 22; Gaps 6;

QY 4 MLLTRILNGFICALLYVSSGLTCGPGRGIGKRRHPPKKLTPLAYKOFIPNVAEKTIGAS 63
Db 2 LLLARCLLVLLVSLVSGLACPGPGRGFGRRHPPKKLTPLAYKOFIPNVAEKTIGAS 61

QY 64 RYEGKTRNSERKEELTPNNPDIFKDEENTGADRMLTQRCKDLNALATSVMNOPGV 123
Db 62 RYEGKTRNSERKEELTPNNPDIFKDEENTGADRMLTQRCKDLNALATSVMNOPGV 121

QY 124 KLRVTEGDEDGHSEESLHYSGRAVDTTSRDRSKYGMALARLAVAGFDWVYESKAH 183
Db 122 KLRVTEGDEDGHSEESLHYSGRAVDTTSRDRSKYGMALARLAVAGFDWVYESKAH 181

Query Match 81.5%; Score 1807; DB 10; Length 475;
Best Local Similarity 77.8%; Pred. No. 5; 3e-159;
Matches 361; Conservative 22; Mismatches 37; Indels 44; Gaps 6;

Db 182 IHCSVKAENSAVAKSGCCPGSATVHLERGGTKLVKOLSPGDRVLADADGRLLYSDFLT 243

QY 244 FLDRMDSSRKLKVYVIEETRQPRLLTAAHLLFVAPOHNOSEATGSTSG-QALFASNVKP 302
Db 242 FLDRDEGAKKVYVYIETLERPRLLTAAHLLFVAP-HNDS---GTPPGPSALFAASRVRP 297
Db 303 GORVVVYIGE--GGQQLPASVSVSLSREASAYAPlTAQGTILINRVLASCYAVIEBS 360
Oy 361 WAHWAFAFPFLAQGLIALCP-----DGAPlTAQGTILINRVLASCYAVIEBS 357
Db 358 WAHRAFAFPFLAHALLAALAPARTDGGSIPAOASATEARGAEPTAGIHWSOLYHI 417
Oy 406 GS梧LDGDAHLHPGMVAPAS 425
Db 418 GTWLDLSETMHPLGMVAKS 437

RESULT 11
US-09-969-520A-1
Sequence 1, Application US/09969520A
Patent NO. US2002017163A1
GENERAL INFORMATION:
APPLICANT: Lamb, Jonathan Robert
APPLICANT: Hoyne, Gerard Francis
APPLICANT: Dallman, Margaret Jane
TITLE OF INVENTION: Therapeutic Use
FILE REFERENCE: 674525-2003
CURRENT APPLICATION NUMBER: US/10/013, 310
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: PCT/GB00/02191
PRIOR FILING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: UK 9913350.6
PRIOR FILING DATE: 1995-06-08
PRIOR APPLICATION NUMBER: UK 9921953.7
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 437
TYPE: PRT
ORGANISM: Mus musculus
US-09-969-520A-1

Query Match 80.7%; Score 1791; DB 9; Length 437;
Best Local Similarity 80.5%; Pred. No. 1.4e-156; Matches 354; Conservative 21; Mismatches 43; Indels 22; Gaps 6;
Oy 4 MILLITRLIGFICALLYVSGLTCGPGRGIGKRRHKPLKLTPLAYKOFIPNVAEKTLGASG 63
Db 2 LILLARCFLVTLASSLIVCPGLACPGPGRGFGKRRHKPLKLTPLAYKOFIPNVAEKTLGASG 61
Oy 64 RYEKTKTRNSERFKELTPNYNPDIKFDENGADRLMTQRCKDKUNALATSVMMQPGV 123
Db 62 RYEKTKTRNSERFKELTPNYNPDIKFDENGADRLMTQRCKDKUNALATSVMMQPGV 121
Oy 124 KLRVTEGWDDEGHHSSESLHYEGRAVDITTSDRDRSKYGMARLAYEAGEDMVYYSKAH 183
Db 122 KLRVTEGWDDEGHHSSESLHYEGRAVDITTSDRDRSKYGMARLAYEAGEDMVYYSKAH 181
Oy 184 IHCSVKAENSYAASKGGCGFCPSATVILEHGCKTQLKLDSPDRVLAADGRLLSDFT 243
Db 182 IHCSVKAENSYAASKGGCGFCPSATVILEQGGTKVLKVDLPGDVRVLAADGRLLSDFT 241
Oy 244 FLDRMDSSRKLKVYVIEETRQPRLLTAAHLLFVAPOHNOSEATGSTSG-QALFASNVKP 302
Db 242 FLDRDEGAKKVYVYIETLERPRLLTAAHLLFVAP-HNDS---GTPPGPSALFAASRVRP 297
Oy 303 GORVVVYIGE--GGQQLPASVSVSLSREASAYAPlTAQGTILINRVLASCYAVIEBS 360
Db 298 GORVVVYIGE--GGQQLPASVSVSLSREASAYAPlTAQGTILINRVLASCYAVIEBS 357
Oy 361 WAHWAFAFPFLAQGLIALCP-----DGAPlTAQGTILINRVLASCYAVIEBS 405
Db 358 WAHRAFAFPFLAHALLAALAPARTDGGSIPAOASATEARGAEPTAGIHWSOLYHI 417
Oy 406 GS梧LDGDAHLHPGMVAPAS 425
Db 418 GTWLDLSETMHPLGMVAKS 437

RESULT 12
US-10-013-310-1
Sequence 1, Application US/10013310
Publication No. US2002019226A1
GENERAL INFORMATION:
APPLICANT: Lamb, Jonathan Robert
APPLICANT: Hoyne, Gerard Francis
APPLICANT: Dallman, Margaret Jane
TITLE OF INVENTION: Therapeutic Use
FILE REFERENCE: 674525-2003
CURRENT APPLICATION NUMBER: US/10/013, 310
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: PCT/GB00/02191
PRIOR FILING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: UK 9913350.6
PRIOR FILING DATE: 1995-06-08
PRIOR APPLICATION NUMBER: UK 9921953.7
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 437
TYPE: PRT
ORGANISM: House Mouse
US-10-013-310-1

Query Match 80.7%; Score 1791; DB 9; Length 437;
Best Local Similarity 80.5%; Pred. No. 1.4e-156; Matches 354; Conservative 21; Mismatches 43; Indels 22; Gaps 6;
Oy 4 MILLITRLIGFICALLYVSGLTCGPGRGIGKRRHKPLKLTPLAYKOFIPNVAEKTLGASG 63
Db 2 LILLARCFLVTLASSLIVCPGLACPGPGRGFGKRRHKPLKLTPLAYKOFIPNVAEKTLGASG 61
Oy 64 RYEKTKTRNSERFKELTPNYNPDIKFDENGADRLMTQRCKDKUNALATSVMMQPGV 123
Db 62 RYEKTKTRNSERFKELTPNYNPDIKFDENGADRLMTQRCKDKUNALATSVMMQPGV 121
Oy 124 KLRVTEGWDDEGHHSSESLHYEGRAVDITTSDRDRSKYGMARLAYEAGEDMVYYSKAH 183
Db 122 KLRVTEGWDDEGHHSSESLHYEGRAVDITTSDRDRSKYGMARLAYEAGEDMVYYSKAH 181
Oy 184 IHCSVKAENSYAASKGGCGFCPSATVILEHGCKTQLKLDSPDRVLAADGRLLSDFT 243
Db 182 IHCSVKAENSYAASKGGCGFCPSATVILEQGGTKVLKVDLPGDVRVLAADGRLLSDFT 241
Oy 244 FLDRMDSSRKLKVYVIEETRQPRLLTAAHLLFVAPOHNOSEATGSTSG-QALFASNVKP 302
Db 242 FLDRDEGAKKVYVYIETLERPRLLTAAHLLFVAP-HNDS---GTPPGPSALFAASRVRP 297
Oy 303 GORVVVYIGE--GGQQLPASVSVSLSREASAYAPlTAQGTILINRVLASCYAVIEBS 360
Db 298 GORVVVYIGE--GGQQLPASVSVSLSREASAYAPlTAQGTILINRVLASCYAVIEBS 357
Oy 361 WAHWAFAFPFLAQGLIALCP-----DGAPlTAQGTILINRVLASCYAVIEBS 405
Db 358 WAHRAFAFPFLAHALLAALAPARTDGGSIPAOASATEARGAEPTAGIHWSOLYHI 417
Oy 406 GS梧LDGDAHLHPGMVAPAS 425
Db 418 GTWLDLSETMHPLGMVAKS 437

RESULT 13
US-09-733-634-16
Sequence 16, Application US/09733634
Publication No. US2003001364A1
GENERAL INFORMATION:
APPLICANT: Massachusetts General Hospital
TITLE OF INVENTION: Method to stimulate insulin production by pancreatic b-cells

; FILE REFERENCE: 17633/1240
; CURRENT APPLICATION NUMBER: US/09/733, 634
; CURRENT FILING DATE: 2000-12-08
; PRIORITY APPLICATION NUMBER: US 60/170, 282
; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16 LENGTH: 437
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-733-634-16

Query Match 80.7%; Score 1791; DB 9; Length 437;

Best Local Similarity 80.5%; Pred. No. 1 4e-156;
Matches 354; Conservative 21; Mismatches 43; Indels 22; Gaps 6;

Qy 4 MILLTRILYVFGTICALLYVSSGLTCGGGRGKRRHKPLKPLAYKOFIPNVAEKTIGASG 63
Db 2 LLLARCFVLVLIASSLIVCPGLACGPGRGKRRHKPLKPLAYKOFIPNVAEKTIGASG 61

Qy 64 RYEKIKTRNSERFKELTPTNYNPDIKFDEENTGADRMLTQRCKDKNIALTSVMNQPGV 123
Db 62 RYEKIKTRNSERFKELTPTNYNPDIKFDEENTGADRMLTQRCKDKNIALTSVMNQPGV 121

Qy 124 KLRVTEGWDGHSESSLHYEGRAVDITTSDRDRSKYGMALARAVEAGFDWVYESKAH 183
Db 122 KLRVTEGWDGHSESSLHYEGRAVDITTSDRDRSKYGMALARAVEAGFDWVYESKAH 181

Qy 184 IHCSVKAENSYAAKSGCGFCGSATVHLEGGTKLYKLSPDRVLAADAGRLLSDFLT 243
Db 182 IHCSVKAENSYAAKSGCGFCGSATVHLEGGTKLYKLSPDRVLAADAGRLLSDFLT 241

Qy 244 FLDRMDSRKLEYVIEPTRQPARLLTAAHLLFVAPOHNOSEATGSTSG-QALPASNVP 302
Db 242 FLDRDSEGAKKYVIEPTRQPARLLTAAHLLFVAPOHNOSEATGSTSG-QALPASNVP 297

Qy 303 GORVVVILGE-GGQQLIPASVHSVSLREEAAGAYPLTAHTGTLINRVLASCYAVIEHS 360
Db 298 GORVVVVAERGGDRRLIPAAVHSVTLREEEAGAYPLTAHTGTLINRVLASCYAVIEHS 357

Qy 361 WAHWAFAFRALQGLAALCP-----DGAIPTA-----ATTTGTHWYSRLYRI 405
Db 358 WAHWAFAFRALAHALLAALAPARTDGGGGSIPAQSATEARGAEPTAGTHWYSOLLYHI 417

Qy 406 GSWLQDGALHPLGMVAPAS 425
Db 418 GTWLLDSETMHPLGMVKS 437

RESULT 14
US-09-021-660A-37

; Sequence 37, Application US/09/021660A

; Patent No. US2001004166A1
; GENERAL INFORMATION:
; APPLICANT: Parrington, S.

; APPLICANT: Belausoft, M.
; TITLE OF INVENTION: METHODS FOR MODULATING HEMATOPOIESIS AND VASCULAR
; TITLE OF INVENTION: GROWTH

; FILE REFERENCE: HUJP-P01-060

; CURRENT APPLICATION NUMBER: US/09/021, 660A
; CURRENT FILING DATE: 2001-08-27

; PRIORITY APPLICATION NUMBER: 60/037, 513
; PRIORITY FILING DATE: 1997-02-10

; PRIORITY APPLICATION NUMBER: 60/049, 763
; PRIORITY FILING DATE: 1997-06-16

; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 37 LENGTH: 437

; TYPE: PRT
; ORGANISM: Mus musculus

US-09-021-660A-37

Query Match 80.7%; Score 1791; DB 10; Length 437;
Best Local Similarity 80.5%; Pred. No. 1 4e-156;
Matches 354; Conservative 21; Mismatches 43; Indels 22; Gaps 6;

Qy 4 MILLTRILYVFGTICALLYVSSGLTCGGGRGKRRHKPLKPLAYKOFIPNVAEKTIGASG 63
Db 2 LLLARCFVLVLIASSLIVCPGLACGPGRGKRRHKPLKPLAYKOFIPNVAEKTIGASG 61

Qy 64 RYEKIKTRNSERFKELTPTNYNPDIKFDEENTGADRMLTQRCKDKNIALTSVMNQPGV 123
Db 62 RYEKIKTRNSERFKELTPTNYNPDIKFDEENTGADRMLTQRCKDKNIALTSVMNQPGV 121

Qy 124 KLRVTEGWDGHSESSLHYEGRAVDITTSDRDRSKYGMALARAVEAGFDWVYESKAH 183
Db 122 KLRVTEGWDGHSESSLHYEGRAVDITTSDRDRSKYGMALARAVEAGFDWVYESKAH 181

Qy 184 IHCSVKAENSYAAKSGCGFCGSATVHLEGGTKLYKLSPDRVLAADAGRLLSDFLT 243
Db 182 IHCSVKAENSYAAKSGCGFCGSATVHLEGGTKLYKLSPDRVLAADAGRLLSDFLT 241

Qy 244 FLDRMDSRKLEYVIEPTRQPARLLTAAHLLFVAPOHNOSEATGSTSG-QALPASNVP 302
Db 242 FLDRDSEGAKKYVIEPTRQPARLLTAAHLLFVAPOHNOSEATGSTSG-QALPASNVP 297

Qy 303 GORVVVILGE-GGQQLIPASVHSVSLREEAAGAYPLTAHTGTLINRVLASCYAVIEHS 360
Db 298 GORVVVVAERGGDRRLIPAAVHSVTLREEEAGAYPLTAHTGTLINRVLASCYAVIEHS 357

Qy 361 WAHWAFAFRALQGLAALCP-----DGAIPTA-----ATTTGTHWYSRLYRI 405
Db 358 WAHWAFAFRALAHALLAALAPARTDGGGGSIPAQSATEARGAEPTAGTHWYSOLLYHI 417

Qy 406 GSWLQDGALHPLGMVAPAS 425
Db 418 GTWLLDSETMHPLGMVKS 437

RESULT 15

US-08-900-220C-13

; Sequence 13, Application US/08/000220C
; Patent No. US20020045206A1
; GENERAL INFORMATION:

; GENERAL APPLICANT: Miao, Ningning
; Wang, Monica
; Mahanthappa, Nagesh K.
; Fang, Kevin
; Jin, Ping

; TITLE OF INVENTION: Method of treating Dopaminergic and
; GABA-ergic Disorders
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & SELIOT LLP
; STREET: ONE POST OFFICE SQUARE
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/900, 220C
; FILING DATE: 24-Jul-1997
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36, 709
; REFERENCE/DOCKET NUMBER: ONV-044.01
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 832-1000
 TELEFAX: (617) 832-7000
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 437 amino acids
 TOPOLGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 13:
 ; US-08-900-220C-13

Query Match 80.6%; Score 1788; DB 8; Length 437;
 Best Local Similarity 80.2%; Pred. No. 2.6e-156; Gaps 6;
 Matches 353; Conservative 22; Mismatches 43; Indels 22;

Qy	4	MULLTRILVGFICALLYSSGLUTCGPGRGIGKRHKPKKLTPPLAYKQFIPNVAEKTGAGS	63
Db	2	LILLARCLFLVILASSLILVPGLAGPGGRGKGKRHKPKKLTPPLAYKQFIPNVAEKTGAGS	61
Qy	64	RYEKITRNSERFELTPWNPDIFKDENTGADRMLTQRCDKLNALISVNQPGV	123
Db	62	RYEKITRNSERFELTPWNPDIFKDENTGADRMLTQRCDKLNALISVNQPGV	121
Qy	124	KLRTEGWDGDGHISPESHYEGRAVDTTSDRRSKYOMLARIAVEAGFDWVYESKAH	183
Db	122	RLRTATEGWDGDGHISSESHYEGRAVDTTSDRRSKYOMLARIAVEAGFDWVYESKAH	181
Qy	184	IHCSCVKAENSAVAKSGGCERGSATVHLEGGTKVVDLSPGDRYLAADGRLLYSDFLT	243
Db	182	IHCSCVKAENSAVAKSGGCERGSATVHLEGGTKVVDLSPGDRYLAADGRLLYSDFLT	241
Qy	244	FLDRMDSSRKLFVYETRORPARIILTAAHLFVAPQHNOSEATGSTSG-QALEASNVKP	302
Db	242	FLDRDEGAKKVVFYVYIETLERPERLILTAHLFVAP-HNDS--GPTPCPSALAFSRVYRP	297
Qy	303	GQRIVVLGE-GGQQLPPAVHSVSLREERASGAYAQLAQGTIIINRVIALSCVAVIEHS	360
Db	298	GQRIVVVAERGGDRLPAVHSVTLREEAQAVPLAHGTILINRVIALSCVAVIEHS	357
Qy	361	WAHRFAFAPERLAAQGILAAALCP-----DGAIPA-----ATTTCGIHWSRLLYRI	405
Db	358	WAHRFAFAPERLAAQGILAAALCP-----DGAIPA-----ATTTCGIHWSRLLYRI	417
Qy	406	GSMWLDGDAHLHPUGLWVAPAS	425
Db	418	GTMWLDSETMHPUGLWVAPAS	437

Search completed: February 20, 2003, 10:14:41
 Job time : 9.62902 secs

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OM protein - protein search, using sw model

Run on: February 20, 2003, 10:08:18 ; Search time 13.9865 Seconds

Post-processing: Minimum Match 0%

Database : Maximum Match 100%
 Listing first 45 summaries

Result No. Score % Query Match Length DB ID Description

1 2218 100.0 425 A49424 PIR73;*
 2 1791 80.7 437 A49425 pir1;*
 3 1780 80.3 437 B53193 pir2;*
 4 1533 69.1 444 S56765 pir3;*
 5 1494 67.4 418 A53193 pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Scoring table: BLOSUM62
 Gapcp 10.0 , Gapext 0.5
 Searched: 283224 seqs, 96134422 residues

RESULTS

RESULT 1

A49424 Patterning protein
 C;Species: Gallus gallus (chicken) Precursor - chicken
 C;Accession: A49424 R;Riddle, R.D.; Johnson, R.L.; Laufer, E.; Tabin, C.
 Cell 75, 1401-416, 1993
 A;Title: Sonic hedgehog mediates the polarizing activity of the ZPA.
 A;Reference number: A49424; MVID:9094333; PMID:869518
 A;Accession: A49424 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-225 <RID>
 A;Cross-references: GB:L28099; NID:9453526; PIDN:AAA72428.1; PID:9453527
 C;Superfamily: sonic hedgehog protein
 F;1-26/Domain: signal sequence #status predicted <SIG>

Query Match 100.0%; Score 2218; DB 2; Length 425;
 Best Local Similarity 100.0%; Pred. No. 1.8e-176;
 Matches 425; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 NVEMMLTRILNVGFCALLVSSGIGKTRGPGRGIGRKRRPKPLTPLAKYQFPIPVAKRTLG 60
 Db 1 NVEMMLTRILNVGFCALLVSSGIGKTRGPGRGIGRKRRPKPLTPLAKYQFPIPVAKRTLG 60

QY 61 ASGRYVGKITRN SERKELP PNP IPI K D E E N T G A D R I M T O R K D K I N A L A I S M P N O W 120
 Db 61 ASGRYVGKITRN SERKELP PNP IPI K D E E N T G A D R I M T O R K D K I N A L A I S M P N O W 120

QY 121 PGVKLRVTEGDEGH HSEESLHYEGRAV DITTS D E D R S K Y G M A R L A V E G F D W Y Y E S 180
 Db 121 PGVKLRVTEGDEGH HSEESLHYEGRAV DITTS D E D R S K Y G M A R L A V E G F D W Y Y E S 180

QY 181 KAHIKCSVKAVNSVA KSGCFFPGS T V H E H G G T R L V K D L S P G R V L A A D D G R U Y S D 240
 Db 181 KAHIKCSVKAVNSVA KSGCFFPGS T V H E H G G T R L V K D L S P G R V L A A D D G R U Y S D 240

QY 241 FLTFLLRMDSSRKL F Y V I E T Q P R A R L L R A H L E V A P Q H N O S E R T G S Q A F E S N V 300
 Db 241 FLTFLLRMDSSRKL F Y V I E T Q P R A R L L R A H L E V A P Q H N O S E R T G S Q A F E S N V 300

QY 301 KPGQRYVVLGGQQQLPASVHSV SREEN S G A Y A P D T A Q C T I L I N R V L A S C Y A V E E H S 360
 Db 301 KPGQRYVVLGGQQQLPASVHSV SREEN S G A Y A P D T A Q C T I L I N R V L A S C Y A V E E H S 360

QY 361 WAHWAFAFPRLAQGLLAALCPDGAIPTAATTGIGIHWYSLYRIGSWLGDALHPLGM 420
 Db 361 WAHWAFAFPRLAQGLLAALCPDGAIPTAATTGIGIHWYSLYRIGSWLGDALHPLGM 420

QY 421 VAPAS 425
 ||||

ALIGNMENTS

Db 421 VAPAS 425

A; Residues: 1-437 <ROR>
 A; Cross-references: GB:L27340; NID:9452122; PIDN:AAA20999.1; PID:9452123
 C; Superfamily: sonic hedgehog protein

RESULT 2
 A49425 Sonic hedgehog protein precursor - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 10-Dec-1999

C;Accession: A49425 R;Echelard, Y.; Epstein, D.J.; St-Jacques, B.; Shen, L.; Mohler, J.; McMahon, J.A.; McMahon, P.A.; Reference number: A49425; MUID:94094334; PMID:7916661

A;Status: Preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA
 A;Residues: 1-437 <ECH>

A;Cross-references: authors translation is shown for the codon TCC at position 436

A;Gene: Shh
 C;Superfamily: sonic hedgehog protein

Query Match 80.7%; Score 1791; DB 2; Length 437;
 Best Local Similarity 80.5%; Pred. No. 5. 9e-141; Matches 354; Conservative 21; Mismatches 43; Indels 22; Gaps 6;
 保守性匹配 80.5%; 预测数. 5. 9e-141; 匹配数 354; 保守性 21; 错配数 43; 缺口数 6;
 保守性相似度 80.5%; 预测号. 5. 9e-141; 匹配数 354; 保守性 21; 错配数 43; 缺口数 6;

Matches 352; Conservatve 22; Mismatches 44; Indels 22; Gaps 6;

Query Match 80.3%; Score 1780; DB 2; Length 437;
 Best Local Similarity 80.0%; Pred. No. 4. 9e-140; Matches 352; Conservative 22; Mismatches 44; Indels 22; Gaps 6;

保守性匹配 80.3%; 预测数. 4. 9e-140; 匹配数 352; 保守性 22; 错配数 44; 缺口数 6;

保守性相似度 80.3%; 预测号. 4. 9e-140; 匹配数 352; 保守性 22; 错配数 44; 缺口数 6;

Query Match 80.3%; Score 1780; DB 2; Length 437;
 Best Local Similarity 80.0%; Pred. No. 4. 9e-140; Matches 352; Conservatve 22; Mismatches 44; Indels 22; Gaps 6;

保守性匹配 80.3%; 预测数. 4. 9e-140; 匹配数 352; 保守性 22; 错配数 44; 缺口数 6;

保守性相似度 80.3%; 预测号. 4. 9e-140; 匹配数 352; 保守性 22; 错配数 44; 缺口数 6;

Query Match 80.3%; Score 1780; DB 2; Length 437;
 Best Local Similarity 80.0%; Pred. No. 4. 9e-140; Matches 352; Conservatve 22; Mismatches 44; Indels 22; Gaps 6;

保守性匹配 80.3%; 预测数. 4. 9e-140; 匹配数 352; 保守性 22; 错配数 44; 缺口数 6;

保守性相似度 80.3%; 预测号. 4. 9e-140; 匹配数 352; 保守性 22; 错配数 44; 缺口数 6;

Query Match 80.3%; Score 1780; DB 2; Length 437;
 Best Local Similarity 80.0%; Pred. No. 4. 9e-140; Matches 352; Conservatve 22; Mismatches 44; Indels 22; Gaps 6;

保守性匹配 80.3%; 预测数. 4. 9e-140; 匹配数 352; 保守性 22; 错配数 44; 缺口数 6;

保守性相似度 80.3%; 预测号. 4. 9e-140; 匹配数 352; 保守性 22; 错配数 44; 缺口数 6;

Query Match 80.3%; Score 1780; DB 2; Length 437;
 Best Local Similarity 80.0%; Pred. No. 4. 9e-140; Matches 352; Conservatve 22; Mismatches 44; Indels 22; Gaps 6;

保守性匹配 80.3%; 预测数. 4. 9e-140; 匹配数 352; 保守性 22; 错配数 44; 缺口数 6;

保守性相似度 80.3%; 预测号. 4. 9e-140; 匹配数 352; 保守性 22; 错配数 44; 缺口数 6;

Query Match 80.3%; Score 1780; DB 2; Length 437;
 Best Local Similarity 80.0%; Pred. No. 4. 9e-140; Matches 352; Conservatve 22; Mismatches 44; Indels 22; Gaps 6;

保守性匹配 80.3%; 预测数. 4. 9e-140; 匹配数 352; 保守性 22; 错配数 44; 缺口数 6;

保守性相似度 80.3%; 预测号. 4. 9e-140; 匹配数 352; 保守性 22; 错配数 44; 缺口数 6;

Query Match 80.3%; Score 1780; DB 2; Length 437;
 Best Local Similarity 80.0%; Pred. No. 4. 9e-140; Matches 352; Conservatve 22; Mismatches 44; Indels 22; Gaps 6;

保守性匹配 80.3%; 预测数. 4. 9e-140; 匹配数 352; 保守性 22; 错配数 44; 缺口数 6;

保守性相似度 80.3%; 预测号. 4. 9e-140; 匹配数 352; 保守性 22; 错配数 44; 缺口数 6;

Query Match 80.3%; Score 1780; DB 2; Length 437;
 Best Local Similarity 80.0%; Pred. No. 4. 9e-140; Matches 352; Conservatve 22; Mismatches 44; Indels 22; Gaps 6;

保守性匹配 80.3%; 预测数. 4. 9e-140; 匹配数 352; 保守性 22; 错配数 44; 缺口数 6;

保守性相似度 80.3%; 预测号. 4. 9e-140; 匹配数 352; 保守性 22; 错配数 44; 缺口数 6;

Query Match 80.3%; Score 1780; DB 2; Length 437;
 Best Local Similarity 80.0%; Pred. No. 4. 9e-140; Matches 352; Conservatve 22; Mismatches 44; Indels 22; Gaps 6;

保守性匹配 80.3%; 预测数. 4. 9e-140; 匹配数 352; 保守性 22; 错配数 44; 缺口数 6;

保守性相似度 80.3%; 预测号. 4. 9e-140; 匹配数 352; 保守性 22; 错配数 44; 缺口数 6;

Query Match 80.3%; Score 1780; DB 2; Length 437;
 Best Local Similarity 80.0%; Pred. No. 4. 9e-140; Matches 352; Conservatve 22; Mismatches 44; Indels 22; Gaps 6;

保守性匹配 80.3%; 预测数. 4. 9e-140; 匹配数 352; 保守性 22; 错配数 44; 缺口数 6;

保守性相似度 80.3%; 预测号. 4. 9e-140; 匹配数 352; 保守性 22; 错配数 44; 缺口数 6;

Query Match 80.3%; Score 1780; DB 2; Length 437;
 Best Local Similarity 80.0%; Pred. No. 4. 9e-140; Matches 352; Conservatve 22; Mismatches 44; Indels 22; Gaps 6;

保守性匹配 80.3%; 预测数. 4. 9e-140; 匹配数 352; 保守性 22; 错配数 44; 缺口数 6;

保守性相似度 80.3%; 预测号. 4. 9e-140; 匹配数 352; 保守性 22; 错配数 44; 缺口数 6;

Query Match 80.3%; Score 1780; DB 2; Length 437;
 Best Local Similarity 80.0%; Pred. No. 4. 9e-140; Matches 352; Conservatve 22; Mismatches 44; Indels 22; Gaps 6;

保守性匹配 80.3%; 预测数. 4. 9e-140; 匹配数 352; 保守性 22; 错配数 44; 缺口数 6;

保守性相似度 80.3%; 预测号. 4. 9e-140; 匹配数 352; 保守性 22; 错配数 44; 缺口数 6;

Query Match 80.3%; Score 1780; DB 2; Length 437;
 Best Local Similarity 80.0%; Pred. No. 4. 9e-140; Matches 352; Conservatve 22; Mismatches 44; Indels 22; Gaps 6;

保守性匹配 80.3%; 预测数. 4. 9e-140; 匹配数 352; 保守性 22; 错配数 44; 缺口数 6;

保守性相似度 80.3%; 预测号. 4. 9e-140; 匹配数 352; 保守性 22; 错配数 44; 缺口数 6;

Query Match 80.3%; Score 1780; DB 2; Length 437;
 Best Local Similarity 80.0%; Pred. No. 4. 9e-140; Matches 352; Conservatve 22; Mismatches 44; Indels 22; Gaps 6;

保守性匹配 80.3%; 预测数. 4. 9e-140; 匹配数 352; 保守性 22; 错配数 44; 缺口数 6;

保守性相似度 80.3%; 预测号. 4. 9e-140; 匹配数 352; 保守性 22; 错配数 44; 缺口数 6;

Query Match 80.3%; Score 1780; DB 2; Length 437;
 Best Local Similarity 80.0%; Pred. No. 4. 9e-140; Matches 352; Conservatve 22; Mismatches 44; Indels 22; Gaps 6;

保守性匹配 80.3%; 预测数. 4. 9e-140; 匹配数 352; 保守性 22; 错配数 44; 缺口数 6;

保守性相似度 80.3%; 预测号. 4. 9e-140; 匹配数 352; 保守性 22; 错配数 44; 缺口数 6;

	Db	415 VNSS 418
Qy	183	HICCSVKAENSAVAKSGCGCPGSAVHLEGGTKVLDLSPGDRVLAADAGRLLYSDEL 242
	181	: :
Db		HICCSVKAENSAVAKSGCGCPGAVRMVERGGTAKVDLRPGDRLVSSDPOGNILYSDFL 240
Qy	243	TFLDRMDSSRKLFFYVETROPRARLLTAHLFVAPQHNOSEAGTSQGALFSNVKG 302
	241	: :
Db		MFIQDODERDVKKLFYVETROPRARLLTAHLFVAPQHNOSEAGTSQGALFSNVKG 294
Qy	303	GORYVVLGEQGQQLPAPSVHSVSLREESAGAYAQLTAQGTILINRVLASCYAVIEHWSA 362
	295	: :
Db		GDLITTDADPKMTLAKVKVKVDSL-EEDTCAYAQLTAQGTILINRVLASCYAVIEHWTWA 353
Qy	363	HWAFAFPRLAQGLALCPDGAIPTAT-----TTG 394
	354	: :
Db		HLFAFPRLFGMSLSSVITYPRODSSPGLPHQVHQVLDQSHHQVLDQSHHQLEG 413
Qy	395	IHWYSLRLYRIGSWSLQDGDAHLPLGMVAPAS 425
	414	: :
Db		IHWYSLQLQYQITWILDNSLHPLGMATKS 444
RESULT 5		
A53193		hedghog homolog vhh-1 - zebra fish
C;Species		Brachydanio rerio (zebra fish)
C;Date		06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 10-Dec-1999
C;Accession		A53193
R;RoleLink		H; Augsburger, A.; Heemskerk, J.; Korzh, V.; Norlin, S.; Ruiz 1 Altaba, A.;
Cell		Cell 76, 761-775, 1994
A;Title		Floor plate and motor neuron induction by vhh-1, a vertebrate homolog of hedgehog protein
A;Reference number		A53193; MUID:94170375; PMID:8124714
A;Accession		A53193
A;Status		preliminary
A;Molecule type		mRNA
A;Residues		1-418 <RQE>
A;Cross-references		GB:L27585; NID:9452159; PID:9452160
C;Superfamily		sonic hedgehog protein
Query Match		
Best Local Similarity		64.4%; Score 1429; DB 2; Length 415;
Matches		283; Conservative 66.4%; Pred. No. 7e-111; Mismatches 72; Gaps 5;
Qy	4	MILLTRILYGFICALLYVSSGLTCGGGRGIGKRRHPPKLTPLAYKQFIPWAEKTLGASC 63
Db	1	MILLTRILYGFICALLYVSSGLTCGGGRGIGKRRHPPKLTPLAYKQFIPWAEKTLGASC 60
Qy	64	RVEGKTRNNSPERKELTTPNPDIFKDEENTGADRMLTORCKDKLNALALISVMHQPGV 123
Db	61	RVEGKTRNNSPERKELTTPNPDIFKDEENTGADRMLTORCKDKLNALALISVMHQPGV 120
Qy	124	KLRVTEGWDDEGHHSLESLIVHEGRADVITTSRDRDSKYGLALARLAVEAGDWVYESKAH 183
Db	121	KLRVTEGWDDEGHHSLESLIVHEGRADVITTSRDRDSKYGLALARLAVEAGDWVYESKAH 180
Qy	184	IHCСVKAENSAVAKSGCGCPGSAVHLEGGTKVLDLSPGDRVLAADAGRLLYSDEL 243
Db	181	: :
Qy	244	FLDRMDSRKLFFYVETROPRARLLTAHLFVAPQHNOSEAGTSQGALFSNVKG 303
Db	241	: :
Qy	304	ORVYVILGEQGQQLPAPSVHSVSLREESAGAYAQLTAQGTILINRVLASCYAVIEHWSA 363
Db	297	: :
Qy	364	WAFAPRLAQGLALCPDGAIPTATTTG-IHWYSLRLYRIGSWSLQDGDAHLPLGMV 421
Db	355	: :
Qy	415	LHPLGM 420
Db	408	LHPLGM 413
RESULT 7		
B4425		desert hedgehog protein precursor - mouse
C;Species		Mus musculus (house mouse)
C;Date		06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 10-Dec-1999
C;Accession		B4425
R;Echard		D.Y.; Epstein, D.J.; St-Jacques, B.; Shen, L.; Mohler, J.; McMahon, J.A.; M
Cell		Cell 75, 1417-1430, 1993
A;Title		Sonic hedgehog, a member of a family of putative signaling molecules, is imp
A;Reference number		A49425; MUID:94094334; PMID:7916661
A;Accession		B4425
A;Status		preliminary
A;Molecule type		RNA
A;Residues		1-396 <ECH>

A;Cross-references: GB:X76292; NID:9443941; PID:CAA53924.1; PID:9443942	Db	181 AFQVITODPPRLAATPHLIFADHNTPEAA---HERATFASHQPGQ---YVLSGV 234
C;Genetics:	Oy	314 QQLIPASVHSVLREASGAYAPLTACTILNRYLASCYAVIEHSAWAHAPAPERLAQ 373
A;Gene: Dhh	C;	325 PGLQPARVAAS-THVALGSYAPLRTHQTLVVEDVASCFAAVADHHLAQAFWLRL- 291
C;superfamily: sonic hedgehog protein	Db	374 GLIALCDGAIPTAA---TTTIGIHYSLYRILYSRWLQDADHLIGMTRAS 425
Query Match	Oy	Db 292 -----FPSSLANGSWTPSEGWHSYPOMLYRLGRULLBLBESTHPLGMSGAGS 336
Best Local Similarity	54.1%; Score 1200; DB 2; Length 396;	Matches 241; Conservative 56; Mismatches 84; Indels 16; Gaps 9;
Pred. No. 7.2e-92;	Oy	QY 12 IYFGIC-ALVSSGLRGCPGRG-IGRRRHKP-LTPLAYKOFIPNVAEKTGASGRYEGK 68
Pred. No. 1.1e-92;	Db	Db 7 LIPPCCLALLALSAQSCGGPGRGPVGRVRRYVKQLVPUYKOFVPSMPERTLGASGPAGR 66
Mismatches	Oy	QY 69 ITRNSERFKEELTPNPYNDITPKDEENGADRLLMTORCKKLNALATSYMNONPGVKLRT 128
Indels	Db	Db 67 VTRGSEFRDLVNVNPYNDITPKDEENGADRLLMTORCKKLNALATSYMNONPGVKLRT 126
Gaps	Oy	QY 129 EGWDDEGHHSERSELSLHVGRADITTSRDSDRSKYGMLARAVEAGFDWVYTESRAHINCSV 188
9;	Db	Db 127 EGWDDEGHHSERSELSLHVGRADITTSRDSDRSKYGMLARAVEAGFDWVYTESRAHINCSV 186
Matches	Oy	QY 189 KAENSVAKSSCCFGPSATVHLEHGKHLVQLDKLSPGDRVLAADDERLYSDFLTLDRM 248
241;	Db	Db 187 KADNSLAVRAGGCFFPGNATVRLSGERKGRLRBLHGRDWWVLAADAGRVVPPVFLFLRD 246
Conservative	Oy	QY 249 DSSRKLFYVIEETRQPRLLTAAHILFVAFQHNOSEATGTSQGQALFASVNVKPGQRVY 308
56;	Db	Db 247 LQRASSFVAVETERPRKLPLTPWHLFVA---RGPAQGDA---PVFAARRAGDS---V 300
Mismatches	Oy	QY 309 LGEGGQOLLPSPVHSYSLREASGAVPLTAQGTILNRVLAACYAVIEHSAWAHAFAP 368
84;	Db	Db 301 LAPGGDALQPARVARVA-REEAVGVPAFLAHGLLVDNLVASCYAVLESHQWAHAFAP 359
Indels	Oy	QY 369 FRLAQGILALCQDPGAPTAATTGTHWYSLYLRT 405
16;	Db	Db 360 LRLHA-LGALLPGGV---QPTGMHWYSLYLRL 390
16;	RESULT	RESULT 9
8	Db	A64400
Residue 49425	Db	segment polarity protein hedgehog - fruit fly (<i>Drosophila melanogaster</i>)
Indian hedgehog protein - mouse (fragment)	Db	Nr. Alternate names: hh protein
C;Species: <i>Mus musculus</i> (house mouse)	Db	C;Species: <i>Drosophila melanogaster</i>
Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000	Db	C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 10-Dec-1999
C;Accession: CA9425	Db	C;Accession: A46400; JN0501; A44480
R;Echelard, Y.; Epstein, D.J.; St-Jacques, B.; Shen, L.; Mohler, J.; McMahon, J.A.; McMahon, A.; Title: Sonic hedgehog, a member of a family of putative signaling molecules, is implicated in the development of the nervous system. Cell 75, 1417-1430, 1993	Db	R;Tashiro, T.; Eaton, S.; Kornberg, T.B.
A;Title: Sonic hedgehog, a member of a family of putative signaling molecules, is implicated in the development of the nervous system.	Db	Genes Dev. 6, 2635-2645, 1992
A;Reference number: A49425; MUID:94094334; PMID:7916661	Db	A;Title: The <i>Drosophila</i> hedgehog gene is expressed specifically in posterior compartmentalized domains. Development 121, 183-189, 1993
A;Accession: C49425	Db	A;Title: Structure and expression of hedgehog, a <i>Drosophila</i> segment-polarity gene required for segment formation. Development 121, 183-189, 1993
A;Status: preliminary	Db	A;Title: Structure and expression of hedgehog, a <i>Drosophila</i> segment-polarity gene required for segment formation. Development 121, 183-189, 1993
A;Molecule type: mRNA	Db	A;Title: Structure and expression of hedgehog, a <i>Drosophila</i> segment-polarity gene required for segment formation. Development 121, 183-189, 1993
A;Residues: 1-336 <ECB>	Db	A;Title: Structure and expression of hedgehog, a <i>Drosophila</i> segment-polarity gene required for segment formation. Development 121, 183-189, 1993
A;Cross-references: GB:X76291	Db	A;Title: Structure and expression of hedgehog, a <i>Drosophila</i> segment-polarity gene required for segment formation. Development 121, 183-189, 1993
C;Superfamily: sonic hedgehog protein	Db	A;Title: Structure and expression of hedgehog, a <i>Drosophila</i> segment-polarity gene required for segment formation. Development 121, 183-189, 1993
Query Match	Db	A;Cross-references: GB:L05404
Best Local Similarity	Db	A;Note: it is uncertain whether Met-1 or Met-51 is the initiator
47.4%; Score 1052; DB 2; Length 336;	Db	A;Note: intron positions were determined from partial DNA sequence
Matches 215; Conservative 60.4%; Pred. No. 1.2e-9;	Db	R;Lee, J.J.; von Kessler, D.P.; Parks, S.; Beachy, P.A.
Mismatches 37; Mismatches 80; Indels 24; Gaps 5;	Db	Cell 71, 33-50, 1992
Db	Db	A;Title: Secretion and localized transcription suggest a role in positional signaling
1	Db	A;Reference number: A34380
ERFKELTPNYPNDITPKDEENGADRLLMTORCKKLNALATSYMNONPGVKLRTGEWDE	Db	A;Accession: A43380
74	Db	A;Status: preliminary; not compared with conceptual translation
ERFKELTPNYPNDITPKDEENGADRLLMTORCKKLNALATSYMNONPGVKLRTGEWDE	Db	A;Molecule type: DNA
133	Db	A;Residues: 1-471 <LEE>
ERFKELTPNYPNDITPKDEENGADRLLMTORCKKLNALATSYMNONPGVKLRTGEWDE	Db	A;Cross-references: GB:L02793; NID:9157609; PID:9157610
133	Db	A;Note: sequence extracted from NCBP backbone (NCBIP:11418)
ERFKELTPNYPNDITPKDEENGADRLLMTORCKKLNALATSYMNONPGVKLRTGEWDE	Db	C;Comment: This protein is required for cell-cell communication.
133	Db	A;Cross-references: FlyBase:FBgn004644
ERFKELTPNYPNDITPKDEENGADRLLMTORCKKLNALATSYMNONPGVKLRTGEWDE	Db	A;Introns: 160/3; 248/1
60	Db	C;Genetics: hh
ERFKELTPNYPNDITPKDEENGADRLLMTORCKKLNALATSYMNONPGVKLRTGEWDE	Db	A;Keywords: transmembrane protein
1	Db	C;Superfamily: sonic hedgehog protein
ERFKELTPNYPNDITPKDEENGADRLLMTORCKKLNALATSYMNONPGVKLRTGEWDE	Db	F;62-82/Domain: transmembrane #status predicted <TM>
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41.7%; Score 925; DB 2; Length 471;	Db	Best Local Similarity
47.8%; Pred. No. 6.8e-69; Mismatches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;	Db	Pred. No. 6.8e-69;
1.1e-92;	Db	Matches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;
Oy	Db	Query Match
6	Db	Best Local Similarity
41.7%; Score 925; DB 2; Length 471;	Db	Pred. No. 6.8e-69;
47.8%; Pred. No. 6.8e-69; Mismatches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;	Db	Matches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;
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41.7%; Score 925; DB 2; Length 471;	Db	Pred. No. 6.8e-69;
47.8%; Pred. No. 6.8e-69; Mismatches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;	Db	Matches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;
Oy	Db	Query Match
6	Db	Best Local Similarity
41.7%; Score 925; DB 2; Length 471;	Db	Pred. No. 6.8e-69;
47.8%; Pred. No. 6.8e-69; Mismatches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;	Db	Matches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;
Oy	Db	Query Match
6	Db	Best Local Similarity
41.7%; Score 925; DB 2; Length 471;	Db	Pred. No. 6.8e-69;
47.8%; Pred. No. 6.8e-69; Mismatches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;	Db	Matches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;
Oy	Db	Query Match
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41.7%; Score 925; DB 2; Length 471;	Db	Pred. No. 6.8e-69;
47.8%; Pred. No. 6.8e-69; Mismatches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;	Db	Matches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;
Oy	Db	Query Match
6	Db	Best Local Similarity
41.7%; Score 925; DB 2; Length 471;	Db	Pred. No. 6.8e-69;
47.8%; Pred. No. 6.8e-69; Mismatches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;	Db	Matches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;
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41.7%; Score 925; DB 2; Length 471;	Db	Pred. No. 6.8e-69;
47.8%; Pred. No. 6.8e-69; Mismatches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;	Db	Matches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;
Oy	Db	Query Match
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41.7%; Score 925; DB 2; Length 471;	Db	Pred. No. 6.8e-69;
47.8%; Pred. No. 6.8e-69; Mismatches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;	Db	Matches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;
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41.7%; Score 925; DB 2; Length 471;	Db	Pred. No. 6.8e-69;
47.8%; Pred. No. 6.8e-69; Mismatches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;	Db	Matches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;
Oy	Db	Query Match
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41.7%; Score 925; DB 2; Length 471;	Db	Pred. No. 6.8e-69;
47.8%; Pred. No. 6.8e-69; Mismatches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;	Db	Matches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;
Oy	Db	Query Match
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41.7%; Score 925; DB 2; Length 471;	Db	Pred. No. 6.8e-69;
47.8%; Pred. No. 6.8e-69; Mismatches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;	Db	Matches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;
Oy	Db	Query Match
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41.7%; Score 925; DB 2; Length 471;	Db	Pred. No. 6.8e-69;
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41.7%; Score 925; DB 2; Length 471;	Db	Pred. No. 6.8e-69;
47.8%; Pred. No. 6.8e-69; Mismatches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;	Db	Matches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;
Oy	Db	Query Match
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41.7%; Score 925; DB 2; Length 471;	Db	Pred. No. 6.8e-69;
47.8%; Pred. No. 6.8e-69; Mismatches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;	Db	Matches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;
Oy	Db	Query Match
6	Db	Best Local Similarity
41.7%; Score 925; DB 2; Length 471;	Db	Pred. No. 6.8e-69;
47.8%; Pred. No. 6.8e-69; Mismatches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;	Db	Matches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;
Oy	Db	Query Match
6	Db	Best Local Similarity
41.7%; Score 925; DB 2; Length 471;	Db	Pred. No. 6.8e-69;
47.8%; Pred. No. 6.8e-69; Mismatches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;	Db	Matches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;
Oy	Db	Query Match
6	Db	Best Local Similarity
41.7%; Score 925; DB 2; Length 471;	Db	Pred. No. 6.8e-69;
47.8%; Pred. No. 6.8e-69; Mismatches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;	Db	Matches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;
Oy	Db	Query Match
6	Db	Best Local Similarity
41.7%; Score 925; DB 2; Length 471;	Db	Pred. No. 6.8e-69;
47.8%; Pred. No. 6.8e-69; Mismatches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;	Db	Matches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;
Oy	Db	Query Match
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41.7%; Score 925; DB 2; Length 471;	Db	Pred. No. 6.8e-69;
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41.7%; Score 925; DB 2; Length 471;	Db	Pred. No. 6.8e-69;
47.8%; Pred. No. 6.8e-69; Mismatches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;	Db	Matches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;
Oy	Db	Query Match
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41.7%; Score 925; DB 2; Length 471;	Db	Pred. No. 6.8e-69;
47.8%; Pred. No. 6.8e-69; Mismatches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;	Db	Matches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;
Oy	Db	Query Match
6	Db	Best Local Similarity
41.7%; Score 925; DB 2; Length 471;	Db	Pred. No. 6.8e-69;
47.8%; Pred. No. 6.8e-69; Mismatches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;	Db	Matches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;
Oy	Db	Query Match
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41.7%; Score 925; DB 2; Length 471;	Db	Pred. No. 6.8e-69;
47.8%; Pred. No. 6.8e-69; Mismatches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;	Db	Matches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;
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41.7%; Score 925; DB 2; Length 471;	Db	Pred. No. 6.8e-69;
47.8%; Pred. No. 6.8e-69; Mismatches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;	Db	Matches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;
Oy	Db	Query Match
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Oy	Db	Query Match
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47.8%; Pred. No. 6.8e-69; Mismatches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;	Db	Matches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;
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47.8%; Pred. No. 6.8e-69; Mismatches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;	Db	Matches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;
Oy	Db	Query Match
6	Db	Best Local Similarity
41.7%; Score 925; DB 2; Length 471;	Db	Pred. No. 6.8e-69;
47.8%; Pred. No. 6.8e-69; Mismatches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;	Db	Matches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;
Oy	Db	Query Match
6	Db	Best Local Similarity
41.7%; Score 925; DB 2; Length 471;	Db	Pred. No. 6.8e-69;
47.8%; Pred. No. 6.8e-69; Mismatches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;	Db	Matches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;
Oy	Db	Query Match
6	Db	Best Local Similarity
41.7%; Score 925; DB 2; Length 471;	Db	Pred. No. 6.8e-69;
47.8%; Pred. No. 6.8e-69; Mismatches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;	Db	Matches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;
Oy	Db	Query Match
6	Db	Best Local Similarity
41.7%; Score 925; DB 2; Length 471;	Db	Pred. No. 6.8e-69;
47.8%; Pred. No. 6.8e-69; Mismatches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;	Db	Matches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;
Oy	Db	Query Match
6	Db	Best Local Similarity
41.7%; Score 925; DB 2; Length 471;	Db	Pred. No. 6.8e-69;
47.8%; Pred. No. 6.8e-69; Mismatches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;	Db	Matches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;
Oy	Db	Query Match
6	Db	Best Local Similarity
41.7%; Score 925; DB 2; Length 471;	Db	Pred. No. 6.8e-69;
47.8%; Pred. No. 6.8e-69; Mismatches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;	Db	Matches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;
Oy	Db	Query Match
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41.7%; Score 925; DB 2; Length 471;	Db	Pred. No. 6.8e-69;
47.8%; Pred. No. 6.8e-69; Mismatches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;	Db	Matches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;
Oy	Db	Query Match
6	Db	Best Local Similarity
41.7%; Score 925; DB 2; Length 471;	Db	Pred. No. 6.8e-69;
47.8%; Pred. No. 6.8e-69; Mismatches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;	Db	Matches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;
Oy	Db	Query Match
6	Db	Best Local Similarity
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47.8%; Pred. No. 6.8e-69; Mismatches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;	Db	Matches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;
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47.8%; Pred. No. 6.8e-69; Mismatches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;	Db	Matches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;
Oy	Db	Query Match
6	Db	Best Local Similarity
41.7%; Score 925; DB 2; Length 471;	Db	Pred. No. 6.8e-69;
47.8%; Pred. No. 6.8e-69; Mismatches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;	Db	Matches 197; Conservative 65; Mismatches 132; Indels 18; Gaps 6;
Oy	Db	Query Match
6	Db	Best Local Similarity
41.7%; Score 925; DB 2; Length 471;	Db	Pred. No. 6.8e-69;
47.8%; Pred. No. 6.8e-69; Mismatches 197; Conservative 65; Mismatches 132;		

QY 186 CSWKAENSAVAKGGCGPSATVHLEGGTKLVKLDLSPGDRVLAAADGRLLYSDELTFL 245
 |||||::|::: ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 243 CSVKSDDSISSHWHGCCTPESTALLSESVRKPLGELSIDGRVLSMTANGOAVTEVILEM 302

QY 246 DRMDSSRKLKYVLTETRPARLLTAHLFLFVAPQHNOSEATGSTSQALFASNVPRQR 305
 ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 303 DRNLEQMQNFVQLHT-DGGAVLTVPAHLVSWWQESQKLIT-----FVERDRIEKKQ 354

QY 306 VYVLGEQGQQLPASVHSV-SLRREEASGAYAAPTQAGTILINRVLASCYAVIEEHSAHW 364
 | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 355 VYLVDEGELRERQVVKVGSR--SRGVVAIATRECTIVVNSVANSCYAVINSQSLAHW 412

QY 365 AFAPFLRLAQGLIA-----ALCPDGAIPTAATTGIGHWSRLYLIGSWM 410
 ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 413 GLAPMRLLUSTLAWLPAKEQQLHSSPKVSSAQOONGIHWHYANALYKVKDYL 464

RESULT 10
 G02735
 desert hedgehog - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 21-DEC-1996 #sequence_revision 06-Jun-1997 #text_change 11-Jan-2000
 C;Accession: G02735
 R;Drummond, I.A.
 submitted to the EMBL Data Library, June 1996
 A;Reference number: HO1643
 A;Accession: G02735
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-94 <DRU>
 A;Cross-references: EMBL:U59748; NID:91401271; PID:91401272
 C;Genetics:
 A;Gene: HDHH
 C;Superfamily: sonic hedgehog protein

Query Match 20.2%; Score 449; DB 2; Length 94;
 Best Local Similarity 84.0%; Pred. No. 2.7e-30; Indels 0; Gaps 0;
 Matches 79; Conservative 13; Mismatches 2;

QY 87 TIRKDEENTGADRMLTORCKDKINNALATISVMQWPGVSKLRYVEGWDGDGHSEESLHYEG 146
 |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 1 IIFKDEENGADRLMRTECKERNLVALAVMMWPGVRLRVTEGWDGDGHHAODSLHYEG 60

QY 147 RAVDITTSRDRDKSKYGMALARLAVEAQDWVYTES 180
 |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 61 RAUDITTSRDRDKRYGLALARLAVEAQDWVYGG 94

RESULT 11
 T29550
 hypothetical protein ZK377.1 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 C;Accession: T29550
 R;Nhan, M.; Hawkins, J.
 submitted to the EMBL Data Library, February 1997
 A;Description: The sequence of C. elegans cosmid ZK377.
 A;Reference number: Z20639
 A;Accession: T29550
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-615 <NR>
 A;Cross-references: EMBL:U88183; PIDN:AAB52656_1; GSPDB:GN00020; CESP:T05C12.10
 A;Experimental source: clone T05C12
 C;Genetics:
 A;Gene: CESP-T05C12.10
 A;Map position: 2
 A;Introns: 31/3; 87/2; 141/3; 180/2; 203/3; 267/1; 776/2; 794/2; 834/2; 1086/3; 1143/
 Query Match 7.5%; Score 166; DB 2; Length 1207;
 Best Local Similarity 29.3%; Pred. No. 3.4e-05;
 Matches 55; Conservative 33; Mismatches 84; Indels 16; Gaps 6;

QY 187 SVKAENSAVAKGGCG-----CPSGSATVHLEGGTKLVKLDLSPGDRVLAAADGRLLYSDELTFL 241
 ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 942 AVLADTPGAGAGGGRSNCFSADSLV-TVTGQKRMDELQGDYVLYPSSGVNLKEVK 1000

QY 242 LTFLDRMDSRSRKLKYVLTETRPARLLTAHLFLFVAPQHNOSEATGSTSQALFASNVPRQR 295
 | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 1001 EMFYHREPPRTTRNFWVLYTKSGR-KLSLIGRHLLPVABCSSQEYQTMNPDGIDVAMRESK 1059

QY 296 FASNVKPGQRVYVLLGEQGQQLPASVHSVSLRREEASGAYAAPTQAGTILINRVLASCYAV 355
 ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 1060 YAKKARKEGCVLIDESGEVIADEIVRG--RMTNGIYSPMVTEGSLIVDVLSSCFSH 1117

QY 356 IEERSWAH 363
 ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 1118 LESHS-AH 1124

RESULT 13
 T24045
 hypothetical protein R08B4.1 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

Query Match 8.6%; Score 191.5; DB 2; Length 615;
 Best Local Similarity 28.9%; Pred. No 9.9e-08;
 Matches 58; Conservative 39; Mismatches 87; Indels 17; Gaps 7;

C;Accession: T24045
 R;White, S.
 submitted to the EMBL Data Library, November 1995
 A;Reference number: Z19834
 A;Accession: T24045
 A;Status: preliminary;
 A;Molecule type: DNA
 A;Residues: 1-1225 <WIL>
 A;Cross-references: EMBL:268008; PIDN:CAA92000.1; GSPDB:GN00028; CESP:R08B4.1
 C;Genetics:
 A;Gene: CESP:R08B4.1
 A;Map position: X
 A;Introns: 53/2; 113/1; 152/3; 204/3; 272/1; 354/1; 389/3; 714/3; 839/3; 877/1; 960/3; 1
 Query Match 7.1%; Score 158; DB 2; Length 1225;
 Best Local Similarity 27.8%; Pred. No. 0.00015; Mismatches 52; Conservative 37; Indels 16; Gaps 7;
 Matches 52; Mismatches 82; Indels 16; Gaps 7;
 Qy 192 NSVAKSGCGCPGSAVHLEHGKTKVLDKLSGPDRVLAADAGRLLSDFLTFLDRMDSS 251
 Db 1012 SALVAAATGACFSLDTW-TTPTGKKRMQDIDGDYVLTADL-KRYFTPTLWTHREPK 1069
 Qy 252 RKLFIYVIETQPRARLLTAHLLE--VAPOHNOSEATGSTSGOALFASNVKGGQRTV 308
 Db 1070 VQEFLTINTMYGKT-LRISRHFMNRKKGKSYQYIKMPHPDRAIFASDLEGDCVWV 1128
 Qy 309 L-GIGGGQQLIPASVHSVSLREEASGAYAALTAGTQTLINRVLASCYAYEETHSWA--H 363
 Db 1129 LYKGIVRQKQIETITRSV---RTGIYSPLTNNGRIVNDMLASCISEIQQNVLQTTF 1183
 Qy 364 WAFAPFR 370
 Db 1184 WAYDKLR 1190

RESULT 14

T34504 hypothetical protein ZK1290.12 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C;Accession: T34504
 R;Batch: A.
 submitted to the EMBL Data Library, July 1995
 A;Description: The sequence of C. elegans cosmid ZK1290.
 A;Reference number: Z21535
 A;Accession: T34504
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-484 <TAI>
 A;Cross-references: EMBL:U21308; PIDN:AAB93321.1; GSPDB:GN00020; CESP:ZK1290.12
 A;Experimental source: strain Bristol N2; clone ZK1290
 C;Genetics:
 A;Gene: CESP:ZK1290.12
 A;Map position: 2
 A;Introns: 66/3; 124/2; 181/2; 392/1
 Query Match 7.0%; Score 155; DB 2; Length 484;
 Best Local Similarity 24.9%; Pred. No. 6.9e-05; Mismatches 50; Conservative 50; Indels 19; Gaps 7;
 Matches 50; Mismatches 82; Indels 19; Gaps 7;
 Qy 194 VAAKSGGCFFPGSATVHLEHGKTKVLDKLSGPDRVLAADAGRLLSDFLTFLDRMDSSRK 253
 Db 283 VASGVACFGIGNSKV-MTPAGEKSMADLSVGDMWMTY-EKMWYTRAVSWLHLPLDTRKA 340
 Qy 254 LFVYVETPOTRPARLLTAHLFVFAPOHNOSEAGTSQQL-FASNYKPGQRVYLGEG 312
 Db 341 AFKLTTEQ-----GAIDMPHOHYKANCVTEMELVAEDMTIGDCMV--KE 389
 Qy 313 GQQLIPASVHSVSLREEASGAYAALTAGTQTLINRVLASCYAYE---EHSWAHWFAP 368
 Db 390 NEKLMNTTSEKSFTYE-TGYVAMTENGDLIVDVYDYLASCHNWKANTSHLFNFTPSV 448

Query Match 6.9%; Score 152.5; DB 2; Length 1021;
 Best Local Similarity 27.7%; Pred. No. 0.00036; Mismatches 49; Conservative 31; Indels 25; Gaps 7;
 Matches 49; Conservative 31; Mismatches 72; Indels 25; Gaps 7;
 Qy 214 GTKLYKDLSGDRVLAADAGRLLSDFLTFLDRMDSSRKLYVTFTRPAPRLLTAH 273
 Db 814 GKKRMDIEGIVLTADLK-TALESAITWIRHREPTEQFLEIKTDGKT-LQLTAGH 871
 Qy 274 LLFVA-----POHNOSEATGS-----TSGOALFASNYKPGQRYVYLGEGQOL 316
 Db 872 PIYATECRRYKPSKNSLNLNSIPERYRHLIDTLPPDSETKASQIKIGECLLI--HNGDOF 929
 Qy 317 LPASVHSVSLREEASGAYAALTAGTQTLINRVLASCYAYE---SWAHWFAPR 370
 Db 930 RMQKIDSIS-KTVSTGIGSYPLTENGRLVNDLASCYSEVOQVNLQTTFWAFDRLR 985

Search completed: February 20, 2003, 10:13:30
 Job time : 17.9865 secs

RESULT 15

T23252 hypothetical protein K02E2.2 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999
 C;Accession: T23252
 R;Lloyd, C.
 submitted to the EMBL Data Library, November 1995
 A;Reference number: Z19716
 A;Accession: T23252
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-1021 <WIL>
 A;Cross-references: EMBL:Z81560; PIDN:CA04547.1; GSPDB:GN00023; CESP:K02E2.1
 A;Experimental source: Clone K02E2
 C;Genetics:
 A;Gene: CESP:K02E2.2
 A;Map position: 5
 A;Introns: 41/1; 79/3; 131/3; 197/1; 262/1; 297/3; 566/3; 610/3; 735/3; 775/3; 834/3;
 Query Match 6.9%; Score 152.5; DB 2; Length 1021;
 Best Local Similarity 27.7%; Pred. No. 0.00036; Mismatches 49; Conservative 31; Indels 25; Gaps 7;
 Matches 49; Conservative 31; Mismatches 72; Indels 25; Gaps 7;
 Qy 214 GTKLYKDLSGDRVLAADAGRLLSDFLTFLDRMDSSRKLYVTFTRPAPRLLTAH 273
 Db 814 GKKRMDIEGIVLTADLK-TALESAITWIRHREPTEQFLEIKTDGKT-LQLTAGH 871
 Qy 274 LLFVA-----POHNOSEATGS-----TSGOALFASNYKPGQRYVYLGEGQOL 316
 Db 872 PIYATECRRYKPSKNSLNLNSIPERYRHLIDTLPPDSETKASQIKIGECLLI--HNGDOF 929

GeneCore version 5.1.3
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OM protein - protein search, using sw model.**Run on:**

February 20, 2003, 10:07:32 ; Search time 13.0329 Seconds
 (without alignments)

1352.533 Million cell updates/sec

Title:

US-09-827-110A-10

Perfect score:

2218

Sequence:

1 MVEMLILTRILLYFICALL.....GSWVLDGDAHLHPLGMVAPAS 425

Scoring table:

BLOSUM2

Gapext

0.5

Searched:

112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters:

112892

Minimum DB seq length:

0

Maximum DB seq length:

200000000

Post-processing:

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SwissProt;40;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2218	100.0	425	1 SHH_CHICK	091035 gallus gallus
2	1807	81.5	462	1 SHH_HUMAN	Q15465 homosapien
3	1791	80.7	437	1 SHH_MOUSE	Q62226 mus musculus
4	1780	80.3	437	1 SHH_RAT	Q3673 rattus norvegicus
5	1603	72.3	432	1 SHH_CYNPY	Q90385 cynops pyrrhura
6	1533	69.1	444	1 SHH_XENLA	Q92000 xenopus laevis
7	1494	67.4	418	1 SHH_BRARE	Q92000 brachydanio
8	1458	65.7	416	1 TWHH_BRARE	Q90419 brachydanio
9	1295	58.4	408	1 DHH_CHICK	Q93938 gallus gallus
10	1286	58.0	409	1 IHH_XENLA	Q91611 xenopus laevis
11	1277	57.6	411	1 IHL_MOUSE	P91812 mus musculus
12	1265	57.1	411	1 IHH_HUMAN	Q14623 homo sapiens
13	1232	55.6	412	1 IHL_BRARE	Q98862 brachydanio
14	1200	54.1	396	1 DHH_MOUSE	Q61488 mus musculus
15	1198	54.0	396	1 DHH_XENLA	Q93323 homo sapiens
16	1129	50.9	395	1 DHHL_XENLA	Q91610 xenopus laevis
17	1119	50.5	398	1 DHH2_XENLA	Q91611 xenopus laevis
18	925	41.7	471	1 HH_DROME	Q02936 drosophila melanogaster
19	876	39.7	481	1 HH_DROME	P56574 drosophila melanogaster
20	603	27.2	121	1 SHH_RASSEL	P79858 rasbora elegans
21	600	27.1	121	1 SHH_CARAU	P79691 carassius auratus
22	271	121	1 SHH_PUNTE	P79850 puntius tetrazona	
23	599	27.0	121	1 SHH_RASHE	P79864 rasbora heteromorpha
24	599	27.0	121	1 SHH_RASPA	P79869 rasbora pavonia
25	598	27.0	121	1 SHH_TANAL	P79915 tanichthys tanichthys
26	597	26.9	121	1 SHH_AMBCH	P79682 amblypharynx pseudoplatensis
27	595	26.8	121	1 SHH_DANAA	Q13235 danio aequipinnatus
28	595	26.8	121	1 SHH_DANAE	Q13234 danio aequipinnatus
29	595	26.8	121	1 SHH_DANAF	Q13245 danio franklini
30	595	26.8	121	1 SHH_DANAK	P79709 danio kerri
31	595	26.8	121	1 SHH_DANER	P79719 danio pulchellum
32	595	26.8	121	1 SHH_DANPU	P79838 puntius conchophilus
33	595	26.8	121	1 SHH_DEVDE	P79839 pseudoraspasias devoratio

ALIGNMENTS

34	595	26.8	121	1 SHH_DEVMA	Q13247 devario malabaricus
35	595	26.8	121	1 SHH_DEVPA	Q13250 devario patersoni
36	591	26.6	121	1 SHH_PUNCO	P79838 puntius conchophilus
37	396	17.9	88	1 DHH_BRARE	P79729 brachydanio
38	293	13.2	58	1 IHL_CARAU	P79693 carassius aurolineatus
39	293	13.2	58	1 IHH_DANAT	Q13240 danio affinis
40	293	13.2	58	1 IHH_DANPE	P79711 danio kerri
41	293	13.2	58	1 IHH_DEVDE	P79719 danio pulchellum
42	293	13.2	58	1 IHH_PUNTE	Q13243 devario devoratio
43	293	13.2	58	1 IHL_RASEL	P79852 puntius tetrazona
44	293	13.2	58	1 SHH_PSEPR	P79860 rasbora elephas
45	289	13.0	58	1 SHH_PSEPR	P79839 pseudoraspasias devoratio

CC THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF
CC A CHOLESTEROL MOETY TO THE C-TERMINAL OF THE NEWLY GENERATED N-
CC TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS
CC TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION
CC OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE
CC ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE
CC C-PRODUCT HAS NO SIGNALING ACTIVITY.
CC -1- SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.

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CC

CC EMBL: L28099; AAA72428.1; -
DR HSSP: 062226; IvhH.
DR MEROPS; C45_001; -
DR Interrho; IPR003320; HH_signal.
DR Interrho; IPR001767; Hedgehog_hint.
DR Interrho; IPR003585; Hedgehog_hintC.
DR Interrho; IPR003587; Hedgehog_hintN.
DR Interrho; IPR002203; Intein.
DR Interrho; IPR001657; SonichH.
DR Pfam; PF01079; Hint; I.
DR PRINTS; PRO0632; SONICHHOC.
DR PRODOM; PD003042; HH_lSignal; 1.
DR SMART; SM00305; HintC; I.
DR PROSITE; PS50817; INFEIN_N_TER; 1.
KW Developmental protein; Autocatalytic cleavage; Hydrolase; Protease;
Signal; Lipoprotein; Palmitate;
Signal

FT 1 26 POTENTIAL.

FT CHAIN 27 425 SONIC HEDGEHOG PROTEIN_N-PRODUCT.
FT CHAIN 27 425 SONIC HEDGEHOG PROTEIN_C-PRODUCT.
FT SITE 200 201 CLEAVAGE (AUTO-) (PROBABLE).
FT SITE 246 246 INVOLVED IN CHOLESTEROL TRANSFER (BY
FT SIMILARITY).

FT SITE 270 270 INVOLVED IN AUTO-CLEAVAGE (BY
FT ACT_SITE 273 273 SIMILARITY).
FT BINDING 200 200 CHOLESTEROL (BY SIMILARITY).
FT DOMAIN 390 393 POLY-THR.
FT LIPID 27 27 PALMITATE (BY SIMILARITY).
FT SEQUENCE 425 AA; 46474 MW; DA9627443D4A0173 CRC64;

Query Match 100.0%; Score 2218; DB 1; Length 425;
Best Local Similarity 100.0%; Prev. No. 1.7e-172;
Matches 425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC

CC 1 MVEMLLITRLITLVGFTCALLVSSGLTCGRGRGIGKRRHPPKLTPLAYKQIPNVAEKTG 60
Db 1 MVEMLLITRLITLVGFTCALLVSSGLTCGRGRGIGKRRHPPKLTPLAYKQIPNVAEKTG 60

CC 61 ASGRREGKTRNSERKELTPTNYNDIIFDEENGADRLMTORCKDKLNALASYANQW 120
Db 61 ASGRREGKTRNSERKELTPTNYNDIIFDEENGADRLMTORCKDKLNALASYANQW 120

CC 121 PGVKLKVTEGDEGHSESLHNGRAVDITTSQRDRSKYGMALARVAGDWYYES 180
Db 121 PGVKLKVTEGDEGHSESLHNGRAVDITTSQRDRSKYGMALARVAGDWYYES 180

CC 181 KAHTICSVKAENSAKSGCFPGSATVHLHGTRKLVKDLSPDRVLAADADRLYSD 240
Db 181 KAHTICSVKAENSAKSGCFPGSATVHLHGTRKLVKDLSPDRVLAADADRLYSD 240

CC 241 FLTFLORMDSRKLKFVIERQPRARLLTAHLIFVAPQHQNEATGSPSQQLAFASWV 300
Db 301 KPGQRYVVLGGQQQLPASVHSVSREESAGAYAPLTAQGTILNVLASCYAVIEHS 360
Db 301 KPGQRYVVLGGQQQLPASVHSVSREESAGAYAPLTAQGTILNVLASCYAVIEHS 360

CC 361 WAHWAFAPIERLAQGLLALCDGAIAPTAATTGTHWYSRLYRIGSWVLDALHPLGN 420
Db 361 WAHWAFAPIERLAQGLLALCDGAIAPTAATTGTHWYSRLYRIGSWVLDALHPLGN 420

Oy 421 VAPAS 425

Db 421 VAPAS 425

RESULT 2

SHH_HUMAN	STANDARD;	PRT;	462 AA.
ID SHH_HUMAN			
AC Q15465;			
DT 15-JUL-1999 (Rel. 38, Created)			
DT 15-JUN-2002 (Rel. 41, Last annotation update)			
DE Sonic hedgehog protein precursor (SHH) (HHG-1).			
GN SHH.			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX NCBI_TaxId=9605;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC TISSUE=Fetal lung;			
RX MEDLINE=96070431; PubMed=7590746;			
RA Marigo V., Roberts D.J., Lee S.M.K., Tsukurov O., Levi T.,			
RA Gastier J.M., Epstein D.J., Gilbert D.J., Copeland N.G., Seidman C.E.,			
RA Jenkins N.A., Seidman J.G., McMahon A.P., Tabin C.,			
RA "Cloning, expression, and chromosomal location of SHH and IHH: two			
RT human homologues of the Drosophila segment polarity gene hedgehog.",			
RT Genomics 28:44-51(1995).			
RN [2]			
RP SEQUENCE FROM N.A.			
RA TATE G., Kishimoto K., Mitsuya T.,			
RA "Expression of Sonic hedgehog and its receptor Patched/Smoothened in			
RT human cancer cell lines and embryonic organs",			
RT J. Biochem. Mol. Biol. Biophys. 4:27-34(2000).			
RN [3]			
RP SEQUENCE OF 1-187 FROM N.A.			
RA Strong C., Graves T., Sutler C., Ozersky P.,			
RA Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.			
RN [4]			
RP SEQUENCE OF 119-167 FROM N.A.			
RX MEDLINE=9236997; PubMed=7720571;			
RA Chang D.T., Lopez A., von Kessler D.P., Chiang C., Simandl B.K.,			
RA Zhao R., Seldin M.F., Fallon J.F., Beachy P.A.,			
RA "Products, genetic linkage and limb patterning activity of a murine			
RT hedgehog gene,"			
RT Development 120:3339-3353(1994).			
RN [5]			
RP PALMITOYLATION			
RX MEDLINE=98256319; PubMed=9593755;			
RA Pepinsky R.B., Zeng C., Wen D., Ryhorn P., Baker D.P., Williams K.P.,			
RA Bixler S.A., Ambrose C.M., Garber E.A., Miatkowski K., Taylor F.R.,			
RA Wang E.A., Galde A.,			
RT "Identification of a palmitic acid-modified form of human Sonic			
RT hedgehog,"			
RT J. Biol. Chem. 273:14037-14045(1998).			
RN [6]			
RP VARIANTS HPE ARG-31; GLY-117 AND ARG-117.			
RX MEDLINE=97051337; PubMed=8895572;			
RA Roessler E., Belloni E., Gaudenz K., Jay P., Berta P., Scherer S.W.,			
RA Tsui L.-C., Muenke M.,			
RT "Mutations in the human Sonic hedgehog gene cause holoprosencephaly.",			
RL Nat. Genet. 14:357-360(1996).			
RN [7]			

RP	VARIANTS HPE ARG-31; GLY-117; ARG-117; GLU-224; THR-226 AND THR-383.	CC	-1- SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.
RX	MEDLINE=88027056; PUBMED=930262;	CC	-1- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
RA	Roesler E., Belloni E., Gaudenz K., Vargas F., Scherer S.W.,	CC	WWW= http://www.infobiogen.fr/services/chromcancer/Genes/SHHID378.html .
RA	Tsui L.-C., Muenke M.;	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
RT	*Mutations in the C-terminal domain of Sonic hedgehog cause	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
RT	holoprosencephaly.;	CC	the European Bioinformatics Institute. There are no restrictions on its
RL	Hum. Mol. Genet. 6:1847-1853(1997).	CC	use by non-profit institutions as long as its content is in no way
RN	[8]	CC	modified and this statement is not removed. Usage by and for commercial
RP	VARIANTS HPE HIS-100; GLN-188 AND ASN-222.	CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@sb-sib.ch).
RX	MEDLINE=9371775; PUBMED=1041331;	CC	-----
RA	Odent S., Atti-Bitach T., Blayau M., Mathieu M., Aug J.,	CC	-----
RA	Delezo de A.L., Gail J.J., Le Marec B., Munich A., David V.,	CC	-----
RA	Vekemans M.;	CC	-----
RT	*Expression of the sonic hedgehog (SHH) gene during early human	CC	-----
RT	development and phenotypic expression of new mutations causing	CC	-----
RT	holoprosencephaly.;	CC	-----
RL	Hum. Mol. Genet. 8:1683-1689(1999).	CC	-----
RN	[9]	CC	-----
RP	VARIANTS HPE V-88; K-115; R-236; 263-R--A-269 DEL; D-290; A-424 AND	DR	MIM: 142045; -.
RX	L-436.	DR	InterPro: IPR00320; HH_signal.
RA	MEDLINE=2002557; PUBMED=1056296;	DR	InterPro: IPR001767; Hedgehog_hint.
RA	Nanni L., Ming J.E., Bocian M., Steinhaus K., Bianchi D.W.,	DR	InterPro: IPR003586; Hedgehog_hinCC.
RA	Die-Smulders C., Giammari A., Imazumi K., Jones K.L., Campo M.D.,	DR	InterPro: IPR003587; Hedgehog_hinM.
RA	Martin R.A., Meinecke P., Pierpoint M.E.M., Robin N.H., Young I.D.,	DR	InterPro: IPR002203; Intein.
RA	Roessler E., Muenke M.;	DR	InterPro: IPR001657; SonicHH.
RT	*The mutational spectrum of the sonic hedgehog gene in	DR	Pfam: PF01079; Hint; 1.
RT	holoprosencephaly: SHH mutations cause a significant proportion of	DR	Pfam: PF01085; HH_signal; 1.
RL	autosomal dominant holoprosencephaly.;	DR	PRINTS; PR00632; SONICHHG.
CC	Mol. Genet. 8:2479-2488(1999).	DR	PRODOM; PD003042; HH_signal; 1.
CC	-1- FUNCTION: BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN	DR	SMART; SM00305; HinCC; 1.
CC	ASSOCIATION WITH SMOOTHED (SMO), TO ACTIVATE THE TRANSCRIPTION	DR	MIM: 600725; -.
CC	OF TARGET GENES. IN THE ABSENCE OF SHH, PTC REPRESSES THE	DR	InterPro: IPR00320; HH_signal.
CC	CONSTITUTIVE SIGNALING ACTIVITY OF SMO. ALSO REGULATES ANOTHER	DR	InterPro: IPR001767; Hedgehog_hint.
CC	TARGET, THE GLI ONCOGENE. INTERCELLULAR SIGNAL: SIGNAL PRODUCED	DR	InterPro: IPR003586; Hedgehog_hinCC.
CC	VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT: SIGNAL PRODUCED	DR	InterPro: IPR003587; Hedgehog_hinM.
CC	BY THE NOTOCHORD THAT INDUCES VENTRAL CELL FATE IN THE NEURAL TUBE	DR	InterPro: IPR002203; Intein.
CC	AND SOMITES, AND THE POLARIZING SIGNAL FOR PATTERNING OF THE	DR	InterPro: IPR001657; SonicHH.
CC	ANTERIOR-POSTERIOR AXIS OF THE DEVELOPING LIMB BUD. DISPLAYS BOTH	DR	Pfam: PF01079; Hint; 1.
CC	FLOOR PLATE-AND MOTOR NEURON-INDUCING ACTIVITY. THE THRESHOLD	DR	Pfam: PF01085; HH_signal; 1.
CC	CONCENTRATION OF N-PRODUCT REQUIRED FOR MOTOR NEURON INDUCTION IS	DR	PRINTS; PR00632; SONICHHG.
CC	5-FOLD LOWER THAN THAT REQUIRED FOR FLOOR PLATE INDUCTION (BY	DR	PRODOM; PD003042; HH_signal; 1.
CC	SIMILARITY).	DR	SMART; SM00305; HinCC; 1.
CC	-1- SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE	DR	MIM: 142045; -.
CC	CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE	DR	InterPro: IPR00320; HH_signal.
CC	CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM	DR	InterPro: IPR001767; Hedgehog_hint.
CC	TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).	DR	InterPro: IPR003586; Hedgehog_hinCC.
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN EPITAL, INTESTINE, LIVER, LUNG, AND	DR	InterPro: IPR003587; Hedgehog_hinM.
CC	KIDNEY. NOT EXPRESSED IN ADULT TISSUES.	DR	InterPro: IPR002203; Intein.
CC	-1- PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY	FT	SMART: SM00306; HintN; 1.
CC	AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN	FT	SMART: SM00307; INTEIN_N_TER; 1.
CC	THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF	FT	SMART: SM00308; INTEIN_N_TER; 1.
CC	A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N-	FT	SMART: SM00309; INTEIN_N_TER; 1.
CC	TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS	FT	SMART: SM00310; INTEIN_N_TER; 1.
CC	TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION	FT	SMART: SM00311; INTEIN_N_TER; 1.
CC	OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE	FT	SMART: SM00312; INTEIN_N_TER; 1.
CC	ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE	FT	SMART: SM00313; INTEIN_N_TER; 1.
CC	C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).	FT	SMART: SM00314; INTEIN_N_TER; 1.
CC	-1- DISEASE: DEFECTS IN SHH ARE THE CAUSE OF HOLOPROSENCEPHALY (HPE).	FT	SMART: SM00315; INTEIN_N_TER; 1.
CC	HPE IS A CLINICALLY VARIABLE AND GENETICALLY HETEROGENOUS	FT	SMART: SM00316; INTEIN_N_TER; 1.
CC	MALFORMATION IN WHICH THE DEVELOPING FOREBRAIN FAILS TO CORRECTLY	FT	SMART: SM00317; INTEIN_N_TER; 1.
CC	SEPARATE INTO RIGHT AND LEFT HEMISPHERES. IN THE MOST SEVERE FORM	FT	SMART: SM00318; INTEIN_N_TER; 1.
CC	(ALOBAR HPE), THERE IS NO INTERHEMISPHERIC FISSURE, A SINGLE BRAIN,	FT	SMART: SM00319; INTEIN_N_TER; 1.
CC	VENTRICLE IS PRESENT. HPE IS ASSOCIATED WITH SEVERAL DISTINCT	FT	SMART: SM00320; INTEIN_N_TER; 1.
CC	FACIES AND PHENOTIC VARIABILITY. IN THE MOST EXTREME CASES,	FT	SMART: SM00321; INTEIN_N_TER; 1.
CC	ANOPHRALMIA OR CYCLOPIA IS EVIDENT ALONG WITH A CONGENITAL	FT	SMART: SM00322; INTEIN_N_TER; 1.
CC	ABSENCE OF THE MATURE NOSE. THE LESS SEVERE FORM FEATURES FACIAL	FT	SMART: SM00323; INTEIN_N_TER; 1.
CC	DYSMORPHIA CHARACTERIZED BY OCULAR HYPERTELORISM, DEFECTS OF THE	FT	SMART: SM00324; INTEIN_N_TER; 1.
CC	UPPER LIP AND/OR NOSE, AND ABSENCE OF THE OLFACTORY NERVES OR	FT	SMART: SM00325; INTEIN_N_TER; 1.
CC	CORPUS CALLOSUM. THE MAJORITY OF HPE CASES ARE APPARENTLY	FT	SMART: SM00326; INTEIN_N_TER; 1.
CC	SPORADIC, ALTHOUGH CLEAR EXAMPLES OF AUTOSOMAL DOMINANT (AD)	FT	SMART: SM00327; INTEIN_N_TER; 1.
CC	INHERITANCE HAVE BEEN DESCRIBED. INTERESTINGLY, UP TO 30% OF	FT	SMART: SM00328; INTEIN_N_TER; 1.
CC	OBIGATE CARRIERS OF HPE GENE IN AD PEDIGREES ARE CLINICALLY	FT	SMART: SM00329; INTEIN_N_TER; 1.
CC	UNAFFECTED.	FT	SMART: SM00330; INTEIN_N_TER; 1.
Query Match	81.5%; Score 1807; DB 1; Length 462;		

Best Local Similarity 77.8%; Pred. No. 4.4e-139; Matches 361; Conservative 22; Mismatches 37; Indels 44; Gaps 6;

Qy 4 MLLTTRILVGRCIALVSSGLCPCRGISRRHPRKPLTPLAYKOPIPNVAEKUGASG 63
 1 MLLARCLLVLVSLVSLVCGIACCPGRRPKLTPLAYKOPIPNVAEKUTGASG 60

Qy 64 RYEKGKTRNSERPEKELPPNYNPDIKEENGADRLMTORCKDKLNALATSYMNPVG 123
 1 ||| :||| ;||| :||| ;||| :||| ;||| :||| ;||| :||| ;||| :||| ;||| :||| ;||| :|||
 61 RYEGKISRNSERPEKELPPNYNPDIKEENGADRLMTORCKDKLNALATSYMNPVG 120

Qy 124 KLRVTEGDEGHSEESLHYGRGAVDITSDRDRSKYGMARLAVERAGEDFDDVYYESKAH 183
 1 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 121 KLRVTEGDEGHSEESLHYGRGAVDITSDRDRSKYGMARLAVERAGEDFDDVYYESKAH 180

Qy 184 IHCSVKAENSAVAKSGCCFPGSATVHLEGGTKLVKOLSPGPDRVLAADGRLLYSDFLT 243
 1 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 181 IHCSVKAENSAVAKSGCCFPGSATVHLEGGTKLVKOLSPGPDRVLAADGRLLYSDFLT 240

Qy 244 FLDRMDSSRKLYVETROPRALLTAHLFLVAPHOHNOSETG-----SNSG----- 292
 1 ||| | :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 241 FLDRDDGAKKVYVETREPRPLLTAAHLFLVAP-HNDS-ATGEPEASSGSGPPSGGA 298

Db 293 --QALLASNVPGQRYTVLGE--GGQQLPRAVSHVSLREERASAYAPLTQGQTLINR 347
 1 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 299 LGPRRALPSRVPGQRYTVVAAEDGDRRLPAVHSVTLSERAGAVAPLTQGTLINR 358

Qy 348 VILASCYAVIEEHSSWAHHAFAPERLAQGLAAL-----CP 381
 1 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 359 VILASCYAVIEEHSSWAHHAFAPERLAQGLAAL-----CP 381

Db 382 DGAAPTAATTGIRHWSRLYRIGSKYVLDSDALHPLGMVAPAS 425
 1 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 419 GAADAPGAGATAGIHWSQLQYQIGTWLDSEALHPLGMVAKSS 462

Qy 419 GAADAPGAGATAGIHWSQLQYQIGTWLDSEALHPLGMVAKSS 462

Db 293 --QALLASNVPGQRYTVLGE--GGQQLPRAVSHVSLREERASAYAPLTQGQTLINR 347

Db 299 LGPRRALPSRVPGQRYTVVAAEDGDRRLPAVHSVTLSERAGAVAPLTQGTLINR 358

RESULT 3

SHH_MOUSE STANDARD; PRT: 437 AA.

ID SHH MOUSE STANDARD; PRT: 437 AA.

AC Q2226; DT 15-JUL-1999 (Rel. 38, Created)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DT SONIC hedgehog protein precursor (SHH) (HhG-1).
 GN SHH OR HhG1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OX Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.
 RN NCBI_TaxID:10090;
 RP [1] SOURCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Embryo;
 RP MEDLINE=94054334; Published=191661;
 RA Echelard Y., Epstein D.J., St Jacques B., Shen L., Mohler J., McMahon J.A., McMahon A.P.;
 RT "Sonic hedgehog, a member of a family of putative signaling molecules, is implicated in the regulation of CNS polarity.";
 RT Cell 75:1417-1430(1993).
 RN [2] REVISION TO 122.
 RP STRAIN=C57BL/6J;
 RA McMahon A.P.;
 RA Submitted (Nov-1997) to the EMBL/GenBank/DDBJ databases.
 [3] SEQUENCE FROM N.A., AND AUTOPROTEOLYTIC CLEAVAGE.
 RX MEDLINE=95256997; Published=7720571;
 RA Chang D.T., Lopez A.R., von Kessler D.P., Chiang C., Simandl B.K., Zhao R., Seidin M.F., Fallon J.P., Beachy P.A.;
 RT "products, genetic linkage and limb patterning activity of a murine hedgehog gene." Development 120:3339-3353 (1994).
 RN [4] FUNCTION, AND AUTOPROTEOLYTIC CLEAVAGE.

RX MEDLINE=95254654; Published=7736596;
 RA Reelink H., Portier J.A., Chiang C., Tanabe Y., Chang D.T., Beachy P.A., Jessell T.M.;
 RT "Floor plate and motor neuron induction by different concentrations of the amino-terminal cleavage product of sonic hedgehog autoproteolysis."; Cell 81:445-455(1995).

RN [5] X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 34-195.
 RX MEDLINE=9605974; Published=477329;
 RA Hall T.M., Portier J.A., Beachy P.A., Leahy D.J.;
 RT "A potential catalytic site revealed by the 1.7-A crystal structure of the amino-terminal signalling domain of Sonic hedgehog."; Nature 378:212-216(1995).

CC -1- FUNCTION: BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENE (SMO), TO ACTIVATE THE TRANSCRIPTION CONSTITUTIVE SIGNALING ACTIVITY OF SMO. ALSO REGULATES ANOTHER TARGET, THE GLI ONCOGENE. INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT. SIGNAL PRODUCED BY THE NOTOCHORD THAT INDUCES VENTRAL CELL FATE IN THE NEURAL TUBE AND SOMITES, AND THE POLARIZING SIGNAL FOR PATTERNING OF THE ANTERIOR-POSTERIOR AXIS OF THE DEVELOPING LIMB BUD. DISPLAYS BOTH FLOOR PLATE AND MOTOR NEURON-INDUCING ACTIVITY. THE THRESHOLD CONCENTRATION OF N-PRODUCT REQUIRED FOR MOTOR NEURON INDUCTION IS 5-FOLD LOWER THAN THAT REQUIRED FOR FLOOR PLATE INDUCTION (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).

CC -1- TISSUE SPECIFICITY: EXPRESSED IN A NUMBER OF EMBRYONIC TISSUES INCLUDING THE NOTOCHORD, VENTRAL NEURAL TUBE, FLOOR PLATE, LONG BUD, ZONE OF POLARIZING ACTIVITY AND POSTERIOR DISTAL MESENCHYME OF LIMBS. IN THE ADULT, EXPRESSED IN LUNG AND NEURAL RETINA.

CC -1- DEVELOPMENTAL STAGE: FIRST DETECTABLE DURING GASTRULATION.

CC -1- INDUCTION: BY RETINOIC ACID.

CC -1- PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N-TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE C-PRODUCT HAS NO SIGNALING ACTIVITY.

CC -1- SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.

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CC -----

DR EMBL; X76290; CAA53922.1; DR
 RL PDB; 1VHH; 29-JAN-96; DR
 DR MEROPS; C46_002/- DR
 DR MGD; MGI:9297; Shh. DR
 DR InterPro; IPR00320; HH_signal. DR
 DR InterPro; IPR001767; Hedgehog_hint. DR
 DR InterPro; IPR005586; Hedgehog_hintC. DR
 DR InterPro; IPR005587; Hedgehog_hintN. DR
 DR InterPro; IPR002203; Intein. DR
 DR InterPro; IPR001657; Sonichh. DR
 DR Pfam; PF01079; Hint; 1. DR
 DR Pfam; PF01005; HH_signal; 1. DR
 DR PRINTS; PR00632; SONICHHOC. DR
 DR PRODOM; PD003042; HH_signal; 1. DR
 DR SMART; SM00305; HintC; 1. DR
 DR SMART; SM00306; HintN; 1. DR
 DR PROSITE; PS5081; INTIN_N-TER; 1.

KW Developmental protein; Autocatalytic cleavage; Hydrolase; Protease;
KW Signal; Lipoprotein; Palmitate; 3D-structure.
RA Ruiz J.; Altaba A.; Tanabe Y.; Placzek M.; Edlund T.; Jessell T.M.;
RA Dodd J.;
RT Floor plate and motor neuron induction by vhh-1, a vertebrate homolog
RT of hedgehog expressed by the notochord.";
RL Cell 76:761-775(1994).
-I_ FUNCTION: BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN
CC ASSOCIATION WITH SMOOTHED (SMO), TO ACTIVATE THE TRANSCRIPTION
CC OF TARGET GENES. IN THE ABSENCE OF SMO, PTC REPRESSES THE
CC CONSTITUTIVE SIGNALING ACTIVITY OF SMO, ALSO REGULATES ANOTHER
CC TARGET, THE GLI ONCOGENE. INTERCELLULAR SIGNAL ESSENTIAL FOR A
CC VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT: SIGNAL PRODUCED
CC BY THE NOTOCHORD THAT INDUCES VENTRAL CELL FATE IN THE NEURAL TUBE
CC AND SOMITES, AND THE POLARIZING SIGNAL FOR PATTERNING OF THE
CC ANTERIOR-POSTERIOR AXIS OF THE DEVELOPING LIMB BUD. DISPLACES BOTH
CC FLOOR PLATE-AND MOTOR NEURON-INDUCING ACTIVITY. THE THRESHOLD
CC CONCENTRATION OF N-PRODUCT REQUIRED FOR MOTOR NEURON INDUCTION IS
CC 5-FOLD LOWER THAN THAT REQUIRED FOR FLOOR PLATE INDUCTION (BY
CC SIMILARITY).
Q9Y4 Best Local Similarity 80.7%; Score 1791; DB 1; Length 437;
Q9Y4 Matches 354; Conservative 21; Mismatches 43; Indels 22; Gaps 6;
Q9Y4 QTY 4 MILLTRILLVGFICALIVSSGLJCGPGRRGIGKRRHPPKKLPLAYQFTIPNVAKTLAGS 63
Db 2 RVEGKTRNSERFKEFLTPNPNDFLIFKDEENTGADRMLTQRCKDKLNALATSYMNQNPVG 61
Q9Y4 64 RVEGKTRNSERFKEFLTPNPNDFLIFKDEENTGADRMLTQRCKDKLNALATSYMNQNPVG 123
Db 62 RVEGKTRNSERFKEFLTPNPNDFLIFKDEENTGADRMLTQRCKDKLNALATSYMNQNPVG 121
Q9Y4 124 KIRVTEGWEDQHHSEESLHYGRAVDITTSRDRSKYGMARLAVEAQFDWVYESKAH 183
Db 122 KLRVTEGWEDQHHSEESLHYGRAVDITTSRDRSKYGMARLAVEAQFDWVYESKAH 181
Q9Y4 184 IHCSVKAENSYAAKSGCCFGPSATVHLEGGTRKLVKDLSPGDRVLAADGRILYSPLT 243
Db 182 IHCSVKAENSYAAKSGCCFGPSATVHLEGGTRKLVKDLSPGDRVLAADGRILYSPLT 241
Q9Y4 244 FLDRMDSSRKLFKVYIETRQPRLLTAHHLFVAPQHNOSEATGSGTSG-QALFASNVPK 302
Db 242 FLDRDEGAKVVFVIEPLEPRERLLTAHHLFVAP-HNDS--GPTPGPSALFASVRP 297
Q9Y4 303 GORVYVIGE--GGQQLIPASVSVSLREEEASAYAQLTAGTQGTILINVLASCVAVIEHS 360
Db 298 GORVYVVAERGSDRRLPAVHVSTLREEAQAYAQLTAGTQGTILINVLASCVAVIEHS 357
Q9Y4 361 WAHWAFAFPFLAQGLLALCP-----DGATPTA-----ATTWNGIHMSRLYR 405
Db 358 WAHWAFAFPFLAHALLALAPARTDGGGGSPAAQASATEARGAEPPTAGIHWISQLIHI 417
Q9Y4 406 GSWVLDGDAHLPLGMVAPAS 425
Db 418 GTWLLDSETMMHPLGMVAKS 437

RESULT 4
SHH_RAT STANDARD; PRT: 437 AA.
ID SHH_RAT
AC Q63673;
DT 15-JUL-1999 (Rel. 38', Created)
DT 15-JUL-1999 (Rel. 38', Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Sonic hedgehog protein precursor (SHH).
GN SHH OR VHH-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TAXID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN="Sprague-Dawley"; TISSUE="Embryonic floor plate";
RD MEDLINE=94170375; PubMed=8124741;
RA Roelink H., Augsburger A., Heemkerk J., Korzh V., Norlin S.,

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CC use by non profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>)
-I_ SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.
EMBL: L27340; AAA0999.1; -.
DR HSSP; Q6226; 1VHH
DR MEROPS; C46.002; -
DR InterPro; IPR000320; HH_signal.
DR InterPro; IPR01767; Hedgehog_hint.
DR InterPro; IPR003580; Hedgehog_hintC.
DR InterPro; IPR03587; Hedgehog_hintN.
DR InterPro; IPR02203; Intein.
DR InterPro; IPR01657; SonicHH.
DR Pfam; PF01079; Hint; 1.
DR Pfam; PF01085; HH_signal; 1.
DR PRINS; PR00632; SonicHHog.
DR PRODOM; PDD00342; HHSignal; 1.
DR SMART; SM00305; HintC; 1.
DR SMARF; SM03036; HintNN; 1.
DR PROSITE; PS50817; INTENIN_N_TER; 1.
DR PROSITE; PS50817; INTENIN_N_TER; 1.
KW Developmental protein; Autocatalytic cleavage; Hydrolase; Protease;
KW Signal; Lipoprotein; Palmitate.
FT SIGNAL 1 24 POTENTIAL
FT CHAIN 25 437 SONIC HEDGEHOG PROTEIN.
FT CHAIN 25 198 SONIC HEDGEHOG PROTEIN N-PRODUCT.
FT CHAIN 199 437 SONIC HEDGEHOG PROTEIN C-PRODUCT.
FT SITE 198 199 CLEAVAGE (AUTO.).
FT SITE 244 244 INVOLVED IN CHOLESTEROL TRANSFER (BY
FT SITE 268 268 INVOLVED IN AUTO-CLEAVAGE (BY
FT ACT_SITE 271 271 ESSENTIAL FOR AUTO-CLEAVAGE (BY
FT BINDING 198 198 CHOLESTEROL (BY SIMILARITY).

FT DOMAIN	383	387	POLY-GLY.	CC
FT LIPID	25	25	PALMITATE (BY SIMILARITY).	CC
SO SEQUENCE	437 AA;	47630 MW;	ODBC19F0D1662AO CRC64;	CC
Query Match Best Local Similarity	80.3%	Score 1780; DB 1; Length 437;		-I -
Matches 352; Conservative	80.0%	Pred. No. 6. 3e-137; Mismatches 44; Indels 22; Gaps 6;		PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N-TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).
Qy 4 MILITRILVPGFICALIVSSGLTGGPGRGICKRRHPRKKLTPLAYKOFIPNVAEKTIGASG	63			-I - INDUCTION: ACTIVATED BY ACTIVIN, BASIC FIBROBLAST GROWTH FACTOR (BFGF) AND PORK HEAD.
Db 2 LILLARCFLVALASSLIVCPGLACFGFCRKHQFKKLTPLAYKOFIPNVAEKTIGASG	61			CC
Qy 64 RYEKGKTRNSERFELTPNYNPDIKEDENTGADLMTORCKDKLNALATSYMOWPGV	123			CC
Db 62 RYEKGKTRNSERFELTPNYNPDIKEDENTGADLMTORCKDKLNALATSYMOWPGV	121			CC
Qy 124 KLRVTECSDWEDGHHSBESLHYEGRADVITTSDRDRSKYGMARLAVEAGEDWVYEFESKAH	183			CC
Db 122 KLRVTECSDWEDGHHSBESLHYEGRADVITTSDRDRSKYGMARLAVEAGEDWVYEFESKAH	181			CC
Qy 184 IHCSVKAENSAAKSGCCFGPSATVHLEHGKTKLWKDLSPDRDVLAADAGRLLNSDFLT	243			CC
Db 182 IHCSVKAENSAAKSGCCFGPSATVHLEHGKTKLWKDLSPDRVLAAADDQGRLLNSDFLT	241			CC
Qy 244 FLDRDSSRSKLFYVYIMTQPRAHLTAHHFLVAFQHNOSEATSTSGR-LFESNVKP	302			CC
Db 242 FLDRDSSRSKLFYVYIMTQPRAHLTAHHFLVAFQHNOSEATSTSGR-LFESNVKP	297			CC
Qy 303 GQRVYVVAERGGDRRLIPAAVHSVTLREEAAGAYAALTAQCTILNRYASCYAYIEHS	360			CC
Db 298 GQRVYVVAERGGDRRLIPAAVHSVTLREEAAGAYAALTAQCTILNRYASCYAYIEHS	357			CC
Qy 361 WAHWAFAFPRLAQGLLALICP-----DGA IPT-----AATTGIGHWYSILYRI	405			CC
Db 358 WAHWAFAFPRLAQGLLALICP-----DGA IPT-----AATTGIGHWYSILYRI	417			CC
Qy 406 GSWVLDODALPLGMVAPAS	425			CC
Db 418 GTWLUDSETLHPLGMVAKSS	437			CC
RESULT 5				
ID SHH_CNPY STANDARD:	PRT;	432 AA.		DR HSSP; 062226; HH.
AC 090385;				DR IPR00520; HH_signal.
DT 15-JUL-1999 (Rel. 38, Created)				DR InterPro; IPR001767; Hedgehog hint.
DT 16-OCT-2001 (Rel. 40, Last annotation update)				DR InterPro; IPR003586; Hedgehog_hintC.
DE SHH.				DR InterPro; IPR002203; Intein.
GN				DR InterPro; IPR00165; SonicHH.
OS Cyprinidae (Japanese common newt).				DR Pfam; PF01019; Hint; 1.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				DR PRINTS; PR00632; SONICHHOG; 1.
OX Amphibia; Batracia; Caudata; Salamandroidea; Salamandridae; Cyprinidae.				DR PRODOM; PD003042; HH_signal; 1.
NCBI_TaxId=8330;				DR SMART; SM00305; HintC; 1.
RN 1] SEQUENCE FROM N.A.				DR PROSITE; PS5081; HintN; 1.
RC TISSUE=Embryo;				KW SMART; SM00306; HintN; 1.
RX MEDLINE=96136334; PubMed=8573168;				KW Developmental protein; Autocatalytic cleavage; Hydrolase; Protease; Signal; Lipoprotein; Palmitate.
RT *Activation of two Cyprinidae genes, fork head and sonic hedgehog, in animal cap explants. ¹				FT SIGNAL 1 26 POTENTIAL.
RT BioPhys. Res. Commun. 218:395-401(1996).				FT CHAIN 27 432 SONIC_HEDGEHOG PROTEIN.
RT Takabatake T., Takashashi T.C., Inoue K., Ogawa M., Takeshima K.;				FT CHAIN 200 432 SONIC_HEDGEHOG PROTEIN_N-PRODUCT.
RT "Activation of two Cyprinidae genes, fork head and sonic hedgehog, in animal cap explants." ¹				FT SITE 200 201 SONIC_HEDGEHOG PROTEIN_C-PRODUCT.
RT BioPhys. Res. Commun. 218:395-401(1996).				FT SITE 268 268 CLEAVAGE (AUTO-) (BY SIMILARITY).
RL				FT ACT_SITE 271 271 INVOLVED IN AUTO-CLEAVAGE (BY SIMILARITY).
CC				FT BINDING 200 200 ESSENTIAL FOR AUTO-CLEAVAGE (BY SIMILARITY).
CC				FT LIPID 27 27 CHOLESTEROL (BY SIMILARITY).
CC				SO SEQUENCE 432 AA; 47847 MW; B455C7E746CB858 CRC64;
Query Match				
Best Local Similarity	72.3%	Score 1603.5; DB 1; Length 432;		Qy 1 MYEMLUITRILVPGFICALIVSSGLTGGPGRGIGKRRHPRKKLTPLAYKOFIPNVEKTIG
Matches 316; Conservative	72.6%	Pred. No. 1. 3e-122; Mismatches 36; Indels 13; Gaps 5;		Db 1 ADMEMIIRRVLVLAGIFCALIVSSGLTGGPGRGIGKRRHPRKKLTPLAYKOFIPNVEKTIG
Qy 1 MYEMLUITRILVPGFICALIVSSGLTGGPGRGIGKRRHPRKKLTPLAYKOFIPNVEKTIG	60			Qy 61 ASGRYEGKIKTRNSERFELTPNYNPDIKEDENTGADLMTORCKDKLNALATSYMOW
Db 1 ADMEMIIRRVLVLAGIFCALIVSSGLTGGPGRGIGKRRHPRKKLTPLAYKOFIPNVEKTIG	60			Db 61 ASGRYEGKIKTRNSERFELTPNYNPDIKEDENTGADLMTORCKDKLNALATSYMOW
Qy 121 PGVKLRYTEGDEDGHRFEEPLLHYEGRADVITTSDRDRSKYGMARLAVEAGEDWVYEFES	180			Qy 121 PGVKLRYTEGDEDGHRFEEPLLHYEGRADVITTSDRDRSKYGMARLAVEAGEDWVYEFES
Db 121 PGVKLRYTEGDEDGHRFEEPLLHYEGRADVITTSDRDRSKYGMARLAVEAGEDWVYEFES	180			Db 121 PGVKLRYTEGDEDGHRFEEPLLHYEGRADVITTSDRDRSKYGMARLAVEAGEDWVYEFES
CC - SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE				Qy 181 RAHICSVKAENSAAKSGCCFGPSATVHLEHGKTKLWKDLSPDRVLAAADDQGRLLNSDFLT
CC CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE				Db 181 RAHICSVKAENSAAKSGCCFGPSATVHLEHGKTKLWKDLSPDRVLAAADDQGRLLNSDFLT

Qy 241 FLTFELDRMDSRKRKFLVYIETRQPRAILTAHHLFLVAPQH--NQS---EATGSGQ 293
 CC CC - I - EXPRESSION IN INTESTINE, BRAIN, AND HIND LIMB.
 ID SHH_XENLA STANDARD PRT; 444 AA.
 AC Q92000; Q91894; PRT; 444 AA.
 CC CC - I - DEVELOPMENTAL STAGE: FIRST DEFECTED AT THE NEURULA (STAGES 16-17).
 DT 15-JUL-1999 (Rel. 38, created)
 CC CC - I - FIRST PEAK OF EXPRESSION AROUND TADPOLE HATCHING (STAGES 33-40).
 DT 15-JUL-1999 (Rel. 38, last sequence update)
 CC CC - I - HIGH EXPRESSION OBSERVED IN INTESTINE AT THE CLIMAX OF
 DT 16-OCT-2001 (Rel. 40, last annotation update)
 DE CC - I - MORPHOGENESIS (STAGES 60-62) WHEN INTESTINE EPITHELIAL UNDERGOES
 CC CC - I - INDUCTION BY THYROID HORMONE.
 CC CC - I - PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY
 CC CC - I - AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN
 CC CC - I - THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF
 CC CC - I - A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N-
 CC CC - I - TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS
 CC CC - I - TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION
 CC CC - I - OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE
 CC CC - I - ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE
 CC CC - I - C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).
 CC CC - I - SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.

RESULT 6

SHH_XENLA STANDARD PRT; 444 AA.

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 CC CC - I - or send an email to license@ebi-sib.ch).

[1] RNN
 RN SEQUENCE FROM N.A.
 RP TISSUE=Intestine;
 RC MEDLINE-9535169; PubMed-7630736;
 RX Stolow M.A., Shu Y.-B.;
 RT "Xenopus sonic hedgehog as a potential morphogen during embryogenesis
 and thyroid hormone-dependent metamorphosis.";
 RL Nucleic Acids Res. 23:2555-2562(1995).
 RN [2]
 SEQUENCE FROM N.A.
 RP TISSUE=Embryo;
 RC MEDLINE-95401852; PubMed-7671800;
 RA Eker S.C., McGraw L.L., Lai C.-J., Lee J.J., von Kessler D.P.,
 RA Moon R.T., Beachy P.A.;
 RT "Distinct expression and shared activities of members of the hedgehog
 gene family of *Xenopus laevis*";
 RT Development 121:2337-2347(1995).
 RL RN [3]
 SEQUENCE FROM N.A.
 RP TISSUE=Notochord;
 RC MEDLINE-96028338; PubMed-7551564;
 RA Ruiz i Altaba A., Jessell T.M., Roelink H.;
 RT "Restrictions to floor plate induction by hedgehog and winged-helix
 genes in the neural tube of frog embryos";
 RL Mol. Cell. Neurosci. 6:106-121(1995).
 CC - I - FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF
 CC - I - PATTERNING EVENTS DURING DEVELOPMENT AND METAMORPHOSIS INVOLVED
 CC - I - IN LIMB FORMATION, PATTERNING OF THE CENTRAL NERVOUS SYSTEM AND
 CC - I - VENTRAL SOMITE DIFFERENTIATION. INDUCES ECTOPIC CEMENT GLAND
 CC - I - FORMATION IN EMBRYOS. BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH
 CC - I - FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE
 CC - I - TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH, PTC
 CC - I - REPRIMSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO (BY
 CC - I - SIMILARITY).
 CC - I - SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE
 CC - I - CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE
 CC - I - CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM
 CC - I - TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).
 CC - I - TISSUE SPECIFICITY: STRONGLY EXPRESSED IN NOTOCHORD AND NEURAL
 CC - I - FLOOR PLATE DURING EMBRYOGENESIS. IN TADPOLE, HIGH EXPRESSION IS
 CC - I - OBSERVED IN PANCREAS/STOMACH, MODERATE EXPRESSION IN TAIL, AND LOW

Qy 411 DCDAHLHPGMVAPAS 425
 CC 418 QEDDTIHPGLMAKS 432

CC CC - I - EXPRESSION IN INTESTINE, BRAIN, AND HIND LIMB.
 CC CC - I - DEVELOPMENTAL STAGE: FIRST DEFECTED AT THE NEURULA (STAGES 16-17).
 CC CC - I - FIRST PEAK OF EXPRESSION AROUND TADPOLE HATCHING (STAGES 33-40).
 CC CC - I - HIGH EXPRESSION OBSERVED IN INTESTINE AT THE CLIMAX OF
 CC CC - I - MORPHOGENESIS (STAGES 60-62) WHEN INTESTINE EPITHELIAL UNDERGOES
 CC CC - I - INDUCTION BY THYROID HORMONE.
 CC CC - I - PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY
 CC CC - I - AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN
 CC CC - I - THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF
 CC CC - I - A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N-
 CC CC - I - TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS
 CC CC - I - TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION
 CC CC - I - OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE
 CC CC - I - ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE
 CC CC - I - C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).
 CC CC - I - SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.

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[1] DR EMBL; U39213; AAC42227; 1;
 DR EMBL; U63114; AAAB5162; 1;
 DR EMBL; L32248; AAA4981; 1;
 DR HSSP; Q62226; 1VHH.
 DR MEROPS; C46_002;
 DR InterPro; IPR00320; HH_signal.
 DR InterPro; IPR001767; Hedgehog_hint.
 DR InterPro; IPR003586; Hedgehog_hinC.
 DR InterPro; IPR00387; Hedgehog_hinC.
 DR InterPro; IPR002203; Intein.
 DR InterPro; IPR001657; SonicHH.
 DR Pfam; PF01079; Hhnt; 1.
 DR Pfam; PF01085; HH_signal; 1.
 DR PRINTS; PR00632; SONICHHG.
 DR PRODOM; PD003042; HH_signal; 1.
 DR SMART; SM00305; HlnC; 1.
 DR PROSITE; PS50817; INTEIN_N_TER; 1.
 DR Developmental Protein; Autocatalytic cleavage; Hydrolase; Protease;
 KW Signal; Lipoprotein; Palmitate; Repeat.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 444 SONIC HEDGEHOG PROTEIN N-PRODUCT.
 FT CHAIN 25 198 SONIC HEDGEHOG PROTEIN C-PRODUCT.
 FT SITE 199 444 CLEAVAGE (AUTO-) (BY SIMILARITY).
 FT SITE 198 199 INVOLVED IN AUTO-CLEAVAGE (BY
 FT SITE 266 266 SIMILARITY).
 FT ACT_SITE 269 269 ESSENTIAL FOR AUTO-CLEAVAGE (BY
 FT DOMAIN 386 409 SIMILARITY).
 FT DOMAIN 386 409 3 X 8 AA TANDEM REPEATS OF Q-V-D-L-Q-S-H-
 FT REPET 386 393 H.
 FT REPET 386 401 1.
 FT REPET 394 401 2.
 FT REPET 403 409 3.
 FT BINDING 198 198 CHOLESTEROL (BY SIMILARITY).
 FT LIPTD 25 25 PALMITATE (BY SIMILARITY).
 FT CONFLICT 5 9 TOSL-> NSNLW (IN REF. 3).
 FT CONFLICT 302 319 DPKTMILKAVKEVDLE-> ESDHDLEGGRGKWRRLIR
 FT CONFLICT 432 432 (IN REF. 3).
 FT SEQUENCE 444 AA; 49453 MW: 7384E4932FA2EF2 CRC64;
 Query Match 69.1%; Score 1533; DB 1; Length 444;
 Best Local Similarity 66.7%; Pred. No. 7.1e-17;
 Matches 301; Conservative 41; Mismatches 73; Indels 36; Gaps 5;

1 MLYTQSILLSLFICITVTPPLGAGPGERGIGRPIKPLAKQTRPPWAKTGAS 60
 RX MEDLINE-#99225345; PubMed-10201136;
 RT Muller F., Chang B., Albert S., Fischer N., Tora L., Strahle U.;
 RT "Intrinsic elements control expression of zebrafish sonic hedgehog in
 RT floor plate and notochord.";
 RL Development 126:2103-2116(1999).
 RN [5]
 RP SEQUENCE OF 30-92 AND 113-170 FROM N.A.
 RC TISSUE="MUSCLE".
 RX MEDLINE-#9107514; PubMed-891540;
 RA Zardoya R., Abouheif E., Meyer A.;
 RT "Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species
 RT Closely related to the zebrafish.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:13036-13041(1996).
 CC - FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF
 CC PATTERNING EVENTS DURING DEVELOPMENT. SIGNAL PRODUCED BY THE
 CC NOTOCHORD THAT INDUCES SOMITE PATTERNING, DORSO-VENTRAL PATTERNING
 CC OF THE BRAIN AND EARLY APPEARING OF THE DEVELOPING FINES, DISPLAYS
 CC FLOOR PLATE-INDUCING ACTIVITY. BINDS TO THE PATCHED (PTC)
 CC RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO
 CC ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH,
 CC PTG REPRESSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO (BY
 CC SIMILARITY).
 CC - SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE
 CC CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE
 CC CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM
 CC TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).
 CC - TISSUE SPECIFICITY: EXPRESSED IN THE VENTRAL MIDLINE OF THE NEURAL
 CC TUBE AND BRAIN. ALSO FOUND IN THE NOTOCHORD AND IN DEVELOPING FIN
 CC BUD. IN THE DEVELOPING BRAIN, EXPRESSION OCCURS IN DOMAINS THAT
 CC INCLUDE A DISCRETE REGION IN THE FLOOR OF THE Diencephalon.
 CC - DEVELOPMENTAL STAGE: FIRST DETECTABLE IN THE INNER CELL LAYER OF
 CC THE EMBRYONIC SHIELD DURING GASTRULATION. BY 9.5 HRS OF
 CC DEVELOPMENT, EXPRESSED IN A CONTINUOUS BAND THAT EXTENDS FROM THE
 CC TAIL TO THE HEAD. THE ANTERIOR BOUNDARY OF EXPRESSION BEING
 CC POSITIONED IN THE CENTER OF THE ANIMAL POLE ANTERIOR TO THE
 CC PRESUMPTIVE MIDBRAIN.
 CC - PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY
 CC AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN
 CC THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF
 CC A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N-
 CC TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS
 CC TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION
 CC OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE
 CC ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE
 CC C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).
 CC - SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.
 CC
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 CC
 RL L27505; AAA20981; --.
 DR EMBL; C46_002; --.
 RT MEROPS; C46_002; --.
 DR DMBL; U30711; AAC59742.1; --.
 DR DMBL; Z35699; CAAB4738.1; --.
 DR EMBL; AF124382; AAD41913.1; --.
 DR DMBL; U51151; AAB38555.1; --.
 DR EMBL; U51370; AAB38533.1; --.
 DR RSP; Q62246; IVHH.
 DR DMBL; L27505; AAA20981; --.
 DR 2FIN; ZDB-GENE-980525-166; shh.
 DR InterPro; IPR003220; HH_signal.
 DR InterPro; IPR001767; Hedgehog_hint.
 DR InterPro; IPR003586; Hedgehog_HintC.
 DR InterPro; IPR003587; Hedgehog_HintN.
 DR InterPro; IPR002203; Intein.
 DR InterPro; IPR001657; SonicHH.
 RL Pfam; PF01079; Hint_1.
 DR Pfam; PF01085; HH_s1ignal_1.
 DR PRINTS; PR00632; SONICHHOG.
 RP SEQUENCE FROM N.A.
 RX MEDLINE-#96083228; PubMed-7579523;
 RA Fiecht M.J., Concordet J.-P., Barbosa R., Johnson R., Krauss S.,
 RA McMahon A.P., Tabin C., Ingham P.W.;
 RA "The hedgehog gene family in Drosophila and vertebrate development.",
 RT Development Suppl. 43-51(1994).
 RN [4]
 RN SEQUENCE FROM N.A.

DR	PRODOM; PD003042; HH_SIGNAL; 1.	RP	SEQUENCE FROM N.A., AND AUTOPROTEOLYTIC CLEAVAGE.
DR	SMART; SM00305; HintN; 1.	RC	TISSUE=Embryo;
DR	SMART; SM00306; HintN; 1.	RX	MEDLINE=96014264; PubMed=7583153;
DR	PROSITE; PS5017; INPEIN_N_TER; 1.	RA	ECKER S.C.; Ungar A.R.; Greenstein P.; von Kessler D.P.;
KW	Developmental protein; Autocatalytic cleavage; Hydrolase; Protease; Signal; Lipoprotein; Palmitate.	RA	Porter J.A.; Moon R.T.; Beachy P.A.;
FT	SIGNAL	RT	"Patterning activities of vertebrate hedgehog proteins in the developing eye and brain."
FT	CHAIN	RL	Curr. Biol. 5:944-955(1995).
FT	CHAIN	CC	-!- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT. INVOLVED IN DORSO-VENTRAL PATTERNING OF THE BRAIN AND IN EARLY PATTERNING OF THE DEVELOPING EYES.
FT	CHAIN	CC	-!- SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURFACE. IS ALSO SECRETED IN EITHER CLEARED OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).
FT	SITE	CC	-!- TISSUE SPECIFICITY: EXPRESSED IN THE VENTRAL MIDLINE OF THE NEURAL TUBE AND BRAIN. IN THE DEVELOPING BRAIN, EXPRESSION OCCURS IN DOMAINS THAT INCLUDE A DISCRETE REGION IN THE FLOOR OF THE DIENCEPHALON. NOT DETECTED IN THE NOTOCORD OR DEVELOPING FIN BUD.
FT	SITE	CC	-!- PTM: THI-C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N-TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).
FT	SITE	CC	-!- SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.
FT	SEQUENCE	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
FT	SEQUENCE	CC	DR EMBL; U30710; AAC59741.1; -.
FT	SEQUENCE	CC	DR HSSP; Q02226; IVHH.
FT	SEQUENCE	CC	DR ZFIN; ZDB-GENE-980526-41; twhh.
FT	SEQUENCE	CC	DR InterPro; IPR003320; HH signal.
FT	SEQUENCE	CC	DR InterPro; IPR001767; Hedgehog_hint.
FT	SEQUENCE	CC	DR InterPro; IPR003586; Hedgehog_hintC.
FT	SEQUENCE	CC	DR InterPro; IPR003587; Hedgehog_hintN.
FT	SEQUENCE	CC	DR InterPro; IPR001657; Sonichh.
FT	SEQUENCE	CC	DR Pfam; PF01085; HH_signal; 1.
FT	SEQUENCE	CC	DR PRINTS; PR00532; SONICHHOG.
FT	SEQUENCE	CC	DR SMART; SM00305; HintC; 1.
FT	SEQUENCE	CC	DR SMART; SM00306; HintN; 1.
FT	SEQUENCE	CC	DR Developmental protein; Autocatalytic cleavage; Hydrolase; Protease; KW Signal; Lipoprotein; Palmitate.
FT	SEQUENCE	CC	FT SIGNAL 1 POTENTIAL.
FT	SEQUENCE	CC	FT CHAIN 27 416 TIGGY-WINKLE HEDGEHOG PROTEIN N-PRODUCT.
FT	SEQUENCE	CC	FT CHAIN 27 200 TIGGY-WINKLE HEDGEHOG PROTEIN N-PRODUCT.
FT	SEQUENCE	CC	FT SITE 201 416 TIGGY-WINKLE HEDGEHOG PROTEIN C-PRODUCT.
FT	SEQUENCE	CC	FT SITE 201 200 CLEAVAGE (AUTO-).
FT	SEQUENCE	CC	FT SITE 270 270 INVOLVED IN AUTO-CLEAVAGE (BY SIMILARITY).
FT	SEQUENCE	CC	FT ACT_SITE 273 273 ESSENTIAL FOR AUTO-CLEAVAGE (BY SIMILARITY).
FT	SEQUENCE	CC	FT BINDING 200 200 CHOLESTEROL (BY SIMILARITY).
FT	SEQUENCE	CC	FT LIPID 27 27 PALMITATE (BY SIMILARITY).
FT	SEQUENCE	CC	FT SQ 416 AA; 46576 MW; 61EC221830CFE59 CRC64;
FT	SEQUENCE	CC	Query Match 65.7%; Score 1458; DB 1; Length 416; Best Local Similarity 68.8%; Pred. No. 7.9e-111; Mismatches 8; Indels 8; Gaps 4; Matches 287; Conservative 36; Mismatches 8; Indels 8; Gaps 4; [1]

QY	5 LILTRILWFGICLNLSSLCGPGRLGRRHPPKLTPLAKQFIPNVAEKTIGASGR 64	CC	- SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.
Db	5 LHLKOFALCFCITSLILLPCLAGCPGGRGGYKRRHKPKLTPLAYKOFIPNVAEKTIGASGR 64	CC	This SWISS-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation of the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
QY	65 YECKITRNSERKEELTPNYPNDIKFDEENGADRMLTQRCKDKLNALAISMNQPGVK 124	CC	DR 65 YECKITRNSERKEELTPNYPNDIKFDEENGADRMLTQRCKDKLNALAISMNQPGVK 124
Db	65 YECKITRNSERKEELTPNYPNDIKFDEENGADRMLTQRCKDKLNALAISMNQPGVK 124	CC	DR 65 YECKITRNSERKEELTPNYPNDIKFDEENGADRMLTQRCKDKLNALAISMNQPGVK 124
QY	125 LRTVEGMDEDGHSEESLHYEGRAVDTTSDRDSKGMLARLAVEAGFDWVYESKAHIC 184	CC	DR 125 LRTVEGMDEDGHSEESLHYEGRAVDTTSDRDSKGMLARLAVEAGFDWVYESKAHIC 184
Db	125 LRTVEGMDEDGHSEESLHYEGRAVDTTSDRDSKGMLARLAVEAGFDWVYESKAHIC 184	CC	DR 125 LRTVEGMDEDGHLEESLHYEGRAVDTTSDRDSKGMLARLAVEAGFDWVYESKAHIC 184
QY	125 LRTVEGMDEDGHSEESLHYEGRAVDTTSDRDSKGMLARLAVEAGFDWVYESKAHIC 184	CC	DR 125 LRTVEGMDEDGHLEESLHYEGRAVDTTSDRDSKGMLARLAVEAGFDWVYESKAHIC 184
Db	125 LRTVEGMDEDGHLEESLHYEGRAVDTTSDRDSKGMLARLAVEAGFDWVYESKAHIC 184	CC	DR 125 LRTVEGMDEDGHLEESLHYEGRAVDTTSDRDSKGMLARLAVEAGFDWVYESKAHIC 184
QY	185 HCSVKAENSAKKGCGPPGSATVHLEGGTKVLDLSPGDRVLAAADGRLLYRIGSVWLGALPLGMV 244	CC	DR 185 HCSVKAENSAKKGCGPPGSATVHLEGGTKVLDLSPGDRVLAAADGRLLYRIGSVWLGALPLGMV 244
Db	185 HCSVKAENSAKKGCGPPGSATVHLEGGTKVLDLSPGDRVLAAADGRLLYRIGSVWLGALPLGMV 244	CC	DR 185 HCSVKAENSAKKGCGPPGSATVHLEGGTKVLDLSPGDRVLAAADGRLLYRIGSVWLGALPLGMV 244
QY	245 LDMDSSKKLFVYETRORPARLLTAHHLFVAPQHNOSEATGSTSQCALFASNVARGQ 304	CC	DR 245 LDMDSSKKLFVYETRORPARLLTAHHLFVAPQHNOSEATGSTSQCALFASNVARGQ 304
Db	245 LDMDSSKKLFVYETRORPARLLTAHHLFVAPQHNOSEATGSTSQCALFASNVARGQ 304	CC	DR 245 LDMDSSKKLFVYETRORPARLLTAHHLFVAPQHNOSEATGSTSQCALFASNVARGQ 304
QY	245 LDMDSSKKLFVYETRORPARLLTAHHLFVAPQHNOSEATGSTSQCALFASNVARGQ 304	CC	DR 245 LDMDSSKKLFVYETRORPARLLTAHHLFVAPQHNOSEATGSTSQCALFASNVARGQ 304
Db	245 LDMDSSKKLFVYETRORPARLLTAHHLFVAPQHNOSEATGSTSQCALFASNVARGQ 304	CC	DR 245 LDMDSSKKLFVYETRORPARLLTAHHLFVAPQHNOSEATGSTSQCALFASNVARGQ 304
QY	245 IDIDPTTPTTYETRPTKTTLAHHLFVAPQHNOSEATGSTSQCALFASNVARGQ 298	CC	DR 245 IDIDPTTPTTYETRPTKTTLAHHLFVAPQHNOSEATGSTSQCALFASNVARGQ 298
Db	245 IDIDPTTPTTYETRPTKTTLAHHLFVAPQHNOSEATGSTSQCALFASNVARGQ 298	CC	DR 245 IDIDPTTPTTYETRPTKTTLAHHLFVAPQHNOSEATGSTSQCALFASNVARGQ 298
QY	305 RYVVLGEQQQLPASVHSVSLREASGAYAPLTAQGILINRLASCYAVIEBHSWAH 364	CC	DR 305 RYVVLGEQQQLPASVHSVSLREASGAYAPLTAQGILINRLASCYAVIEBHSWAH 364
Db	305 RYVVLGEQQQLPASVHSVSLREASGAYAPLTAQGILINRLASCYAVIEBHSWAH 364	CC	DR 305 RYVVLGEQQQLPASVHSVSLREASGAYAPLTAQGILINRLASCYAVIEBHSWAH 364
QY	365 AFAPPFLAQGLLALACPGPAIPTATTGIGWYSRRLYRIGSVWLGALPLGMV 421	CC	DR 365 AFAPPFLAQGLLALACPGPAIPTATTGIGWYSRRLYRIGSVWLGALPLGMV 421
Db	365 AFAPPFLAQGLLALACPGPAIPTATTGIGWYSRRLYRIGSVWLGALPLGMV 421	CC	DR 365 AFAPPFLAQGLLALACPGPAIPTATTGIGWYSRRLYRIGSVWLGALPLGMV 421
QY	358 AFAPVFLRCKLMLTWLPF-ARESNVNFQEDDGHWSYNSNMFLHIGSWLDRDFHPLGL 413	CC	DR 358 AFAPVFLRCKLMLTWLPF-ARESNVNFQEDDGHWSYNSNMFLHIGSWLDRDFHPLGL 413
RESULT 9			
IH_CHEM	STANDARD;	PRP;	408 AA.
ID	Q98938; 15-JUL-1999 (Rel. 38, Created)	FT	SEQUENCE FROM N.A.
DT	15-JUL-1999 (Rel. 38, Last sequence update)	FT	PRIMERS; PR000532; SONICHHOG.
DT	16-OCT-2001 (Rel. 40, Last annotation update)	FT	PR0003042; HH_SIGNAL; 1.
DE	Indian hedgehog protein precursor (IHH).	FT	SMART; SNO0305; HHNC; 1.
GN	GALUS GALLUS (Chicken).	FT	SMR00306; HINTN; 1.
OS	GALUS GALLUS (Chicken).	FT	Developmental protein; Autocatalytic cleavage; Hydrolase; Protease; KW SIGNAL; Lipoprotein; Palmitate.
OC	Archosauvia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; OC GALLUS; NCBI_TAXID=9031;	FT	FT SIGNAL 1 23 POTENTIAL.
RN	[1]; RP SEQUENCE FROM N.A.	FT	INDIAN HEDGEHOG PROTEIN.
RP	MEDLINE:96325423; PubMed=8662546;	FT	INDIAN HEDGEHOG PROTEIN N-PRODUCT.
RX	Vortkamp A., Lee K., Lanske B., Segre G.V., Kronenberg H.M.,	FT	INDIAN HEDGEHOG PROTEIN C-PRODUCT.
RA	Tabin C.J.; Regulation of rate of cartilage differentiation by Indian hedgehog and pth-related protein.,	FT	CLEAVAGE (AUTOMATIC) (BY INVOLVED IN CHOLESTEROL TRANSFER (BY SIMILARITY)).
RT	RL Science 273,613-622(1996).	FT	INVOLVED IN AUTO-CLEAVAGE (BY SIMILARITY).
RT	- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT. BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IMPLICATED IN ENDOCHEONDRAL OSSIFICATION: MAY REGULATE THE BALANCE BETWEEN GROWTH AND OSSIFICATION OF PARATHYROID HORMONE RELATED PROTEIN (PTHrP).	FT	SIMILARITY).
RT	- SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).	FT	ESTERIFICATION OF DEVELOPING BONES IN THE LIMB.
RT	- TISSUE SPECIFICITY: EXPRESSED IN DEVELOPING MIDGUT, LUNG AND CARTILAGE OF DEVELOPING LONG BONES IN THE LIMB.	FT	- PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N- TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).
QY	9 RILWLGFTICLNLSSLCGPGRLGRRHPPKLTPLAKQFIPNVAEKTIGASGR 64	CC	DR 9 RILWLGFTICLNLSSLCGPGRLGRRHPPKLTPLAKQFIPNVAEKTIGASGR 64
Db	5 RLLILSGCALLAPAVRCGCPGRVGSRVRPRKLIFPLAYKOFSPNPKEKTIGASGR 64	CC	DR 5 RLLILSGCALLAPAVRCGCPGRVGSRVRPRKLIFPLAYKOFSPNPKEKTIGASGR 64
QY	67 GKTRNSERKEELTPNYPNDIKFDEENGADRMLTQRCKDKLNALAISMNQPGVK 186	CC	DR 67 GKTRNSERKEELTPNYPNDIKFDEENGADRMLTQRCKDKLNALAISMNQPGVK 186
Db	65 GKLARNSEERKEELTPNYPNDIKFDEENGADRMLTQRCKDKLNALAISMNQPGVK 186	CC	DR 65 GKLARNSEERKEELTPNYPNDIKFDEENGADRMLTQRCKDKLNALAISMNQPGVK 186
QY	127 VTEGMDEDGHSEESLHYEGRAVDTTSDRDSKGMLARLAVEAGFDWVYESKAHIC 186	CC	DR 127 VTEGMDEDGHSEESLHYEGRAVDTTSDRDSKGMLARLAVEAGFDWVYESKAHIC 186
Db	127 VTEGMDEDGHSEESLHYEGRAVDTTSDRDSKGMLARLAVEAGFDWVYESKAHIC 186	CC	DR 127 VTEGMDEDGHSEESLHYEGRAVDTTSDRDSKGMLARLAVEAGFDWVYESKAHIC 186
QY	187 SVAENSAKKGCGPPSOTAVHLEGGTKVLDLSPGDRVLAAADGRLLYRIGSVWLGALPLGMV 306	CC	DR 187 SVAENSAKKGCGPPSOTAVHLEGGTKVLDLSPGDRVLAAADGRLLYRIGSVWLGALPLGMV 306
Db	187 SVAENSAKKGCGPPSOTAVHLEGGTKVLDLSPGDRVLAAADGRLLYRIGSVWLGALPLGMV 306	CC	DR 187 SVAENSAKKGCGPPSOTAVHLEGGTKVLDLSPGDRVLAAADGRLLYRIGSVWLGALPLGMV 306
QY	247 RDMDSSKKLFVYETRORPARLLTAHHLFVAPQHNOSEATGSTSQCALFASNVARGQ 306	CC	DR 247 RDMDSSKKLFVYETRORPARLLTAHHLFVAPQHNOSEATGSTSQCALFASNVARGQ 306
Db	247 RDMDSSKKLFVYETRORPARLLTAHHLFVAPQHNOSEATGSTSQCALFASNVARGQ 306	CC	DR 247 RDMDSSKKLFVYETRORPARLLTAHHLFVAPQHNOSEATGSTSQCALFASNVARGQ 306
QY	307 IV LGEGGQQLLPASVHSVSLREASGAYAPLTAQGILINRLASCYAVIEBHSWAH 365	CC	DR 307 IV LGEGGQQLLPASVHSVSLREASGAYAPLTAQGILINRLASCYAVIEBHSWAH 365
Db	307 IV LGEGGQQLLPASVHSVSLREASGAYAPLTAQGILINRLASCYAVIEBHSWAH 365	CC	DR 307 IV LGEGGQQLLPASVHSVSLREASGAYAPLTAQGILINRLASCYAVIEBHSWAH 365
QY	366 FAPPLAQGLLALACPGPAIPTATTGIGWYSRRLYRIGSVWLGALPLGMV 402	CC	DR 366 FAPPLAQGLLALACPGPAIPTATTGIGWYSRRLYRIGSVWLGALPLGMV 402
Db	366 FAPPLAQGLLALACPGPAIPTATTGIGWYSRRLYRIGSVWLGALPLGMV 402	CC	DR 366 FAPPLAQGLLALACPGPAIPTATTGIGWYSRRLYRIGSVWLGALPLGMV 402
QY	358 FWPLRYHSLLGGPVQG-----DGHWYSGSLYRLGRMLPPDFHPLG 402	CC	DR 358 FWPLRYHSLLGGPVQG-----DGHWYSGSLYRLGRMLPPDFHPLG 402

RESULT 10
IHH_XENLA STANDARD; PRT; 409 AA.
 ID IHH_XENLA STANDARD; PRT; 409 AA.
 AC 091612; 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Indian hedgehog protein precursor (IHH) (Banded hedgehog protein) (X-BHH).
 DE IHH OR BH.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
 Xenopodinae; Xenopus.
 NCBI_Taxid=8355;
 RN [1] SEQUENCE FROM N A.
 RC TISSUE=Embryo;
 RX MEDLINE=95401852; PubMed=7671800;
 RA ECKER S.C., McGREW L.L., Lai C.-J., Lee J.J., von Kessler D.P.,
 Moon R.T., Beachy P.A.;
 RT "Distinct expression and shared activities of members of the hedgehog gene family of *Xenopus laevis*";
 Development 121: 2337-2347, 1995.
 -I- FUNCTION: SIGNAL INVOLVED IN THE EARLY INDUCTION AND PATTERNING OF ANTERODORSAL ECTODERM, NERVOUS SYSTEM AND SOMITES. INDUCES ECTOPIC CEMENT GLAND FORMATION IN EMBRYOS.
 -I- SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURFACE. HEDGEHOG PROTEIN IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).
 -I- DEVELOPMENTAL STAGE: DETECTABLE WITHIN THE EARLY GASTRULA. AT STAGE 14 NEURULA, HIGH EXPRESSION IN NEUROECTODERM EXPRESSED THROUGHOUT THE NEURAL PLATE AND SUBSEQUENTLY IN BOTH THE NERVOUS SYSTEM AND IN THE DERMATOME OF SOMITES.
 -I- INDUCTION: BY ACTIVIN.
 -I- PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N- TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).
 -I- SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.

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RESULT 11
IHH_MOUSE STANDARD; PRT; 411 AA.
 ID IHH_MOUSE STANDARD; PRT; 411 AA.
 AC 0917812; Q61724; 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Indian hedgehog protein precursor (IHH) (HHG-2).
 DE IHH.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC MEROPS; CA6_UPNP; InterPro; IPR00320; HH signal.
 DR InterPro; IPR001767; Hedgehog_hintC.
 DR InterPro; IPR003586; hedgehog-hintC.
 DR InterPro; IPR003587; Hedgehog_hintN.
 DR Pfam; PF01079; Hint_1.
 DR Pfam; PF01085; HHsignal_1.
 DR PRINTS; PRO00632; SONICHHG.
 DR PRODOM; PDO03042; HH signal; 1.
 DR SMART; SM00305; HintN_1.
 DR Developmental protein; Autocatalytic cleavage; Hydrolase; Protease; Signal; Lipoprotein; Palmitate.

RN [1] SEQUENCE FROM N A., AND AUTOPROTEOLYTIC CLEAVAGE.
 RN STRAIN=CD-1; TISSUE=Kidney;
 RX MEDLINE=9736802; PubMed=9079674;
 RA Valentini R.P., Brookhiser W.T., Park J., Yang T., Briggs J.,
 RA Dressler G., Holzman L.B.;
 RT "Post-translational processing and renal expression of mouse Indian hedgehog";
 RL J. Biol. Chem. 272:8466-8473 (1997).
 RN [2] SEQUENCE OF 76-411 FROM N A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=94094334; PubMed=7916661;

RA Echelard Y., Epstein D.J., St Jacques B., Shen L., Mohler J.,
 RA McMahon J.A., McMahon A.P.;
 RT "Sonic hedgehog, a member of a family of putative signaling
 molecules, is implicated in the regulation of CNS polarity.";
 RL Cell 75:1417-1430(1993).
 RN [3]
 RP REVISIONS.
 RC STRAIN=C57BL/6J;
 RA St. Jacques B.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
 RP [4]
 RX SEQUENCE OF 124-172 FROM N.A.
 RA Chang D.T., Lopez A., von Kessler D.P., Chiang C., Simandl B.K.,
 RA Zhao R., Seidin M.F., Fallon J.F., Beachy P.A.;
 RT "Products, genetic linkage and limb patterning activity of a murine
 hedgehog gene";
 RL Development 120:3339-3353(1994).
 CC -1- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF
 CC PATTERNING EVENTS DURING DEVELOPMENT. BINDS TO THE PATCHED (PTC)
 CC RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO
 CC ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IMPLICATED IN
 CC ENDODCHONDRAL OSSIFICATION; MAY REGULATE THE BALANCE BETWEEN GROWTH
 CC AND OSSIFICATION OF THE DEVELOPING BONES. INDUCES THE EXPRESSION
 CC OF PARATHYROID HORMONE RELATED PROTEIN (PTHrP).
 CC -1- SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE
 CC CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE
 CC CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM
 CC TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: IN THE EMBRYO, DEFECTED IN THE DEVELOPING GUT,
 CC THE GROWTH ZONE OF CARTILAGE OF DEVELOPING LONG BONES, EPITHELIUM,
 CC AND UROGENITAL SINUS. IN THE ADULT KIDNEY, FOUND IN PROXIMAL
 CC CONVOLUTED AND DISTAL STRAIGHT TUBULE.
 CC -1- DEVELOPMENTAL STAGE: DEFECTED AT 10 DAYS POST COITUM (DPC) IN
 CC DEVELOPING GUT. AT 14.5 DAYS DPC IN THE CARTILAGE PRIMORDIUM AND
 CC IN THE DEVELOPING UROGENITAL SINUS. EXPRESSION INCREASES WITH
 CC GESTATIONAL AGE IN KIDNEY AND DUODENUM, BECOMING MAXIMAL IN
 CC ADULTHOOD.
 CC -1- PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYTIC ACTIVITY
 CC AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN
 CC THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF
 CC A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N-
 CC TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS
 CC TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION
 CC OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE
 CC ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE
 CC C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.
 CC -----
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 CC -----
 CC RESULT 12
 ID IH_HUMAN
 AC 014623; 043322;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUN-2000 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Indian hedgehog protein precursor (IHh) (HHG-2).
 GN IHH.
 OS Homo sapiens (Human).
 DR MGI: 96533; Inhh.
 DR InterPro: IPR000320; HH_signal.
 DR InterPro: IPR01767; Hedgehog_hint.
 DR InterPro: IPR03386; Hedgehog_hintC.
 DR InterPro: IPR003587; Hedgehog_hintN.
 DR InterPro: IPR02203; Intein.
 DR MERSP; C46_003; .
 DR MGD: MG_1079; Inhh.
 DR InterPro: IPR000320; HH_signal.
 DR InterPro: IPR01767; Hedgehog_hint.
 DR InterPro: IPR03386; Hedgehog_hintC.
 DR SMART; SM00305; HhntC; I.
 DR PROSITE; PS50817; INTEIN_N_TER; I.
 DR -----
 KW Developmental protein; Auto-catalytic cleavage; Hydrolase; Protease;
 KW Signal; Lipoprotein; Palmitate.
 FT SIGNAL 1
 FT CHAIN 28 411
 FT CHAIN 28 202
 FT CHAIN 203 411
 FT SITE 202 203
 FT SITE 248 248
 FT SITE 272 272
 FT ACT_SITE 275 275
 FT BINDING 202 202
 FT LIPID 28 28
 FT CONFLICT 383 383
 SQ SEQUENCE 411 AA; 45485 MW; 08B7AD8507C0D9B CRC64;
 DB Query Match 57.6%; Score 1277.5; DB 1; Length 411;
 DB Best Local Similarity 62.4%; Pred. No. 3.4e-5;
 DB Matches 257; Conservative 42; MisMatches 88; Indels 25; Gaps 6;
 DB Qy 19 LLVSSGLCTGGPGRCIG-KRRRHKPLTPAKQFTPNVAEKTUGASGRGEKTRNSERPK 77
 DB Db 20 LLVPAARGCGPGRVGSRRPPRKLVPLAYKQFSPPNVEKTIKGASGRGEKTRNSERPK 79
 DB Qy 78 ELTPNPNIDIFKDEENGTGADRIMTQRDKKLNALATSVMNMOPGVKLRTVSGWDEGHH 137
 DB Db 80 ELTPNPNIDIFKDEENGTGADRIMTQRDKKLNALATSVMNMOPGVKLRTVSGWDEGHH 139
 DB Qy 138 SEBSLYHGRGAVDITTSRDRSKYGLMLKVLKOLSPGDRVLAADAGBLYSUPLTLDMSRSKKFV 197
 DB Db 140 SEBSLYHGRGAVDITTSRDRSKYGLMLKVLKOLSPGDRVLAADAGBLYSUPLTLDMSRSKKFV 199
 DB Qy 198 SGCCFGPGSATVHLFEHGGPKLVKOLSPGDRVLAADAGBLYSUPLTLDMSRSKKFV 257
 DB Db 200 TGGCPAGAQVRLENGervalSAVKGDPDRVLAAGEDGTPTPSDVLIFDRPDRNRLAFQV 259
 DB Qy 258 IETRQPRARLLTAHLIFVAFPHQHNOSEATGTSQGALFASNVKPGORVYVIGEGQQLL 317
 DB Db 260 IETQDPERPLLPALHFLIDHTPERA---HFRATEASHVQPG---YVLSVGPGLO 313
 DB Qy 318 PASHSVSLREASGAYAFLTAQGTLINRVLASCYVTEISWAHRAFAPIRLLAOGLLA 377
 DB Db 314 PARVAAVS-THVALGSVAPLIRGTLVVEDWVASCRAVADHLAQLAFWPRL---- 366
 DB Qy 378 ALCPDGALIPTAA---TTTGTTIHWYSLRYLIGSWVLDGALHPLGVAPAS 425
 DB 367 -----FPSSLANGSWTPSEGVHWPOMLYRGLLBESTFHPLGMSGAGS 411

MEDLINE=96070431; PubMed=7590746;
RA Mairig V., Roberts D.J., Lee S.M.K., Tsukurov O., Levi T.,
Gaster J.M., Epstein D.J., Gilbert D.J., Copeland N.G., Seidman C.E.,
Jenkins N.A., Seidman J.G., McMahon A.P., Tabin C.;
***Cloning, expression, and chromosomal location of SHH and IHH: two**
human homologues of the Drosophila segment polarity gene hedgehog.*;
Genomics 28:44-51(1995).

[3]
SEQUENCE OF 124-172 FROM N.A.
MEDLINE=9232697; PubMed=7720571;
RA Chang D.T., Lopez A., von Kessler D.P., Chiang C., Simandl B.K.,
Zhao R., Seldin M.F., Fallon J.F., Beachy P.A.;
"Products, genetic linkage and limb patterning activity of a murine
hedgehog gene.;"
RT Development 10: 3339-3353(1994).
RL CC
CC FUNCTION: INTERCELLULAR SIGNAL, ESSENTIAL FOR A VARIETY OF
PATTERNING EVENTS DURING DEVELOPMENT. BINDS TO THE PATCHED (PTC)
RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO
ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IMPLICATED IN
ENDOCHEONDRAL OSSIFICATION: MAY REGULATE THE BALANCE BETWEEN GROWTH
AND OSSIFICATION OF THE DEVELOPING BONES. INDUCES THE EXPRESSION
OF PARATHYROID HORMONE-RELATED PROTEIN (PTHrP) (BY SIMILARITY).
CC CC
CC -1- PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY
AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN
THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF
A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N-
TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS
TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION
OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE
ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE
C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).

-1- SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.

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EMBL: AB018076; BAA3523_2; -
 DR EMBL; AB010092; BAA3523_2; JOINED.
 DR EMBL; AB018075; BAA3523_2; JOINED.
 DR L38517; AAA62178.1; -.
 HSSP; Q6226; 1VRR.
 MEROPS; C46_003; -.
 Genew; HGNC:5956; IHH.
 MIM; 600726; -.
 DR InterPro; IPR000320; HH_signal.
 DR InterPro; IPR01767; Hedgehog_hint.
 DR InterPro; IPR03586; Hedgehog_hintC.
 DR InterPro; IPR03587; Hedgehog_hintN.
 InterPro; IPR02203; Intein.
 Pfam; PF01079; Hint_1.
 Pfam; PF01085; HH_signal_1.
 DR SMART; SM00305; HintC_1.
 DR SMART; SM00305; HintN_1.
 PROSITE; PS55081; INPH_N_TER; 1.
 DR Developmental protein: Autocatalytic cleavage; Hydrolase; Protease;
 KW signal; Lipoprotein; Palmitate.
 FT SIGNAL_1 27 POTENTIAL.
 FT CHAIN 28 411 INDIAN HEDGEHOG PROTEIN
 FT CHAIN 28 202 INDIAN HEDGEHOG PROTEIN N-PRODUCT.
 FT CHAIN 203 411 INDIAN HEDGEHOG PROTEIN C-PRODUCT.
 FT SITE 202 203 CLEAVAGE (AUTOM-) (BY SIMILARITY).
 SITE 248 248 INVOLVED IN CHOLESTEROL TRANSFER (BY

	SITE	272	272	SIMILARITY.
FT	SITE	272	272	INVOLVED IN AUTO-CLEAVAGE (BY SIMILARITY).
FT	ACT_SITE	275	275	ESSENTIAL FOR AUTO-CLEAVAGE (BY SIMILARITY).
FT	BINDING	202	202	CHOLESTEROL (BY SIMILARITY).
FT	LIPID	28	28	PALMITATE (BY SIMILARITY).
FT	CONFLICT	100	100	D -> R (IN REF. 2).
FT	CONFLICT	246	246	L -> F (IN REF. 2).
FT	CONFLICT	309	309	A -> V (IN REF. 2).
SO	SEQUENCE	411 AA;	45188 MW;	14C904A36C34ADEA CRC64;
Query Match			57.1%;	Score 1265.5; DB 1; Length 411;
Best Local Similarity			62.7%;	Pred. No. 3.2e-95;
Matches			256;	Conservative 38; Mismatches 97; Indels 17; Gaps
QY	19	LLVSSGLNGGGKPGKG-KRHPKKPLTPLAKOFTINVAEKTIGASGRYEGKTRNTERFK	77	
Db	20	LVVPAAMGCCGPGGRVGUSRSRKPRPKVPLAKOFSNVPETLIGASGRYEGKTRNTERFK	79	
QY	78	ELTPNYPDIFIKDEENNTGADRMLTQRCKDLNLAISVNQWPGVKLRVTEGMWDEGH	137	
Db	80	ELTPNYPDIFIKDEENNTGADRMLTQRCKDLNLAISVNQWPGVKLRVTEGMWDEGH	139	
QY	138	SEESLHYGGRAVDITTSDDDRSKVIGMLARLAVEAGFDWWVYTESKAHICSVKAENVA	197	
Db	140	SEBSLHYGGRAVITTSDDDRSKVIGMLARLAVEAGFDWWVYTESKAHICSVKSERAAK	199	
QY	198	SGCCFPGPAGQVRLESGARVALSAVRPGRDVLFLAMGEDGSPTEFSDVLLDRLPRLR	257	
Db	200	TGGCCFPGPAGQVRLESGARVALSAVRPGRDVLFLAMGEDGSPTEFSDVLLDRLPRLR	259	
QY	258	IETOPRARLLTAHHLFVAPQHNOSEATGSTSQALAFSNVKPCQRRVVLGEQGOQL	317	
Db	260	IETOPRARLLTAHHLFVAPQHNOSEATGSTSQALAFSNVKPCQRRVVLGEQGOQL	319	
QY	318	PASVHSVAREEASGAYAFLTAQGTLILRNVLASCYAVIEEHSHSWAIWAFAFRFLAQGL	377	
Db	314	PARVAATS-THVALGAYAFLTKHGTLYWDVWASCPAAVADHHLQALFWPLRLFHSLAW	372	
QY	378	ALCPDGDAIFTAATTGIGIHWYSRULYRICSSWVLDGDLAHLPGMVA	425	
Db	373	G-----SWTPEGEVWVWPQYLRGSLMLLEBGSFHFGMSGAGS	411	
RESULT 13				
IHH_BRARE				
ID	IHH_BRARE		STANDARD:	PRT;
AC	Q88862;			412 AA.
DT	15-JUL-1999	(Rel. 38, Created)		
DT	15-JUL-1999	(Rel. 38, last sequence update)		
DT	16-OCT-2001	(Rel. 40, last annotation update)		
DE	Indian hedgehog protein precursor (IHH) (Echidna hedgehog protein).			
GN	EHH.			
OS	Danio rerio (Zebrafish) (Danio rerio); Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Neopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.			
OC				
OC				
OX				
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE:96310864; PubMed=8684485;			
RA	Currie P.D., Ingham P.W.;			
RA	"Evolutionary analyses of a specific muscle cell type by a hedgehog-like protein in zebrafish."			
RT	Nature 382:452-455(1996).			
RT	[2]			
RN	SEQUENCE OF 113-170 FROM N.A.			
RC	TISSUE=MUSCLE;			
RX	MEDLINE:97075114; PubMed=8917540;			
RA	Zardoya R., Abouheif E., Meyer A.;			
RT	"Evolutionary analyses of a specific muscle cell type by a hedgehog-like protein in zebrafish," closely related to the zebrafish.;			

DR EMBL; AB010993; BAA24866.1; JOINED.
 DR EMBL; 059748; AAB03398.1; -.
 DR HSSP; -.
 DR MEROPS; C45_004; -.
 DR Gener; HGNC:2865; DHH.
 DR MIM; 605423; -.
 DR MIM; 607080; -.
 DR InterPro; IPR000320; HH_signal.
 DR InterPro; IPR01767; Hedgehog_hint.
 DR InterPro; IPR03586; Hedgehog_hintC.
 DR InterPro; IPR003587; Hedgehog_hintN.
 DR InterPro; IPR01657; Sonichh.
 DR Pfam; PF01079; Hint; 1.
 DR Pfam; PF01085; HH_Signal; 1.
 DR PRINTS; PRO0632; SONICHHOG.
 DR PRODOM; PDO03042; HH_Signal; 1.
 DR SMART; SM00305; HintC; 1.
 DR SMART; SM00306; HintN; 1.
 KW Developmental protein; Autocatalytic cleavage; Hydrolase; Protease;
 KW Signal; Lipoprotein; Palmitate.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 396 DESERT HEDGEHOG PROTEIN.
 FT CHAIN 23 398 DESERT HEDGEHOG PROTEIN N-PRODUCT.
 FT CHAIN 199 396 DESERT HEDGEHOG PROTEIN C-PRODUCT.
 FT SITE 198 199 CLEAVAGE (AUTO-) (BY SIMILARITY).
 FT SITE 244 INVOLVED IN CHOLESTEROL TRANSFER (BY
 FT SITE 268 268 SIMILARITY).
 FT ACT_SITE 271 271 INVOLVED IN AUTO-CLEAVAGE (BY
 FT BINDING 198 198 SIMILARITY).
 FT LIPID 23 23 CHOLESTEROL (BY SIMILARITY).
 FT CONFLICT 177 177 PALMITATE (BY SIMILARITY).
 SQ SEQUENCE 396 AA; 43577 MW; FCE4FB21972C3ADS CRC64;

 Query Match 54.0%; Score 1198; DB 1; Length 396;
 Best Local Similarity 59.4%; Pred. No. 9; 2e-90;
 Matches 244; Conservative 56; Mismatches 91; Indels 20; Gaps 0
 Qy 4 MILLTRILLVGSFIC-ALLVSSGLTGPGGRG-IGKRHHPKK-LTPLAYKQFIPNVAEKT 59
 Db 1 MALLTNLPP--LCLCLALLALPAQSCGPGRGPGRYARRQQLVPLLYKQVPGPERYL 57
 Qy 60 GASGRYEGKTRNNSERPEKLTQPNYNPDIKEDEENTGADRLMTORCKDKLVALATSYMQ 119
 Db 58 GASGPAGRVARGRGSRERFDLVNPYNPDIFKDEENSGADRMLTERCKERVNLAIAWMN 117
 Qy 120 WPGKVLRVTEGWDDEGHHSSESLHYGRANWITTSQRDRSKYGMALARLAVAGFDAYYE 179
 Db 118 WPGVRURVTEGWDDEGHHSQDLSHYGRANWITTSQRDRSKYGMALARLAVAGFDAYYE 177
 Qy 180 SKAHICSVKAENSAVAKSGCGCFPGSATVHLHGGTKLVDLSPGDVLADADGRULY 239
 Db 178 SRNHVHVSKADNSLAVRAGGCFCFGNAHATRVLWSGERKGLERLHRGDWVLAADASGRVPT 237
 Qy 240 DFLTFDMDSSRKLTIVETRQPRLLTAAHLLFVAPQHNOSEATGTSQGOLFASH 299
 Db 238 PVLFLFLDRDQRRASTFWAVETEWPPRKLILPWHFLVFAA--RGPAAPAGPDA--PVFARR 293
 Qy 300 VPKGQRYIVLGGQOPLLPSVSYHSVSLREEEAGAKPLTQGTILNRLVASCYAVIEEH 359
 Db 294 LLAGDS--VLPAGGDLRPARVARYA--REAVGVFPLTAHGTLLVNDVLASCYAVLESH 350
 Qy 360 SWAHWAEPFPLAQGLIAALCPDGAITAATTGJHWYLRLYRGSWL 410
 Db 351 QWAHRAEPAPRLILHA-LGALIPLGGAV---OPTGHWHWYSLYLRYLAELL 395

Search completed: February 20, 2003, 10:12:37
Job time : 14.0329 secs

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OM protein - protein search, using sw model

Run on: February 20, 2003, 10:06:28 : Search time 27,3373 seconds
(w/o alignments)
3203.314 Million cell updates/sec

Title: Perfect score: US-09-827-110A-10

Sequence: 1 MEMMLTRILVGFICLL.....GSWVLGDGDAHLFLGWMARAS 425

Scoring table: Blosum62

Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPREMBL_21:
1: sp_archea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_micr:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rabbit:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_virus:
16: sp_bacteriapl:
17: sp_archeab:

Pred. No. 19 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	1590.5	71.7	434	13	057404 pleurodeles
2	1499	67.6	414	13	09w799 parallichthy
3	1313.5	59.2	406	13	057567 notophthalm
4	1099	49.5	415	5	090526 branchiost
5	1095	49.4	415	5	017499 branchiost
6	1059	47.7	442	13	073803 fugu rubrip
7	1044.5	47.1	447	5	Q9GRAB gryllus bim
8	906	40.8	410	5	061676 lyticeinus
9	832	37.5	161	11	Q9R179 rattus norv
10	737	33.2	150	13	Q9YGV7 ambyctoma m
11	735	-33.1	139	6	Q9XS16 bos taurus
12	713	32.1	13	Q9W6C1 eleutherod	
13	697	31.4	177	11	Q9WV29 rattus norv
14	682	30.7	137	13	042234 coturnix co
15	624	28.1	185	5	056693 junonia coe
16	531	23.9	99	13	Q8QGN4 scylliorhinu

ALIGNMENTS

RESULT 1

ID	PRIMARY;	PRT;	434 AA.
057404	057404; DT 01-JUN-1998 (TREMBLrel. 06, Created) DT 01-JUN-1998 (TREMBLrel. 06, last sequence update) DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)		
AC	SONIC_HEDGEHOG		
DE	Sonic hedgehog-related protein. FW SHH.		
GN	pleurodeles waltl (Iberian ribbed newt); Eukaryote; Metazoa; Vertebrata; Euteleostomi; Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Pleurodeles.		
OS			
OC			
OC			
OC			
OX			
RN			
RP	SEQUENCE FROM N.A.		
RA	Cauvit X., Nicolas S., Le Parco Y.;		
RT	Pleurodeles sonic hedgehog."		
RL	Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.		
DR	EMBL; AF003532; AAB94412.1; -;		
DR	HSSP; Q6226; IVHH.		
DR	MEROPS; C46.002; -;		
DR	InterPro; IPR01767; Hedgehog_hint.		
DR	InterPro; IPR003586; Hedgehog_hintC.		
DR	InterPro; IPR003587; Hedgehog_hintN.		
DR	InterPro; IPR00020; HH_Signal.		
DR	InterPro; IPR002203; Intcain.		
DR	IntexPro; IPR001657; SonicHH.		
DR	PFam; PF01085; HH_Signal; 1.		
DR	PFam; PF01079; Hint; 1.		
DR	PRINTS; PR00632; SONICHHG.		
DR	PIR002042; HH_Signal; 1.		
DR	SMART; SM00305; HintC; 1.		
DR	SMART; SM00306; HintN; 1.		
SQ	SEQUENCE 434 AA; 48421 MW; A9495E367151AE74 CRC64;		

Query Match 71.7%; Score 1590.5; DB 13; Length 434;
Best Local Similarity 71.5%; Pred. No. 9.1e-123;
Matches 311; Conservative 40; Mismatches 73; Indels 11; Gaps 3;

Query Match 67.6%; Score 1499; DB 13; Length 414;
 Best Local Similarity 69.3%; Pred. No. 3e-115; Indels 8; Gaps 5;
 Matches 289; Conservative 52; Mismatches 68;

QY	1 MYEMLILTRILINGFICALLYSSGLGCGPGRIGKRRHKKLTPPLAYKOFIPNAAEKTIG 60
Db	1 MCEMILURRDGGFISPLVPLGCGPGRIGKRRHKKLTPPLAYKOFIPNAAEKTIG 60
QY	61 ASGRYEGNITRNSERFEKLTPTNNPDITFKDENTGADRMTORCKDLNAISVMNQW 120
Db	61 ASGRYEGNITRNSERFEKLTPTNNPDITFKDENTGADRMTORCKDLNAISVMNQW 120
QY	121 PEVYLRTVEGWDGHISEESLHYEGRAVIDTSDRSRSKGMLARLAVEAGFDWVYES 180
Db	121 PEVYLRTVEGWDGHISEESLHYEGRAVIDTSDRSRSKGMLARLAVEAGFDWVYES 180
QY	181 KAHINCSVKAENSAKSGGCFPGSATVLEGGTKLVKDLSPGDRVLADADGRILYSD 240
Db	181 KAHINCSVKAENSAKSGGCFPGSATVLEGGTKLVKDLSPGDRVLADADGRILYSD 240
QY	241 FLMFLDRMDSSRKLFYIETROPRARLLTAHLFLVAPOHNOSEATGSTSG-----Q 293
Db	241 FLMFLDRMDSSRKLFYIETROPRARLLTAHLFLVAPOHNOSEATGSTSG-----Q 293
QY	301 SMPSASSRPGRVLTEDREGGRIRAEFYDVRVL-EETGAYAPVTANGIVVUDRLASCY 359
Db	301 SMPSASSRPGRVLTEDREGGRIRAEFYDVRVL-EETGAYAPVTANGIVVUDRLASCY 359
QY	354 AVTEEHSHWAHAFAPFLAQGLIALACP--DGAIPTAATTGIIHWYSRLYRIGSWL 410
Db	360 AVTEEHSHWAHAFAPLRVGFGLSFFSPDYSSHPPAPSQAEGVHWYSELYRIGTWL 419
QY	411 DGDALHPLGMVARPS 425
Db	420 QADTHPLGMAAKSS 434

RESULT 2

ID	Q9W7Q9 PRELIMINARY; PRT: 414 AA.
AC	Q9W7Q9; 039709; 01-NOV-1999 (Tremblrel. 12, Created)
DT	01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE	Sonic hedgehog.
SH1	Paralichthys olivaceus (Flounder).
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Neoteleostei; Acanthopterygii; Acanthopterygii; Percomorphi; Pleuronectiformes; Pleuronectoidei; Paralichthyidae; Paralichthys.
OX	NCBI_TaxID=6255;
RN	[1] SEQUENCE FROM N.A.
RP	MEDLINE:9928226; Pubmed=10223710;
RX	Suzuki T., Ichiro O., Kurokawa T., "Retinoic acid given at late embryonic stage depresses sonic hedgehog and Hoxa-4 expression in the pharyngeal area and induces skeletal malformation in flounder (Paralichthys olivaceus) embryos.", Dev. Growth Differ., 41:143-152(1999).
RT	Dev. Growth Differ., 41:143-152(1999).
RL	EMBL; AB029448; BRA82560.1; -.
DR	O62226; 1VHH.
DR	MEROPS: C46_001; -.
DR	InterPro: IPR00167; Hedgehog_hint.
DR	InterPro: IPR03386; Hedgehog_hintC.
DR	InterPro: IPR003587; Hedgehog_hintN.
DR	InterPro: IPR00320; HH_signal.
DR	InterPro: IPR02203; Intein.
DR	InterPro: IPR001657; SonichH.
PFam	PF01085; HH_signal; 1.
PRINTS	PRO0632; SONICHOG.
DR	PRODom; PD003042; HH_signal; 1.
DR	SMART; SM00305; HintC; 1.
SEQUENCE	414 AA; 45945 MW; 50607BR3DB7CODA3 CRC64;

RESULT 3

ID	Q57567 PRELIMINARY; PRT: 406 AA.
AC	Q57567; 037567; 01-JUN-1998 (Tremblrel. 06, Created)
DT	01-JUN-1998 (Tremblrel. 06, Last sequence update)
DE	Hedgehog segment polarity homolog.
OS	Notophthalmus viridescens (Baster next) (Triturus viridescens).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Notophthalmus.
OX	NCBI_TaxID=8316;
RN	[1] SEQUENCE FROM N.A.
RA	Stark D. R., Gates P. B., Brookes J. P., Ferretti P.;
RT	"Hedgehog homologue from Notophthalmus viridescens.", Dev. Dyn. 0:0-0 (1998).
RL	-1 SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE PHOSPHORIBOSYLTRANSFERASE FAMILY.
CC	EMBL; AE047466; AAC03108.1; -.
DR	062226; 1VHH.
DR	InterPro: IPR00167; Hedgehog_hint.
DR	InterPro: IPR03586; Hedgehog_hintC.
DR	InterPro: IPR00387; Hedgehog_hintN.
DR	InterPro: IPR00320; HH_signal.
DR	InterPro: IPR00320; HH_signal.
DR	InterPro: IPR02375; PR_PyR_Transf.
DR	InterPro: IPR00157; SonichH.
DR	Pfam; PF01085; HH_signal; 1.
DR	PRINTS; PRO0632; SONICHOG.
DR	PRODom; PD003042; HH_signal; 1.
DR	SMART; SM00305; HintC; 1.
DR	PROSITE; PS00103; PUR_Pyr_PR_TRANSFER; 1.
KW	Glycosyltransferase; Transferase.
SEQUENCE	406 AA; 45072 MW; 5842CCAD5314D40 CRC64;

Query Match 59.2%; Score 1313.5; DB 13; Length 406;

Best Local Similarity 62.9%; Pred. No. 5.8e-100; Matches 265; Conservative 43; Mismatches 94; Indels 19; Gaps 5;

Qy 7 LTRTLVPGTICALVS--SGLTCGGGRGKRRPKKLTPLAYKOPIPNVAEKTIGASGR 64
Db 3 LLALPLILAVACALLGGCGPGRVIGRRRPPRPIPLSKQFLRHPEKTLGASR 62

Qy 65 YEGKITRNSERFKELTPWNPDIFKDEENTGADRMLTQRCDDKLNALAISVNQWPGK 124
Db 63 YEGKITRNSERFKELTPWNPDIFKDEENTGADRMLTQRCDDKLNALAISVNQWPGK 122

Qy 125 LRVTEGWDGHHSBESLHVEGRADVDTTSDRDRSKYOMLARIAVEAGFDWVYYESKHLI 184
Db 123 LRVTEGWDGHHSBESLHVEGRADVDTTSDRDRSKYOMLARIAVEAGFDWVYYESKHLI 182

Qy 245 LDRMDSSRKLFLVYVETROPRARLLTAHLFLVPAQHNOSEATGSTSQALFASNVPGQ 304
Db 243 LDRRSTAVKEFYVWETRDPPRLAHLFLVDAFNFTVPLTDFT---VFASHVOPGQ 298

Qy 305 RYVVLGEQGQQLIRASVHSVSLREAAASCAYAPITAOGLTILINVLASCYAVIEEHSHAH 364
Db 299 --VILTEGVGLQPARVSVTQD-SGAYAPLTSGHSPGLLVDDWVSCAEVQVKHQAQL 355

Qy 365 AFAPFRLLAQGLLALACPDAQTAAUTGIGHLYRIGSWWLDGALPLGMVAPLA 424
Db 356 AFWFLRLYH-----SVGRRETQPEGMHWTSLLXLRKGVLUMKEQFHFGMSTK 405

Qy 425 S 425
Db 406 S 406

RESULT 4

ID Q0526	PRELIMINARY;	PRT; 415 AA.
AC Q0526;		
DT 01-MAY-2000 (TREMBLREL. 13, Created)		
DT 01-DEC-2001 (TREMBLREL. 19, Last sequence update)		
DT 01-JUN-2002 (TREMBLREL. 21, Last annotation update)		
DE Hedgehog protein.		
GN HEDGEHOC.		
OS Branchiostoma belcheri (Amphioxus).		
OC Branchiostoma;		
OX NCBI_TAXID:7741;		
RP	SEQUENCE FROM N.A.	
RA MAO B., Zhang Y., Zhang S., Zhang H.,	"A preliminary study on Qingdao amphioxus hedgehog gene.",	
RT Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RL EMBL; AU245862; CAB58231.2; -.		
DR 062226; 1VHH.		
DR InterPro; IPR001767; Hedgehog_hint.		
DR InterPro; IPR003586; Hedgehog_hintC.		
DR InterPro; IPR003587; Hedgehog_hintN.		
DR InterPro; IPR00320; HH_signal.		
DR InterPro; IPR002203; Intein.		
DR InterPro; IPR001657; SonichH.		
DR Pfam; PF01085; HH_signal; 1.		
DR PRINTS; PRO0632; SONICHHOG.		
DR InterPro; IPR00320; HH_signal.		
DR InterPro; IPR002203; Intein.		
DR Pfam; PF01079; HIntN; 2.		
DR PRINTS; PRO0632; SONICHHOG.		
DR ProDom; PD003042; HH_signal; 1.		
DR SMART; SM00305; HIntC; 1.		
DR SMART; SM00306; HIntN; 1.		
DR SEQUENCE 415 AA; 46912 MW; 588D2BD215BDD931 CRC64;		

Query Match Best Local Similarity 49.4%; Score 1095; DB 5; Length 415; Matches 221; Conservative 54; Mismatches 123; Indels 18; Gaps 6;

Qy 11 LLVGFICALLVSGGL-----TCGPQRGIGKRRRHKLTPLAYKOPIPNVAEKTIGAS 62
Db 4 VLAARMWMLVLAISALGTHMGPSBACGFGGRGRRRHKLTPVYKQMPAVSENTFGAS 63

Query Match Best Local Similarity 55.6%; Pred. No. 2.9e-82; Matches 218; Conservative 51; Mismatches 113; Indels 10; Gaps 5;

Qy 27 CGPRGIGKRRHPKKLTPLAYKOPIPNVAEKTIGASGRVEGKITRNSERFKELTPWNPD 86
Db 28 CGPCTTRYGRHRPKLTPVYKQMPAVSENTFGASGLENGRTDRSERFTLQNFNT 87

Qy 87 IIFDEEKTGADRMLTQRCDDKLNALAISVNQWPG 146
Db 88 IIFDEEKTGADRMLTQRCDDKLNALAISVNQWPGVILRVTSWMDGCHHSLESHLVEG 147

Qy 147 RAVDITTSDRRSKRYGMLARLAVERAGEDWVYYESKHLI 206
Db 148 RAVDITTSDRRSKRYGMLARLAVERAGEDWVYYESKHLI 207

Qy 207 TVHLEGGTKVLVKDLSPGDRVLAADAGRLLSDFLTFLDRMDSRKLFLVYVIETRQPR 266
Db 208 WYTRDGRKRMVRPQGDVKLSMSDAGHPVFSVLTMDRSRGWPWYTTKEDRWT 267

Qy 323 REE-KGAVAPLTAGTILINVLASCYAVIEENSWHAFAPRLAQLLALCPDGAI 386
Db 379 SHDOTLQSGVHWPSFFERYGISLVEPTLHP 410

Qy 387 T-AATTGIGHWSRLYRIGSWWLDGALHP 417

Db 64 GLFNGRITDOSERFILKONENTDIFKDFEKTGADFMTQRCOKLNALAISTMNQWEG 123
 Qy 123 VKLRTYEGWEDGHSEESHYEGRAVDTSDRSRSKGMLARAVEAGFDWYHESKA 182
 Db 124 VKLRTEGWEDGHSEESHYEGRAVDTSDRSRSKGMLARAVEAGFDWYHESKA 183
 Qy 183 HHCSCVKAENSAKASGGCPGSATVHLEGGTKLVKDLSPGDRVLADADGRLLYSDFL 242
 ||||| : ||||| ; ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
 Db 184 HHCSCVKAESDTTATGGCSEAHSWTRDGNRINRDYRPGDKVLSMSGGHPVSEVL 243
 Qy 243 TFLDRMDSSKRKYIETROPRARLLTAAHILFWAPOHNQSEATGSTSQALFASNVKP 302
 ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
 244 TMFDRBSPRGPHWVYIHTDRNITYATPSHLVFTESRL---SSPRIAKNSDARP 298
 Qy 303 GORVYVLGEGLPQQLLPASVSVLSEASAYAPTAQGTLINRVLASCYAVTEHWA 362
 ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
 Db 299 GEFLIPDSDGGFGRKVTVSVMHE-KGAYAPI-TVHGIVVVWDVAMSYALISQAL 357
 ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
 Qy 363 HWAFAFPPLAQGLLACPCGAIP-AATTGIGHWSRLYRIGSWLGDALHP 417
 ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
 Db 358 HWVAFPPRLYQOLTSLW-DG--PSHDOTLOEGVHWPSFEYRGISLVEPTLHP 410
 ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||

RESULT 6

ID 073803 PRELIMINARY; PRT; 442 AA.
 AC 073803;
 DT 01-AUG-1998 (TREMBLel. 07, Created)
 DT 01-AUG-1998 (TREMBLel. 07, last sequence update)
 DE 01-JUN-2002 (TREMBLel. 21, last annotation update)
 DE Fugu hedgehog.
 FN Fugu.
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopercyidae; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Takifugu.
 OC NCBI_TaxID=31033;
 RN [1] SEQUENCE FROM N.A.
 RX MEDLINE-9917347; PubMed=1007531;
 RA Geliner K.; Brenner S.;
 RT "Analysis of 148 kb of genomic DNA around the wnt1 locus of Fugu
 rubripes.";
 RL Genome Res. 9:251-258(1999).
 EMBL: AF05116; AAC:4384.1; -.
 DR HSSP: 06226, 1VHH.
 DR InterPro: IPR001767; Hedgehog_hint.
 DR InterPro: IPR003586; Hedgehog_hintC.
 DR InterPro: IPR003587; Hedgehog_hintN.
 DR InterPro: IPR000320; HH_signal.
 DR InterPro: IPR002203; Intein.
 DR Pfam: PF01085; HH_signal; 1.
 DR Pfam: PF01079; Hint; 1.
 DR PRODOM: PD003042; HH_signal; 1.
 DR SMART: SM00305; HH_C; 1.
 DR SMART: SM00306; HintN; 1.
 DR SMART: SM00306; HH_Signal; 1.
 SQ SEQUENCE 442 AA; 4926 MW; 1CB2B423B4B748E8 CRC64;

Query Match Best Local Similarity 50.5%; Score 1059; DB 13; Length 442;
 Matches 223; Conservative 56; Mismatches 115; Indels 48; Gaps 9;

Qy 11 LIVGFTICALVASSGLTCGPGRGIGKRRHPRKLTPIAYKOPIPNVAEKTGASGRREGKIT 70
 ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
 Db 14 LLAANSCVWLVOG---CGPGPYGYTRPRPKLAKMYKQFEPNLSENLLGASGRAEGKIT 70
 71 RNSERKEELTPNYNDIIFDEENGADRLMTQRDKLNALASVANQPGVKURTEG 130
 71 RNSERKEELTPNYNDIIFDEENGADRLMTQRDKLNALASVANQPGVKURTEA 130
 Qy 131 WDEDGHHSESSLHYGRAVDITSDRSRSKYMGLARLAVEAQFDWVYESKAHICSVKA 190

Db 131 WDEDGHHPGSLHYGRAVDITDDRETERYGLQQLAVABGFDWYHESKAHICSVKA 190
 ||||||| : ||||||| : ||||||| : ||||||| : ||||||| : ||||||| : ||||||| : |||||||
 Qy 191 ENSVAKSGCCEPGSATVHLEGGTKLVKDLSPGDRVLADADGRLLYSDFL 250
 ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
 Db 191 DRSVAVEKGGCPGMSRVTAGFORKSLSSLTGDRVMALAVEAGFDWYHESKA 183
 ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
 Qy 251 SRKLFVVIETQPRARLLTAHLLEVAPOHNQSEA--TGTSQALFASNVKPGQRY 307
 ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
 Db 251 SRWRFLSLOTFEDGR-RLAVENTPHLUF----SDAHCPDSQYQAOFASRAGTGTCVL 302
 ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
 Qy 308 VLGEQQQLPAPASVHSVLSEASAYAPTAQGTLINRVLASCYAVTEHWA 367
 ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
 303 VHTAGG-EVHSRIVSIT-BEEVGAYAPLTEAGSVFVDGLASSYALVEDHOLAHWAFC 360
 ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
 Qy 368 PFRL-----AGGLALACPGKA-----PSAATWTG-----I 395
 ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
 Db 361 PVRLSSVSQOLLWABEPEERSDGSKTPQPLPVALVRDRVKARNISVSRSBAGPRGTSEV 420
 ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
 Qy 396 HWYSLRLYRIGSWLGDALHP 417
 ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
 Db 421 HWYAOULHRLGWIVLNPDLFHP 442
 ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||

RESULT 7

ID OGRRAB PRELIMINARY; PRT; 447 AA.
 AC OGRRAB;
 DT 01-MAR-2001 (TREMBLel. 16, Created)
 DT 01-MAR-2001 (TREMBLel. 16, last sequence update)
 DE 01-JUN-2002 (TREMBLel. 21, last annotation update)
 DE Hedgehog protein (Fragment).
 OS Gryllus bimaculatus (Two-spotted cricket).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae;
 OC Gryllinae; Gryllus.
 OC NCBI_TaxID=6999;
 RN [1] SEQUENCE FROM N.A.
 RX MEDLINE-20461145; PubMed=11003837;
 RA Niwa N.; Inoue Y.; Nozawa A.; Saito M.; Misumi Y.; Ohuchi H.,
 RA Yoshioka H.; Noji I.S.;
 RT "Correlation of diversity of leg morphology in Gryllus bimaculatus
 (cricket) with divergence in dpp expression pattern during leg
 development.";
 RT Development 127: 4373-4381 (2000).
 RL EMBL: AB044709; BAB19658.1; -.
 DR HSSP: Q6226, 1VHH.
 DR InterPro: IPR001767; Hedgehog_hint.
 DR InterPro: IPR003586; Hedgehog_hintC.
 DR InterPro: IPR003587; Hedgehog_hintN.
 DR InterPro: IPR000320; HH_signal.
 DR InterPro: IPR001657; SonichH.
 DR Pfam: PF01085; HH_Signal; 1.
 DR Pfam: PF01079; Hint; 1.
 DR PRINTS: PR00632; SONICHHOG.
 DR PRODOM: PD003042; HH_Signal; 1.
 DR SMART: SM00305; HH_C; 1.
 DR SMART: SM00306; HintN; 1.
 DR SMART: SM00306; HH_Signal; 1.
 FT NON_TER 1
 SQ SEQUENCE 447 AA; 48008 MW; 29AEFB061C3EB6F0 CRC64;
 Query Match Best Local Similarity 47.1%; Score 1044.5; DB 5; Length 447;
 Matches 220; Conservative 48; Mismatches 123; Indels 17; Gaps 8;

Qy 3 EMLLUTRILNGFICALLYSSGLTCGPGRGIGKRRHPRKLTPIAYKOPIPNVAEKTGASGRREGKIT 62
 ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
 Db 14 KMLPLRWL---LILLMOCARACGPGRGARRRASRRLTPVQHQHVNSENTLGA 70
 ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
 Qy 63 GRYECKITRNSERKEELTPNYNDIIFDEENGADRLMTQRDKLNALASVANQPGVKURTEA 122
 ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
 71 GPAERRVVARUDPFRDLPVNWADIVFKDDEGTTGADRMLTORCKERLNTLAISTMNQWP 130
 ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||

OY	123 VKLRTVEGDEODCHHSESESHYGRADVDTTSRDRSKYMLARLAVENGEDWYYESKA 182
Db	131 VRLVIEGWDDEEGHGAADSLHBYGRAVDWTTSRDRSKYMLARLAVENGEDWYYESKA 190
Db	183 HINGSVRAENSAVAKSGCCFPGSATVHLERGGTKLVKDLSPGR-VLAADADGRLLYSDF 241
QY	191 HINGSVRAENSAVAKSGCCFPGSATVHLERGGTKLVKDLSPGR-VLAADADGRLLYSDF 249
Db	242 LTFDLDRMOSRSKRFYVTRPRAVLITAAHLLFVAPOHNOSEATGSTSGOALFASWK 301
QY	244 LTFDLDRMOSRSKRFYVTRPRAVLITAAHLLFVAPOHNOSEATGSTSGOALFASWK 301
Db	250 LTFDLDRDPAAPTLLRV-RVASGR-LAIIPLSHLPVA-----RAGGEPEARFADAWR 300
QY	302 PGSRVYVIGELEGGQLPASVHSISREASGAYAPLTAQTLINRLASCYAVIEWSW 361
Db	301 PGIDALLVADAGGAVAPRDPDVYDAETRGGVVAPLTAQTLINRLASCYAVIWSW 360
OY	362 AHWFAPPFRLAQILLA-NLCPCGA-IPTAATTGIAHWYSLRYRIG 406
Db	361 AHWFAPPFRLAQILLA-NLCPCGA-IPTAATTGIAHWYSLRYRIG 408
RESULT 8	
ID	061676 PRELIMINARY; PRT; 410 AA.
AC	061675; OC
DT	01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE	Hedgehog.
OS	Lutrechinius variegatus (Sea urchin).
OC	Eukaryota; Metazoa; Echinodermata; Echinozoa; Echinoidea; Echinoidae; Echinoidea; Euechinoidea; Echinacea; Temnopleuroidea; Toxopneustidae; OCBI-TAXID=7654;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Heitzler P.L.; McClay D.R.; RT
RL	"A sea urchin hedgehog homolog.", Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AR059606; AAC15065.1; -.
DR	InterPro; IPR001767; Hedgehog_domain.
DR	InterPro; IPR001767; Hedgehog_hinc.
DR	InterPro; IPR003566; Hedgehog_hinc.
DR	InterPro; IPR003587; Hedgehog_hinc.
DR	InterPro; IPR003590; HH_Signal.
DR	InterPro; IPR002203; Intein.
DR	InterPro; IPR001657; SonichH.
PFam	PF0105; HH_Signal; 1.
PRINTS	PR00632; SONICHHOG.
DR	PRODom; PDD003042; HH_Signal; 1.
PT	NON_TER 1
PT	NON_TER 1
SQ	SEQUENCE 410 AA; 46071 MW; 875CF889DA6FDBED CRC64;
Query Match	37.5%; Score 832; DB 11; Length 161;
Best Local Similarity	98.1%; Pred. No. 7.3e-61;
Matches	158; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY	87 LTFKBDENTGADRLLMTCRCKDLNALAISTYNQWQVVKLRTVEGWDDEGHSEESLYEG 146
Db	1 LTFKBDENTGADRLLMTCRCKDLNALAISTYNQWQVVKLRTVEGWDDEGHSEESLYEG 60
QY	147 RAVDITTSRDRSKYMLARLAVEAGFDWYYESKAHINCVAKNSVAKSGCCFPGSA 206
Db	61 RAVDITTSRDRSKYMLARLAVEAGFDWYYESKAHINCVAKNSVAKSGCCFPGSA 120
QY	207 TVHLERGGTKLVKDLSPGRDVLAAADGRLLYSDFLTFLDR 247
Db	121 TVHLERGGTKLVKDLSPGRDVLAAADGRLLYSDFLTFLDR 161
RESULT 10	
ID	091677 PRELIMINARY; PRT; 150 AA.
AC	091676; OC
DT	01-MAY-1999 (TREMBLrel. 10, Created)
DT	01-MAY-1999 (TREMBLrel. 20, Last sequence update)
DE	Sonic hedgehog (Fragment).
Db	357 ASFADIRWYIWHM--GIDTDITGQEQVRHWIYTOGLKLGKVW-SDRLFP 406
QY	358 ASFADIRWYIWHM--GIDTDITGQEQVRHWIYTOGLKLGKVW-SDRLFP 408
RESULT 9	
ID	09R179 PRELIMINARY; PRT; 161 AA.
AC	09R179; OC
DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE	Sonic hedgehog protein (Fragment).
OS	Rattus norvegicus (Rat).
RA	Garges P.L.; Meyer R.A. Jr.; Brown C.A.; Price D.K.; RA
RL	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=SPRAGUE-DAWLEY; TISSUE=KIDNEY;
RA	Stinson hedgehog in the rat.", Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AF062915; AAD5373.1; -.
DR	HSSP; 062226; IVHH.
DR	MEROPS; C416.002;
DR	InterPro; IPR001767; Hedgehog_hinc.
DR	InterPro; IPR000320; HH_Signal.
DR	InterPro; IPR001657; SonichH.
DR	Pfam; PF001085; HH_Signal; 1.
DR	PRINTS; PR00632; SONICHHOG.
DR	PRODom; PDD003042; HH_Signal; 1.
PT	NON_TER 1
PT	NON_TER 1
SQ	SEQUENCE 161 AA; 17906 MW; DF06D85FB45AE4DB CRC64;
Query Match	40.8%; Score 906; DB 5; Length 410;
Best Local Similarity	48.1%; Pred. No. 2.4e-65;
Matches	199; Conservative 65; Mismatches 134; Indels 16; Gaps 10;
QY	7 LTFLVLFCC-LVSSGLTCGPGKGKRRH-PKKITPLAYQFINVAEKTILGASCR 64
Db	6 MVKWLTVQITTAICLIALTOACHPGRS-GKTSRHPRNRPHQPLQKQKVNPNEQFGASGP 64
QY	65 YEGKITRNFELPNTPNINPDITFKDEBTNGADRLLMTCRCKDLNALAISTYNQWQVVKLRTVEGWDDEGHSEESLYEG 124
Db	65 PEGRIDDDERFSKLSPNNDDIVFKDSEGTGADRLLMTCRCKDLNALAISTYNQWQVVKLRTVEGWDDEGHSEESLYEG 124
QY	125 LRYTEGWDGDGHSEESLYEGRAVDITTSRDRSKYMLARLAVEAGFDWYYESKAHINCVAKNSVAKSGCCFPGSA 184
Db	125 LRYVEAWDED-QPNVPELHAEGRAVDITTSRDRSKYMLARLAVEAGFDWYYESKAHINCVAKNSVAKSGCCFPGSA 183
QY	185 HCSVKAENSAVAKSGCCFPGSAVHLERGGTKLVKDLSPGRDVLAAADGRLLYSDFLTFLDR 244

OS Ambystoma mexicanum (Axolotl); Craniata; Vertebrata; Euteleostomi;
 OC Eukaryota; Metazoa; Chordata; Salamandroidea; Ambystomatidae;
 OC Ambystoma;
 OC NCBI_TAXID=8296;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tork M.A., Izquierdo Belmonte J.C., Gardiner D.M., Bryant S.V.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: AF031480; AAD18128.1; -.
 DR HSSP: 062256; IYHH.
 DR InterPro: IPR001767; Hedgehog-hint.
 DR InterPro; IPR000320; HH_signal.
 DR InterPro; IPR001657; SonicHH.
 DR Pfam: PF01079; Hntc_1.
 DR Prints; PRO0632; SONICHHOC.
 DR Prodrom; PDO03042; HH_signal; 1.
 FT NON_TER 1 1
 FT NON_TER 150 150
 SQ SEQUENCE 150 AA; 16599 MW; 986F65037A69A8AC CRC64;
 Query Match Best Local Similarity 33.2%; Score 737; DB 13; Length 150;
 Matches 140; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
 QY 86 DIFFDEENTGADRIMTORCKDKLNALISWNPQGVKLRVTEGWDDEGHHSERSESLHYE 145
 Db 1 DIFFDEENTGADRIMTORCKDKLNALISWNPQGVKLRVTEGWDDEGHHSERSESLHYE 60
 QY 146 GRAVIDITTSDRSKYGMARLAVERGFDWVYFESKAHIHCSCVKANSAKSGCCFPAS 205
 Db 61 GRAVIDITTSDRSKYGMARLAVERGFDWVYFESKAHIHCSCVKANSAKSGCCFPAS 120
 QY 206 ATVHLHGGTLYKVLSPGDRVLAADAGR 235
 Db 121 AKVTLHGVTTRPVKDLRPGDVRVLAADGQR 150
 RESULT 11
 Q9X516 ID Q9X516 PRELIMINARY; PRT; 139 AA.
 AC Q9X516.
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DE Sonic hedgehog (Fragment).
 OS Bos taurus (Bovine).
 OC Bovidae; Bovine; Bos.
 OC NCBI_TAXID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 DR T.F., Richardson M.K., Olsson L., Schlosser G., Klymkowsky M.W.,
 RA Hanken J.;
 RT "Differences in vertebrate limb development revealed by studies of the
 direct developing frog *E. coqui*".
 DR Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: AF113403; AAD3436.1; -.
 DR HSSP: 062226; IYHH.
 DR InterPro; IPR000320; HH_signal.
 DR Eleutherodactylidae;
 DR Pfam: PF01085; HH_signal; 1.
 DR Prints; PRO0632; SONICHHOC.
 DR Prodrom; PDO03042; HH_signal; 1.
 FT NON_TER 1 1
 FT NON_TER 138 138
 SQ SEQUENCE 138 AA; 15751 MW; FF4156A17F4681FF0 CRC64;
 Query Match Best Local Similarity 32.1%; Score 713; DB 13; Length 138;
 Matches 134; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 51 IPNVAEKTGLGASGRYEGKTRNNSERKELETPNYNDIIFKDEENTGADRIMTORCKDKLN 110
 Db 1 IPNVAEKTGLGASGRYEGKTRNNSERKELETPNYNDIIFKDEENTGADRIMTORCKDKLN 60
 QY 111 ALAISYMNOPQGVKLRVTEGWDDEGHHSERSESLHYEGRADVITTSDRSKYGMARLAVE 170
 Db 61 ALAISVNLNGVGKLRVTEGWDDEGHHSERSESLHYEGRADVITTSDRSKYGMARLAVE 120
 DR Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: AF114100; AAD33926.1; -.
 DR HSSP: 062226; IYHH.
 DR InterPro; IPR000320; HH_signal.
 DR InterPro; IPR001657; SonicHH.
 DR Pfam: PF01085; HH_signal; 1.
 DR Prints; PRO0632; SONICHHOC.
 DR Prodrom; PDO03042; HH_signal; 1.
 FT NON_TER 1 1
 FT NON_TER 139 139
 SQ SEQUENCE 139 AA; 15961 MW; C83B0B96982046B1 CRC64;
 Query Match Best Local Similarity 33.1%; Score 735; DB 6; Length 139;
 Q9WV29 ID Q9WV29 PRELIMINARY; PRT; 177 AA.
 AC Q9WV29.
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Indian hedgehog protein (Fragment).
 OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Murida; Murinae; Rattus
 Rattus_taxid=1011;
 [1] SEQUENCE FROM N.A.
 RP STRAINS-SPRAGUE-DANLEY; TISSUE=KIDNEY;
 RA Carges P.L., Meyer R.A. Jr., Brown C.A., Price D.K.;
 RT "Indian hedgehog in rat;"
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF162914; ASN45372.1; -.
 DR IHSV; Q62226; IVHH.
 DR MEROPS; C46_003; -.
 DR InterPro: IPRO01767; Hedgehog_hint.
 DR InterPro: IPRO03587; Hedgehog_hintN.
 DR InterPro: IPRO0320; HH_signal.
 DR InterPro: IPRO01657; SonICHH.
 DR PFAM: PF01085; HH_signal; 1.
 DR PFAM: PF01079; Hint; 1.
 DR PRINTS: PRO0632; SONICHOG.
 DR PRODOM: PD000404; HH_signal; 1.
 DR SMART: SM00306; HIntN; 1.
 FT NON_TER 177 AA; HintN; 1.
 SQ SEQUENCE 177 AA: 19739 MW; CA5871626A565F65 CRC64;
 Query Match 31.4%; Score 697; DB 11; Length 177;
 Best Local Similarity 74.6%; Pred. No. 1. 2e-49;
 Matches 132; Conservative 14; Mismatches 31; Indels 0; Gaps 0;
 OY 100 LMWQCRQDKPLNLATISVMQPGVQLRVTGWDDEGHHSSEBSLHYEGRAVDTTSQRDRN 600
 Db 1 LMWQCRQDKPLNLATISVMQPGVQLRVTGWDDEGHHSSEBSLHYEGRAVDTTSQRDRN 600
 QY 160 KGMLARLAVEAGEDWVYESKATHCSTKAENSTAAGSGCCFGPSATVHLEGGTKLVK 211
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Sonic hedgehog (fragment).
 GN SHH.
 OS Coturnix coturnix (common quail).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauvia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Coturnix.
 OX NCBI_TAXID=9091;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:98167603; PUBMED=9435297;
 RA Bortucki A.G., Mendham L., Emerson C.P. Jr.;
 RT "Control of somite patterning by Sonic hedgehog and its downstream
 signal response genes.";
 RL Development 125: 777-790 (1998).
 DR MEROPS; C46_002; -.
 DR InterPro: IPRO01767; Hedgehog_hint.
 DR InterPro: IPRO01657; SonICHH.
 DR PFAM: PF01079; Hint; 1.
 DR PRINTS: PR00632; SONICHOG.
 DR SMART: SM00305; HIntN; 1.
 FT NON_TER 1 137 AA; 14571 MW; 7FD29DF815AF1532 CRC64;
 SQ SEQUENCE 137 AA: 14571 MW; 7FD29DF815AF1532 CRC64;

		Query Match	30.7%	Score 692;	DB 13;	Length 137;	
Best Local Similarity	95.6%	Pred. No.	1.3e-13;				
Matches	130;	Conservative	1;	Mismatches	5;	Indels	0;
							Gaps 0;
QY	290	TSGQALFASNVNPGORYVVLGGQQLIPASVHSVSREASGAYPLTAQDTILINRVL	349				
Db	2	TSGQAFFASNVKPGORYVVLGGGRQLLPASVHSVSREASGAYPLTAQDTILINRVL	61				
QY	350	ASCYAVIEEHSAWHAFAFPFLAQGLLAICDGAIPTATTGIGHWSRLYRIGSW	409				
Db	62	TSCYAVIEEHSAWHAFAFPFLAQGLLAICPDGAIFAGTTTGIHWYSRLYHIGSW	121				
QY	410	LDGDALIHPGMVAPAS	425				
Db	· 122	LDGDALIHPGMVAPAS	137				
RESULT	15						
Q66699							
ID	Q66699	PRELIMINARY;		PRN;	185 AA.		
AC	Q66699;						
DT	01-MAY-1999	(TREMBLrel. 10, Created)					
DT	01-MAY-1999	(TREMBLrel. 10, Last sequence update)					
DT	01-JUN-2001	(TREMBLrel. 17, Last annotation update)					
DE	Hedgehog protein (Fragment).						
GN	Junonia coenia (Peacock butterfly) (Precis coenia).						
OS	Eukaryota; Metazoa; Anthropoda; Tracheata; Hexapoda; Insecta;						
OC	Papilionoidea; Nymphalidae; Nymphalinae; Junonia.						
OX	NBII-TAXID-39708;						
RN	1)						
RP	SEQUENCE FROM N.A.						
RA	Kings D.N., Lewis D.L., Selegue J.E., Pearson B.J., Goodrich L.V.,						
RA	Johnson R.L., Gates J., Scott M.P., Carroll S.B.,						
RT	"recruitment of a hedgehog regulatory circuit in butterfly eyespot evolution."						
RT	Science 0:0-0 (1999).						
DR	EMBL: AF117474; AAD08931.1; -.						
DR	DBLP; 062226; IVMH.						
DR	Interpro; IPR000320; HH_signal.						
DR	Interpro; IPR010157; SonichHH.						
DR	PFAM; PF01085; HH_signal; 1.						
PRINTS	PRO0632; SONICHHG.						
DR	PRODOM; PDD03042; HH_signal; 1.						
FT	NON_TER 1						
FT	NON_TER 1						
SQ	SEQUENCE 185 AA;	20745 MW;	E9BF94CE2FAAE662 CRC64;				
Query Match	28.1%	Score 624;	DB 5;	Length 185;			
Best Local Similarity	68.8%	Pred. No.	1.3e-43;				
Matches	117;	Conservative	21;	Mismatches	30;	Indels	2;
							Gaps 2;
QY	61	ASGRYEKGTRNTERKFPLTPNYPDIFKDEINTGADRMLTORCKDLNLAISVNW	120				
Db	3	ASCPPEGIGITRDEKEFRDQDVNPNDPIDEFKDDEGTGADRMLTORCKDLNLAISVNW	62				
QY	121	PSYKLRTVEGWDDEGHSEESLHYEGRADWITSDRDRSKYMLARLAWEAGEDWVYES	180				
Db	63	PSYVLRTVEGWDDEBNEDSHLNLYHEGRADWITSDRDRSKYMLARLAWEAGEDWVYES	122				
QY	181	KALIHCCSVKAENSAVAKSGGCFFGSATVHLEHGCTKLVRDLSRGDRVLA	230				
Db	123	RSYIHCSVVKTESSVGT-GAGCFFPSGAVWHTENGSPXD-IASLKKGNKVLA	170				

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ON protein - protein search, using sw model

Title: US-09-827-110A-13

Perfect score: 2289

Sequence: 1 MILLARCFLVILLASSLLVC. GTWLILDSETMHPIGMAYKSS 437

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_101002:
1: /SIDS2/gcdatal/geneseq/geneseq-emb1/AA1980.DAT: *
2: /SIDS2/gcdatal/geneseq/geneseq-emb1/AA1981.DAT: *
3: /SIDS2/gcdatal/geneseq/geneseq-emb1/AA1982.DAT: *
4: /SIDS2/gcdatal/geneseq/geneseq-emb1/AA1983.DAT: *
5: /SIDS2/gcdatal/geneseq/geneseq-emb1/AA1984.DAT: *
6: /SIDS2/gcdatal/geneseq/geneseq-emb1/AA1985.DAT: *
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13: /SIDS2/gcdatal/geneseq/geneseq-emb1/AA1993.DAT: *
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17: /SIDS2/gcdatal/geneseq/geneseq-emb1/AA1997.DAT: *
18: /SIDS2/gcdatal/geneseq/geneseq-emb1/AA1998.DAT: *
19: /SIDS2/gcdatal/geneseq/geneseq-emb1/AA1999.DAT: *
20: /SIDS2/gcdatal/geneseq/geneseq-emb1/AA2000.DAT: *
21: /SIDS2/gcdatal/geneseq/geneseq-emb1/AA2001.DAT: *
22: /SIDS2/gcdatal/geneseq/geneseq-emb1/AA2002.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2289	100.0	437 16 AAR77339	Mouse sonic hedgehog
2	2289	100.0	437 20 AAY05857	Mouse Sonic hedgehog
3	2289	100.0	437 20 AAY05513	Mouse Sonic hedgehog
4	2289	100.0	437 20 AYW97768	Mouse Sonic hedgehog
5	2289	100.0	437 20 AYW94471	Mouse Shh hedgehog
6	2289	100.0	437 21 AAY95975	Mouse Sonic hedgehog
7	2289	100.0	437 21 AAY95284	Mouse Sonic hedgehog
8	2289	100.0	437 21 AAY96246	Partial mouse Shh.
9	2289	100.0	437 21 AAY70579	Mouse sonic hedgehog
10	2289	100.0	437 22 MAG65746	Mouse sonic hedgehog

RESULT 1

ID AAR77339 standard; Protein: 437 AA.
XX
AC AAR77339;
XX
DT 08-MAR-1996 (first entry)
XX
DE Mouse sonic hedgehog protein.
XX
KW Mouse; sonic hedgehog protein; probe; primer; diagnostic;
KW nervous system disorder; gene therapy; antibody.
OS mus musculus.

XX
FH Key Location/Qualifiers
FT Peptide 1..24
FT Peptide /note= "signal peptide"
FT Peptide 25..30
FT Modified-site /note= "conserved sequence (AAR77349)"
FT /note= "N-linked glycosylation site"

XX
PN W09518856-A1.

XX
PD 13-JUL-1995.

XX
PF 30-DEC-1994; 94WO-US14992.

XX
PR 14-DEC-1994; 94US-0356060.

PR 30-DEC-1993; 93US-0176427.

PA (HARD) HARVARD COLLEGE.

PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
 XX
 PT Ingham PW, McMahon AP, Tabin CJ;
 XX
 WPI; 1995-255060/33.
 DR N-PSDB; AAQ91637.

XX Hedgehog-like protein(s) and nucleic acid(s) encoding them - useful
 PT to treat degenerative nervous system disorder(s) and in gene
 PT therapy.
 XX

Claim 17; Page 139-41; 210pp; English.

SQ Sequence 437 AA:

Query Match	100.0%	Score	2289;	DB	16;	Length	437;
Best local Similarity	100.0%	Pred.	No.	9.	4e-226;	Indels	0;
Matches	437;	Mismatches	0;	Gaps	0;		

Qy 1 MILLARCFLVILASSLIVCPGLACGPGRGFKRRHKPLKLTPLAYKOFIPNVAEKTIGAS 60
 Db 1 MILLARCFLVILASSLIVCPGLACGPGRGFKRRHKPLKLTPLAYKOFIPNVAEKTIGAS 60
 Qy 61 GRYEGKTRNSENRFELTPNYNPDIKFDEENIGADRMLTORCKDKLNALATSVMNQPG 120
 Db 61 GRYEGKTRNSENRFELTPNYNPDIKFDEENIGADRMLTORCKDKLNALATSVMNQPG 120
 Qy 121 VRVRYTVEGDEDHHSESLBSLHREGRAVDTTSRDRSKYGMALARLAVEAGDWYYESKA 180
 Db 121 VRVRYTVEGDEDHHSESLBSLHREGRAVDTTSRDRSKYGMALARLAVEAGDWYYESKA 180
 Qy 181 HICCSVKIENSVAKSQGCGFPESATVILEOGSGKVLKDRLPDRDVLAADDQGRLLSDFL 240
 Db 181 HICCSVKIENSVAKSQGCGFPESATVILEOGSGKVLKDRLPDRDVLAADDQGRLLSDFL 240
 Qy 241 TFDRDEGAKKVYVIELEPERLUTTAHILFVAPHDNSFTPGSALERASVRQGQR 300
 Db 241 TFDRDEGAKKVYVIELEPERLUTTAHILFVAPHDNSFTPGSALERASVRQGQR 300
 Qy 301 VVVAERGGDRILPAAHSTVREEEAGAVALTAGTILINRVLASCAYTEEHWAH 360
 Db 301 VVVAERGGDRILPAAHSTVREEEAGAVALTAGTILINRVLASCAYTEEHWAH 360
 Qy 361 RATAFPLRHALALAPARTDGGGGSIPAAQASATEARGAEETAGIHWYSQOLYHGTW 420
 Db 361 RATAFPLRHALALAPARTDGGGGSIPAAQASATEARGAEETAGIHWYSQOLYHGTW 420
 Qy 421 LLSETMPLGMWKSS 437
 Db 421 LLSETMPLGMWKSS 437

RESULT 2

AAV05857 AAV05857 standard; Protein; 437 AA.

XX
 AC AAV05857;
 XX
 DT 02-AUG-1999 (first entry)
 DÉ Mouse Sonic hedgehog Shh protein.
 XX
 KW Sonic hedgehog; Shh; mouse; epithelial tissue; epithelium;
 KW cutaneous tissue; skin; hair; wound healing; vulnery;
 KW

XX The sequence represents a mouse sonic hedgehog protein, homologous to a *Drosophila* hedgehog protein (AAQ77337), and is encoded by a cDNA isolated from an 8-5-day post coitum mouse cDNA library. Probes and primers derived from the sonic hedgehog gene may be used as diagnostic agents for neuromuscular, autonomic or central nervous system disorders, and the gene may also be used in gene therapy. Antibodies generated from the protein may be used as therapeutic or research reagents.

XX Sequence 437 AA:

Query Match	100.0%	Score	2289;	DB	16;	Length	437;
Best local Similarity	100.0%	Pred.	No.	9.	4e-226;	Indels	0;
Matches	437;	Mismatches	0;	Gaps	0;		

Qy 1 MILLARCFLVILASSLIVCPGLACGPGRGFKRRHKPLKLTPLAYKOFIPNVAEKTIGAS 60
 Db 1 MILLARCFLVILASSLIVCPGLACGPGRGFKRRHKPLKLTPLAYKOFIPNVAEKTIGAS 60
 Qy 61 GRYEGKTRNSENRFELTPNYNPDIKFDEENIGADRMLTORCKDKLNALATSVMNQPG 120
 Db 61 GRYEGKTRNSENRFELTPNYNPDIKFDEENIGADRMLTORCKDKLNALATSVMNQPG 120
 Qy 121 VRVRYTVEGDEDHHSESLBSLHREGRAVDTTSRDRSKYGMALARLAVEAGDWYYESKA 180
 DR N-PSDB; AAQ91620.

XX Use of hedgehog polypeptides on patched therapeutics

PS Claim 26; Page 124-125; 14pp; English.

XX The present sequence represents mouse Sonic hedgehog protein sub. The invention relates to a method for modulating the growth state an epithelial cell by ectopically contacting the epithelial cell, in vitro or in vivo, with a hedgehog therapeutic (i.e. a hedgehog polypeptide or gene therapy construct) or ptc therapeutic (i.e. a small organic molecule that mimics the effect of hedgehog proteins on patched signalling, or activates or potentiates patched signalling) in an amount effective to alter the rate of proliferation of the epithelial cell. The hedgehog therapeutic preferably comprises at least a bioactive extracellular portion of a hedgehog protein (see AAV0584-62) encoded by a vertebrate hedgehog gene (see AAV25617-25). Especially a human hedgehog gene. Promotion of proliferation of epithelial cells can be used to control a wound healing process in e.g. burn treatment, skin regeneration, skin grafting, pressure sore treatment, dermal ulcer treatment, post surgery scar reduction or treatment of ulcerative colitis (claimed). It can also be used to induce hair growth for the treatment of alopecia (claimed). Inhibition of the growth of epithelial tissue can be used to treat or prevent hyperplastic or neoplastic conditions, e.g. psoriasis, keratosis, acne, comedogenic lesions, folliculitis and pseudo-folliculitis, keratoacanthoma, callosities, Darier's disease, keloid, hypertrophic scars, or autoimmune disorders, e.g. aphthous ulcers, pemphigus vulgaris, pemphigus foliaceus, pemphigus vegetans, pemphigus erythematosus, epidermolysis, lupus lesions, desquamative lesions or carcinomas. The methods can also be used to counteract the effects of ageing on skin.

XX Sequence 437 AA:

Query Match	100.0%	Score	2289;	DB	20;	Length	437;
Best Local Similarity	100.0%	Pred.	No.	9.	4e-226;	Indels	0;
Matches	437;	Mismatches	0;	Gaps	0;		

Qy 1 MILLARCFLVILASSLIVCPGLACGPGRGFKRRHKPLKLTPLAYKOFIPNVAEKTIGAS 60
 Db 1 MILLARCFLVILASSLIVCPGLACGPGRGFKRRHKPLKLTPLAYKOFIPNVAEKTIGAS 60
 Qy 61 GRYEGKTRNSENRFELTPNYNPDIKFDEENIGADRMLTORCKDKLNALATSVMNQPG 120
 Db 61 GRYEGKTRNSENRFELTPNYNPDIKFDEENIGADRMLTORCKDKLNALATSVMNQPG 120
 Qy 121 VRVRYTVEGDEDHHSESLBSLHREGRAVDTTSRDRSKYGMALARLAVEAGDWYYESKA 180
 KW burn, skin grafting; pressure sore; ulcer; ulcerative colitis;
 KW alopecia; psoriasis; keratosis; acne; comedogenic lesion;
 KW folliculitis; pseudofolliculitis; keratoacanthoma; callosities;
 KW Darier's disease; sat; autoimmune disease; pemphigus;
 KW dermatomylosis; lupus lesion; desquamative lesion; carcinoma;
 KW therapy; hedgehog therapeutic; ptc therapeutic; parched.
 XX OS Mus musculus.
 PN WO9920298-A1.
 XX PD 29-APR-1999.
 XX PF 20-OCT-1998; 98WO-US22227.
 XX PR 11-SEP-1998; 98US-0151999.
 XX PR 20-OCT-1997; 97US-055552.
 XX PA (ONTO-) ONTOGENY INC.
 XX PI Wang EA;
 XX DR WPI; 1999-288170/24.
 XX N-PSDB; AAQ91620.
 KW

Db	121	VRIERVTEGWDDEGHHSBESLHVYEGRAVDTITSDRDRSKYGMARLAVAEAGFDWWVYESKA	180	CC	Inhibit growth of myoblastic-derived tissue to provide treatment of
Oy	181	HICCSVKAENSAVAKSGCFCPGSATVHLEQGGTKLVKDLRPGDRVLADDQGRLLYSDL	240	CC	hyperplastic or neoplastic growth of muscle tissue such as in
Db	181	HICCSVKAENSAVAKSGCFCPGSATVHLEQGGTKLVKDLRPGDRVLADDQGRLLYSDL	240	CC	myoblastic sarcoma (also claimed). The hedgehog therapeutic
Oy	241	TRLDREGAKKVYVVIETLEPRERLUTAHLIFVAPLTAIGTILINRVLASCYAVIEEHWAH	300	CC	preferably comprises at least a bioactive extracellular portion of
Db	241	TRLDREGAKKVYVVIETLEPRERLUTAHLIFVAPLTAIGTILINRVLASCYAVIEEHWAH	300	CC	a hedgehog protein (see AAX05510-19) encoded by a vertebrate hedgehog
Oy	301	VVVAERGDRRLPAAVHVSVLTREEEAGAYAPLTAIGTILINRVLASCYAVIEEHWAH	360	CC	gene (see AAX25088-107), especially a human hedgehog gene.
Db	301	VVVAERGDRRLPAAVHVSVLTREEEAGAYAPLTAIGTILINRVLASCYAVIEEHWAH	360	XX	Sequence 437 AA:
Oy	361	RAFAPFLAHALLAALAPARTDGGGSSIPAAQSATEARGAFTAGTHWSOLLYHGTW	420	SQ	Query Match 100.0%; Score 2289; DB 20; Length 437;
Db	361	RAFAPFLAHALLAALAPARTDGGGSSIPAAQSATEARGAFTAGTHWSOLLYHGTW	420	AC	Best Local Similarity 100.0%; Pred. No. 9, 4e-226; Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	421	LIDSETMFLGMAVKSS	437	XX	DB 241 TFLDRDEGAKKVYVVIETLEPRERLUTAHLIFVAPLTAIGTILINRVLASCYAVIEEHWAH
Db	421	LIDSETMFLGMAVKSS	437	XX	QY 1 MULLARCFVLVILLASLIVCPGLACGPGRRGFKRRHDKKKLTPLAYKOFIPNVAEKTIGS 60
Oy	421	LIDSETMFLGMAVKSS	437	XX	Db 1 MULLARCFVLVILLASLIVCPGLACGPGRRGFKRRHDKKKLTPLAYKOFIPNVAEKTIGS 60
Db	61	GRYEGKTRNSERFKELTPPNYNPDTIIRDEENGTADRLMTQRCKDKNALAISVMQWPG	120	QY 61. GRYEGKTRNSERFKELTPPNYNPDTIIRDEENGTADRLMTQRCKDKNALAISVMQWPG 120	
Oy	61	GRYEGKTRNSERFKELTPPNYNPDTIIRDEENGTADRLMTQRCKDKNALAISVMQWPG	120	DB 121 VRIERVTEGWDDEGHHSBESLHVYEGRAVDTITSDRDRSKYGMARLAVAEAGFDWWVYESKA 180	
Db	121	VRIERVTEGWDDEGHHSBESLHVYEGRAVDTITSDRDRSKYGMARLAVAEAGFDWWVYESKA	180	DB 241 TFLDRDEGAKKVYVVIETLEPRERLUTAHLIFVAPLTAIGTILINRVLASCYAVIEEHWAH	
Oy	181	HICCSVKAENSAVAKSGCFCPGSATVHLEQGGTKLVKDLRPGDRVLADDQGRLLYSDL	240	DB 301 VVVAERGDRRLPAAVHVSVLTREEEAGAYAPLTAIGTILINRVLASCYAVIEEHWAH	
Db	181	HICCSVKAENSAVAKSGCFCPGSATVHLEQGGTKLVKDLRPGDRVLADDQGRLLYSDL	240	AC AAX05513;	
XX				XX 05-JUL-1999 (first entry)	
DT				XX Mouse Sonic hedgehog protein Shh.	
XX				XX Sonic hedgehog; Shh protein; mouse; hedgehog therapeutic;	
KW				KW ptc therapeutic; patched; signal transduction; muscle atrophy; cachexia; muscular myopathy; myoblastic sarcoma; therapy.	
XX				OS Mus sp.	
XX				XX WO9910004-A2.	
PN				XX 04-MAR-1999.	
PD				XX 28-AUG-1998; 98WO-US17922.	
XX				XX 29-AUG-1997; 97US-0057394.	
PR				XX (ONTO-) ONTOGENY INC.	
PA				XX Bladgen CS, Currie PD, Hughes SM, Ingham PW;	
PT				XX WPT; 1999-243557/20.	
XX				DR N-PSDB; AAX25101.	
XX				XX A new method to regulate muscle growth	
PT				XX Disclosure; Page 115-116; 130pp; English.	
PS				XX The present sequence is mouse Sonic hedgehog protein Shh. The invention relates to a method for modulating the formation and/or maintenance of muscle tissue by ectopically contacting muscle cells, especially muscle stem/progenitor cells, in vitro or in vivo, with a hedgehog therapeutic (i.e. hedgehog polypeptides and gene therapy constructs) or ptc therapeutic (i.e. a small organic molecule that mimics the effect of hedgehog proteins on patched signalling, or activates or potentiates patched signalling) in an amount effective to alter the growth state of the treated cells. Also claimed is a method for treatment or prevention of disorders of, or surgical or cosmetic repair of, such muscle tissues, by administering a hedgehog polypeptide or ptc therapeutic. The disorder may be muscle atrophy, in particular skeletal muscle atrophy or cardiac muscle atrophy, cachexia, or muscular myopathy (all claimed). The hedgehog polypeptide or ptc therapeutic can	
XX				CC inhibit growth of myoblastic-derived tissue to provide treatment of hyperplastic or neoplastic growth of muscle tissue such as in myoblastic sarcoma (also claimed). The hedgehog therapeutic preferably comprises at least a bioactive extracellular portion of a hedgehog protein (see AAX05510-19) encoded by a vertebrate hedgehog gene (see AAX25088-107), especially a human hedgehog gene.	
XX				CC Sequence 437 AA:	
QY	1	MULLARCFVLVILLASLIVCPGLACGPGRRGFKRRHDKKKLTPLAYKOFIPNVAEKTIGS	60	Query Match 100.0%; Score 2289; DB 20; Length 437;	
Db	1	MULLARCFVLVILLASLIVCPGLACGPGRRGFKRRHDKKKLTPLAYKOFIPNVAEKTIGS	60	Best Local Similarity 100.0%; Pred. No. 9, 4e-226; Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Oy	61	GRYEGKTRNSERFKELTPPNYNPDTIIRDEENGTADRLMTQRCKDKNALAISVMQWPG	120	Db 61. GRYEGKTRNSERFKELTPPNYNPDTIIRDEENGTADRLMTQRCKDKNALAISVMQWPG 120	
Db	61	GRYEGKTRNSERFKELTPPNYNPDTIIRDEENGTADRLMTQRCKDKNALAISVMQWPG	120	QY 121 VRIERVTEGWDDEGHHSBESLHVYEGRAVDTITSDRDRSKYGMARLAVAEAGFDWWVYESKA 180	
Db	121	VRIERVTEGWDDEGHHSBESLHVYEGRAVDTITSDRDRSKYGMARLAVAEAGFDWWVYESKA	180	Db 121 VRIERVTEGWDDEGHHSBESLHVYEGRAVDTITSDRDRSKYGMARLAVAEAGFDWWVYESKA 180	
Oy	181	HICCSVKAENSAVAKSGCFCPGSATVHLEQGGTKLVKDLRPGDRVLADDQGRLLYSDL	240	Db 121 VRIERVTEGWDDEGHHSBESLHVYEGRAVDTITSDRDRSKYGMARLAVAEAGFDWWVYESKA 180	
Db	181	HICCSVKAENSAVAKSGCFCPGSATVHLEQGGTKLVKDLRPGDRVLADDQGRLLYSDL	240	AC AAX05513;	
XX				XX 05-JUL-1999 (first entry)	
DT				XX Mouse Sonic hedgehog protein Shh.	
XX				XX Sonic hedgehog; Shh protein; mouse; hedgehog therapeutic;	
KW				KW ptc therapeutic; patched; signal transduction; Parkinson's disease; Huntington's disease; amyotrophic lateral sclerosis; cerebral ischaemia; hypoxia; neuroprotective; therapy.	
XX				OS Mus sp.	
XX				XX WO994775-A2.	
PN				XX 04-FEB-1999.	
PD				XX 24-JUL-1998; 98WO-US15419.	
XX				XX 24-JUL-1997; 97US-0900220.	
PR				XX PA (ONTO-) ONTOGENY INC.	

				RESULT 5
PI				AAW94471
XX				ID AAW94471 standard; Protein; 437 AA.
DR				XX
WPI; 1999-142578/12.				AC AAW94471;
N-PSDB; AAX07274.				XX
X				DT 29-APR-1999 (first entry)
PT				XX
Increasing the survival of neuronal, dopaminergic and GABA-nergic				DE Mouse Shh hedgehog protein sequence.
cells - by using a ptc therapeutic such as a protein kinase				XX
inhibitor, or an agent derived from hedgehog polypeptides, useful in				XX
the treatment of parkinson's disease				XX
PS				XX
X				XX
XX				XX
This polypeptide is mouse Shh Sonic hedgehog protein. The				Patched; hedgehog; ptc therapeutic; neuroprotective; neuronal cell;
Invention is based on the finding that hedgehog proteins are useful				brain infarction; cerebral infarction; transient ischaemic attack;
as protective agents in the treatment and prophylaxis of				haemorrhage; encephalomyelitis; coronary bypass; cerebral hypoxia.
neurodegenerative disorders resulting from the loss of dopaminergic				OS Mus sp.
and/or GABA-nergic neurons, or the general loss of tissue from the				XX
substantia nigra. Exemplary disorders include Parkinson's disease,				PN WO9900117-A2.
Huntington's disease (both claimed), amyotrophic lateral sclerosis				XX
and cerebral ischaemia. The Invention relates to hedgehog				PD 07-JAN-1999.
therapeutics (i.e. hedgehog polypeptides and gene therapy constructs				XX
e.g. constructs encoding recombinant hedgehog polypeptides and				PF 26-JUN-1998; 98WO-US13387.
trans-activation constructs for altering hedgehog gene regulatory				XX
sequences) and ptc therapeutics (i.e. agents which mimic the effect				PR 27-JUN-1997; 97US-0883656.
of naturally occurring hedgehog proteins on patched signalling)				PA (ONTO-) ONTOGENY INC.
that are effective in both human and animal subjects. Human Ihh				XX
and Ihh polypeptides (see AW97763-64) are preferred. The products				PI Mahanthappa NK;
can also be used for the maintenance of differentiated neurons in				XX
cultures, and to enhance the implantation of such neuronal cells in				DR WPI; 1999-095458/08.
an animal. They can be used to prevent or treat neurodegenerative				DR N-PSDB; AAX16185.
conditions arising from the use of certain drugs, and in the				XX
prevention and/or treatment of hypoxia, e.g. as a neuroprotective				XX
CC				PT Method for limiting damage to neurons caused by ischaemic or epoxic
XX				PT conditions - is used for the treatment and prevention of e.g.
Sequence 437 AA:				PT cerebral infarction, stroke and transient ischaemic attacks
SQ				XX Disclosure; Page 68-70; 104pp; English.
Query Match	100 %	Score 2289;	DB 20;	Length 437;
Best Local Similarity	100 %;	Pred. No. 9.4e-226;		
Matches 437;	Conservative	0;	Mismatches 0;	Indels 0;
Db				Gaps 0;
QY	1	MILLIARCELVILIASSLVCPGLACGPGRGFGKRRHPRKKLTPLAYQFIPNVAEKTLAS 60		
Db	1	MILLIARCELVILIASSLVCPGLACGPGRGFGKRRHPRKKLTPPLAYQFIPNVAEKTLAS 60		
QY	61	GRYEGKITRNSERFKEPLTPNYNFDIKFDEENGADRMLTORCKDKLNALATSVMNQPG 120		
Db	61	GRYEGKITRNSERFKEPLTPNYNFDIKFDEENGADRMLTORCKDKLNALATSVMNQPG 120		
QY	121	VRLRVTEGWDDEGHHSERSLSERLVEGRAVDITSDRSRKYGMALARLAVEAGEDWWVYESKA 180		
Db	121	VRLRVTEGWDDEGHHSERSLSERLVEGRAVDITSDRSRKYGMALARLAVEAGEDWWVYESKA 180		
QY	181	RIHCSYTKAENSAVAKSGCFPOSATWLEQGGTLYKLDRLRGDRVLAADDGGRLLYSDL 240		
Db	181	RIHCSYTKAENSAVAKSGCFPOSATWLEQGGTLYKLDRLRGDRVLAADDGGRLLYSDL 240		
QY	241	TFLDRDEGAKKVYVETLERRERLTAHLFLYAPHTAHLFVPHNDSGPTPGPSAFAFASRYRPGQR 300		
Db	241	TFLDRDEGAKKVYVETLERRERLTAHLFLYAPHTAHLFVPHNDSGPTPGPSAFAFASRYRPGQR 300		
QY	301	VVVAERGGDQLPAPAVHSTREEAGAYAPPATAHTLILINRLASCYAVIERSWAH 360		
Db	301	VVVAERGGDQLPAPAVHSTREEAGAYAPPATAHTLILINRLASCYAVIERSWAH 360		
QY	361	RAFAFRFLAHALLALAPARTDGCGGSIPAQGATEARGAEPAGTHIYSQLYHICW 420		
Db	361	RAFAFRFLAHALLALAPARTDGCGGSIPAQGATEARGAEPAGTHIYSQLYHICW 420		
QY	421	LIDDETMHDGLMAKSS 437		
Db	421	LIDDETMHDGLMAKSS 437		
QY	121	VRLRVTEGWDDEGHHSERSLSERLVEGRAVDITSDRSRKYGMALARLAVEAGEDWWVYESKA 180		

KW	Sonic hedgehog; Shh; mouse; excitotoxicity; parkinson's disease; Huntington's disease; neuronal degeneration; neuroprotective; dopaminergic; GABAergic; substantia nigra; therapy.
XX	
OS	Mus musculus.
PN	WO200035948-A1.
PD	22-JUN-2000.
XX	
PP	03-DEC-1999; 99WO-US28721.
XX	
PR	03-DEC-1998; 98WO-US25576.
XX	
PR	27-JAN-1999; 99US-0231243.
PR	03-JUN-1999; 99US-0325602.
XX	
PA	(BIOJ) BIOTRON INC.
PA	(ONTO-) ONTOGENY INC.
XX	
PI	Galdes A, Mahanthappa N;
XX	
DR	WPI: 2000-431570/37.
XX	
PT	Treating disorders involving exotoxicity, e.g. trauma, hypoglycemia, senile dementia and Korsakoff's disease, by using lipophilic modified hedgehog polypeptide - Disclosure: Page 154-155; 174pp; English.
XX	
PS	The present sequence of that of mouse sonic hedgehog (Shh) protein. The invention relates to a method for promoting the survival and/or functional performance of neuronal cells, especially substantia nigra, dopaminergic or GABAergic neurons that are susceptible to exotoxicity, by contacting the cells, <i>in vitro</i> or <i>in vivo</i> , with a lipophilic (e.g. cholesterol) modified hedgehog polypeptide. The method is used to treat or prevent parkinson's disease, Huntington's disease, domic acid poisoning, spinal cord trauma, hypoglycemia, mechanical trauma to the nervous system, senile dementia, Korsakoff's disease, schizophrenia, AIDS dementia, multi-infarct dementia, mood disorders, depression, chemical toxicity, neuronal damage associated with uncontrolled seizures such as epileptic seizures, neuronal injury associated with HIV and AIDS, neurodegeneration associated with Down's syndrome, neuropathic pain syndrome, olivopontocerebral atrophy, amyotrophic lateral sclerosis, mitochondrial abnormalities, Alzheimer's disease, hepatic encephalopathy, Tourette's syndrome and drug addiction (all claimed). The lipophilic modified hedgehog polypeptide is also useful for promoting survival and/or functional performance of neuronal cells susceptible to exotoxicity.
XX	
SQ	Sequence 437 AA:
Query Match	100.0%; Score 2289; DB 21; Length 437;
Best Local Similarity	100.0%; Pred. No. 9; 4e-226;
Matches	437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	
Db	1 MLLLARCLFLVILASSILVCPGLACGGPGGKRRPKKLTPLAYKOPIPNVAEKTGAS 60
QY	61 GRYEGKTRNSRERKELTNNPYNDIKDEENIGADRMLTQORCKDKLNALATSVMNQPG 120
Db	61 GRYEGKTRNSRERKELTNNPYNDIKDEENIGADRMLTQORCKDKLNALATSVMNQPG 120
QY	121 VLRVTEGWDGCHHSEBSLHVEGRADITTSQRDRSKYGMALARLAVEAGFDWVYRSKA 180
Db	121 VLRVTEGWDGCHHSEBSLHVEGRADITTSQRDRSKYGMALARLAVEAGFDWVYRSKA 180
QY	181 HTHCSVKRNENYAAKSGCFCRSATVILEQSGTKLVDRCDRVLAADDQCRUYSDFL 240
Db	61 GRYEGKTRNSRERKELTNNPYNDIKDEENIGADRMLTQORCKDKLNALATSVMNQPG 120
QY	181 HTHCSVKRNENYAAKSGCFCRSATVILEQSGTKLVDRCDRVLAADDQCRUYSDFL 240
CC	This sequence inhibits expression of the patched gene which has been implicated in neuromuscular disorders (neuropathies). This sequence may therefore be used for treating neuromuscular disorders i.e. preventing degradation in function of motor or sensory nerves and protecting peripheral nerve cells under conditions that normally cause neuropathy.
QY	241 TELDRDEGAKKVYFTLETLPERRLERRTAHLFVARHNDSCPTPQSALFASRVRGOR 300
Db	361 RAFAPEFLAHALLALAPARDGGGSIPQAQSATEARGAEPTGHWQSOLIHGTW 420
QY	301 VVVVAERGGDRRLPAVHSVLREERAGAYAAPTANTGTLINRVLASCYAVIEHSAWH 360
Db	301 VVVAERGGDRRLPAVHSVLREERAGAYAAPTANTGTLINRVLASCYAVIEHSAWH 360
QY	361 RAFAPEFLAHALLALAPARDGGGSIPQAQSATEARGAEPTGHWQSOLIHGTW 420
Db	361 RAFAPEFLAHALLALAPARDGGGSIPQAQSATEARGAEPTGHWQSOLIHGTW 420
QY	421 LIDSEMPHIGMAVKSS 437
Db	421 LIDSEMPHIGMAVKSS 437
RESULT	8
ID	AAY96345
XX	
AC	AAY96246;
XX	
DT	11-SEP-2000 (first entry)
XX	
DE	Partial mouse Shh.
XX	
KW	Mouse; sonic hedgehog; Shh; neuromuscular disorder; neuropathy; Guillain-Barre syndrome; peripheral neuropathy; diabetes; alcoholism; chronic inflammatory demyelinating polyneuropathy; CIDP; gene therapy; infection; inflammation; hereditary neuropathy; Charcot-Marie-Tooth disease; vasculitis; lung cancer; tumour; multiple myeloma; nutritional imbalance; kidney disease; hypothyroid neuropathy; trauma; Reitnau's disease; Abetalipoproteinemia; Tangier disease; Krabbe's disease; Metachromatic leukodystrophy; Fabry's disease; CMT; GBS; Deyérine-Sottas syndrome; acute neuropathy; Amyotrophic lateral sclerosis; ALS; Miller-Fisher syndrome; amyotodosis; Hereditary sensory neuropathy Type II; HSN II; B-cell lymphoma; Waldenström's Macroglobulinaemia; Chronic Lymphocytic Leukaemia; neuroprotective; cytoprotective; patched-mediated signal transduction.
XX	
OS	Mus sp.
XX	
PN	WO200027422-A2.
XX	
PD	18-MAY-2000.
XX	
PF	08-NOV-1998; 99WO-US26334.
XX	
PR	06-NOV-1998; 98US-0187387.
XX	
PA	(BIOJ) BIOTRON INC.
PA	(ONTO-) ONTOGENY INC.
XX	
PI	Galdes A, Mahanthappa N;
XX	
DR	WPI: 2000-387341/33.
XX	
PT	Novel method of preventing deterioration of peripheral nerves, useful for treating or preventing neuropathy, e.g. where associated with diabetes or viral infection, by administering hedgehog or patched agent
PT	Claim 7: Page 131-132; 152pp; English.
XX	
CC	The present sequence is the partial mouse sonic hedgehog protein, Shh. This sequence inhibits expression of the patched gene which has been implicated in neuromuscular disorders (neuropathies). This sequence may therefore be used for treating neuromuscular disorders i.e. preventing degradation in function of motor or sensory nerves and protecting peripheral nerve cells under conditions that normally cause neuropathy.

CC syndrome; GBS; peripheral neuropathy; diabetic neuropathy;
 alcohol-induced neuropathy; chronic inflammatory demyelinating
 polyneuropathy; CIDP; infection-induced neuropathy, including HIV
 infection; inflammation-induced neuropathy; hereditary neuropathy e.g.
 Charcot-Marie-Tooth disease (CMT); Familial Amyloidotic neuropathy,
 Refsum's disease, Metachromatic leukodystrophy, Fabry's disease, Dejerine-Sottas
 syndrome, Hereditary sensory neuropathy Type II (HSN II) and Amyotrophic
 lateral sclerosis (ALS); acute neuropathy e.g. Miller-Fisher syndrome;
 neuropathy caused by vasculitis; neuropathy associated with tumours e.g.
 lung cancer, multiple myeloma, B-cell Lymphoma, Waldenstrom's
 disease, Macroglobulinaemia, Chronic lymphocytic leukaemia; neuropathy associated
 with: amyloidosis, nutritional imbalance, kidney disease, trauma; and
 hypothyroid neuropathy. The coding sequence may be used in gene therapy
 of the above disorders.

XX SQ Sequence 437 AA:
 Query Match 100.0%; Score 2289; DB 21; Length 437;
 best Local Similarity 100.0%; Pred. No. 9.4e-226; Indels 0; Gaps 0;
 Matches 437; Conservative 0; Mismatches 0; Gaps 0;

Db 1 MLLARCFVLASSILVCPGLACGPGRGKRRHPPKKLTPLAYKQFTPVNAEKTGAS 60
 QY |||||||MLLARCFVLASSILVCPGLACGPGRGKRRHPPKKLTPLAYKQFTPVNAEKTGAS 60
 61 GRYEGKITRNSERFKELTPTNPINPDIFKDEENTGADRMLTORCKDKLNALATSMNQWPG 120
 Db 121 VRLRVTEGWDGHSESELHYGRAVDITTSDRDSKGMLARLAVEGFDWYIESKA 180
 QY |||||VRLRVTEGWDGHSESELHYGRAVDITTSDRDSKGMLARLAVEGFDWYIESKA 180
 121 VRLRVTEGWDGHSESELHYGRAVDITTSDRDSKGMLARLAVEGFDWYIESKA 180
 Db 181 HHCSCVKAENSAVAKSGCCFPGSATVHLEQGTTKLVKDLRGDRVLAADDQGRLLYSDFL 240
 QY |||||HHCSCVKAENSAVAKSGCCFPGSATVHLEQGTTKLVKDLRGDRVLAADDQGRLLYSDFL 240
 Db 181 HHCSCVKAENSAVAKSGCCFPGSATVHLEQGTTKLVKDLRGDRVLAADDQGRLLYSDFL 240
 QY 241 TFLDRDEGAKKVVFYVTELEPRERLLTAAHLLFVAPHNDSGPTPGPSALFASRVRPGQR 300
 121 TFLDRDEGAKKVVFYVTELEPRERLLTAAHLLFVAPHNDSGPTPGPSALFASRVRPGQR 300
 Db 301 VVVAERGGDRRLPAVHSVTLREBEEAGAYAAPTANTGTILINRVLASCYAVIEHSWAH 360
 QY |||||VVVAERGGDRRLPAVHSVTLREBEEAGAYAAPTANTGTILINRVLASCYAVIEHSWAH 360
 361 RAPAPRFLAHALLAALAPARTDGCGGSTPAQSATEARGAEPTAGIHWSQLIHYHIGTW 420
 Db 361 RAPAPRFLAHALLAALAPARTDGCGGSTPAQSATEARGAEPTAGIHWSQLIHYHIGTW 420
 QY 421 LLQSETMHPGLMAVKSS 437
 421 LLQSETMHPGLMAVKSS 437

RESULT 9
 AAY70679 standard; Protein: 437 AA.
 XX AC AAY70679;
 XX DT 18-JUL-2000 (first entry)
 XX DE Mouse Sonic hedgehog (Shh) protein.
 XX
 KW Sonic hedgehog; Shh; mouse; growth modulator; therapeutic agent;
 KW anti-proliferative; anticancer; vasoactive; antirheumatic; hypotensive;
 KW anti-inflammatory; antiasthmatic; antiarthritic; tubercostatic; asthma;
 KW antimicrobial; antiallergy; treatment; prevention; lung diseases; cancer;
 KW cystic fibrosis; bronchitis; emphysema; respiratory distress syndrome;
 KW tuberculosis; wound healing; lung transplantation.

OS Mus sp.
 XX PN WO200015246-A2.
 XX PD 23-MAR-2000.
 XX PR 11-SEP-1998; 98US-0099952.
 XX PA (HARD) HARVARD COLLEGE.
 XX PI Pepicelli C, Lewis P, McMahon AP;
 DR XX WPI: 2000-271252/23.
 DR N-PSDB; AA7252260.

PT Modulation of lung tissue or cell growth rate used for treating or
 preventing damage to lung tissue comprises ectopically contacting
 tissue with hedgehog therapeutic, patched therapeutic or fibroblast
 growth factor-10

XX PS Claim 14; Page 119-121; 143pp; English.

CC The patent discloses a method for modulating the growth state of
 epithelial or mesenchymal cells of the lung, by ectopically contacting
 the tissue with a therapeutical agent, that can effectively alter the rate
 of proliferation of cells. This agent can be selected from hedgehog (hh)
 patched (ptc) or fibroblast growth factor (fgf)-10 therapeutics. It
 involves a direct or indirect antagonism of patched-mediated regulation
 of gene expression. This method is useful for the treatment or prevention
 of lung diseases, like cancer, cystic fibrosis, bronchopneumonitis,
 bronchiitis, bronchospasm, sarcoidosis, silicosis, eosinophilic granulomatosis,
 ankylosing spondylitis, emphysema, tuberculosis, respiratory distress
 syndrome, allergic rhinitis, asthma, pulmonary fibrosis and primary
 pulmonary hypertension. It is also used to control wound healing or other
 reformation processes in the lung and augment lung transplantation. The
 present sequence is the mouse sonic hedgehog (Shh) protein, essential
 for development of the respiratory system. Hedgehog polypeptides can be
 used to control the formation and/or maintenance of the lung tissue.

XX SQ Sequence 437 AA:
 Query Match 100.0%; Score 2289; DB 21; Length 437;
 best Local Similarity 100.0%; Pred. No. 9.4e-226; Indels 0; Gaps 0;
 Matches 437; Conservative 0; Mismatches 0; Gaps 0;

Db 1 MLLARCFVLASSILVCPGLACGPGRGKRRHPPKKLTPLAYKQFTPVNAEKTGAS 60
 QY |||||||MLLARCFVLASSILVCPGLACGPGRGKRRHPPKKLTPLAYKQFTPVNAEKTGAS 60
 61 GRYEGKITRNSERFKELTPTNPINPDIFKDEENTGADRMLTORCKDKLNALATSMNQWPG 120
 Db 121 VRLRVTEGWDGHSESELHYGRAVDITTSDRDSKGMLARLAVEGFDWYIESKA 180
 QY |||||VRLRVTEGWDGHSESELHYGRAVDITTSDRDSKGMLARLAVEGFDWYIESKA 180
 121 VRLRVTEGWDGHSESELHYGRAVDITTSDRDSKGMLARLAVEGFDWYIESKA 180
 Db 181 HHCSCVKAENSAVAKSGCCFPGSATVHLEQGTTKLVKDLRGDRVLAADDQGRLLYSDFL 240
 QY |||||HHCSCVKAENSAVAKSGCCFPGSATVHLEQGTTKLVKDLRGDRVLAADDQGRLLYSDFL 240
 Db 181 HHCSCVKAENSAVAKSGCCFPGSATVHLEQGTTKLVKDLRGDRVLAADDQGRLLYSDFL 240
 QY 121 VRLRVTEGWDGHSESELHYGRAVDITTSDRDSKGMLARLAVEGFDWYIESKA 180
 121 VRLRVTEGWDGHSESELHYGRAVDITTSDRDSKGMLARLAVEGFDWYIESKA 180
 Db 181 HHCSCVKAENSAVAKSGCCFPGSATVHLEQGTTKLVKDLRGDRVLAADDQGRLLYSDFL 240
 QY |||||HHCSCVKAENSAVAKSGCCFPGSATVHLEQGTTKLVKDLRGDRVLAADDQGRLLYSDFL 240
 Db 241 TFLDRDEGAKKVVFYVTELEPRERLLTAAHLLFVAPHNDSGPTPGPSALFASRVRPGQR 300
 QY |||||TFLDRDEGAKKVVFYVTELEPRERLLTAAHLLFVAPHNDSGPTPGPSALFASRVRPGQR 300
 Db 301 VVVAERGGDRRLPAVHSVTLREBEEAGAYAAPTANTGTILINRVLASCYAVIEHSWAH 360
 QY |||||VVVAERGGDRRLPAVHSVTLREBEEAGAYAAPTANTGTILINRVLASCYAVIEHSWAH 360
 361 RAPAPRFLAHALLAALAPARTDGCGGSTPAQSATEARGAEPTAGIHWSQLIHYHIGTW 420

Db	361 RAFAPFRILAHALLAALAPARTDGGGSIPAAQSATEARGAEPHTAGIHWYSQOLYHIGTW	420	QY	181 HHCSCVKENSYAAKSGCFCGSAATVHLEQGCKLKVLDLRPCDRVLADDGCRLLISDFL	240
QY	421 LLIDSETMHPGLMAVKSS	437	ID	181 HHCSCVKENSYAAKSGCFCGSAATVHLEQGCKLKVLDLRPCDRVLADDGCRLLISDFL	240
Db	421 LLIDSETMHPGLMAVKSS	437	QY	181 HHCSCVKENSYAAKSGCFCGSAATVHLEQGCKLKVLDLRPCDRVLADDGCRLLISDFL	240
RESULT 10			QY	241 TFLDRDGAKKYVYETLEPERLILTAHLFVAPNPHNDSGPTCPGFSALFASRVPRQR	300
AAG65746			ID	241 TFLDRDGAKKYVYETLEPERLILTAHLFVAPNPHNDSGPTCPGFSALFASRVPRQR	300
ID	AAG65746 standard; Protein: 437 AA.		XX	301 VVVAERGGDRRLPAVHSVTLREEEAGAYAPLTAGTILINRYLASCTAVIEHSHWAH	360
AC	AAG65746;		XX	301 VVVAERGGDRRLPAVHSVTLREEEAGAYAPLTAGTILINRYLASCTAVIEHSHWAH	360
Oy			DT	07-JAN-2002 (first entry)	
XX			DE	Mouse sonic hedgehog (Shh) polypeptide.	
XX			XX	Adipocyte; hedgehog polypeptide; desert hedgehog; Indian hedgehog; Dhh; Ihh; sonic hedgehog; Shh; therapeutic; cytostatic; tumor. MUS sp.	
OS			XX	Mus sp.	
XX			XX	W0200164238-A2.	
PD			XX	07-SEP-2001.	
XX			PF	28-FEB-2001; 2001WO-US06450.	
XX			XX	29-FEB-2000; 200005-186058P.	
PA			PA	(CURI-) CURIS INC.	
XX			PI	Zehentner B, Lesser-Reiff U, Burtscher H;	
XX			XX	WPI; 2001-607352/09.	
PS			DR	N-PSDB; AAI66774.	
PT	Method for regulating formation and/or maintenance of adipocyte tissue by contacting pre-adipocyte or adipocyte cells with a hedgehog polypeptide or ptc therapeutic		XX	XX	
PT	Disclosure; Page 97-99; 132pp; English.		XX	XX	
XX			XX	XX	
CC	The invention provides a method for regulating formation and/or maintenance of adipocyte tissue that comprises contacting pre adipocyte or adipocyte cells with a hedgehog polypeptide or ptc therapeutic		XX	XX	
CC	method is used for regulating the growth state of an adipocyte stem/progenitor cell, and treating or preventing disorders of, or surgical or cosmetic repair of, adipocyte tissues, e.g., for treating or preventing hyperplastic or neoplastic conditions affecting adipocyte tissue, such as soft tissue tumors, especially adipose cell tumors, e.g., lipomas, fibrolipomas, lipoblastomas, lipomatosis, hibernomas, hemangiomas and/or liposarcomas. Hedgehog polypeptides can be used in combination with other therapeutic agents. The present sequence represents a mouse sonic hedgehog (Shh) polypeptide.		XX	XX	
SQ	Sequence 437 AA;		XX	XX	
Query Match	100.0%; Score 2289; DB 22; Length 437;		XX	XX	
Best Local Similarity	100.0%; Pred. No. 9.4e-226;		XX	XX	
Matches	437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		XX	XX	
OY			XX	XX	
1	MULLARCFVTLASSLUVCPGLACGPGRGPKRKRHKPKLTPLAQKQFTPVNAEKTGAS	60	CC	The invention relates to nucleic acids encoding hedgehog proteins selected from sonic hedgehog (Shh), Indian hedgehog (Ihh), desert hedgehog (Dhh) polypeptides. The hedgehog genes are involved in the formation of ordered spatial arrangements of differentiated tissue in vertebrates. The nucleic acid sequences are useful for producing hedgehog proteins, used for promoting differentiation of, or survival of differentiated, neuronal cells, and for promoting proliferation, survival particularly chondrocytes, or testicular germ line cells. The present	
Db	1 MULLARCFVTLASSLUVCPGLACGPGRGPKRKRHKPKLTPLAQKQFTPVNAEKTGAS	60	CC	sequence represents a mouse Shh polypeptide.	
Oy	61 GRVCKITRNCSRKEELTPNYPDIFKDEENTGADRMLTQDKLVALAISWANQPG	120	CC		
Db	61 GRVCKITRNCSRKEELTPNYPDIFKDEENTGADRMLTQDKLVALAISWANQPG	120	CC		
Oy	121 VRURVTEGDEDGHSESSLHYEGRAVDTTSRDRSKYMLARLAVAFGDWVYWSKA	180	CC		
Db	121 VRURVTEGDEDGHSESSLHYEGRAVDTTSRDRSKYMLARLAVAFGDWVYWSKA	180	CC		

SQ	Sequence	437 AA:	PT	Modulating immune function comprises administration of a hedgehog or Ptc agent, for treating e.g. diabetes, eczematous dermatitis, urticaria or vasculitis -
Query Match	100.0%	Score 2289; DB 22; Length 437;	PT	PtC agent, for treating e.g. diabetes, eczematous dermatitis, urticaria or vasculitis -
Best Local Similarity	100.0%	Pred. No. 9.4e-226; Mismatches 0; Indels 0; Gaps 0;	PT	PtC agent, for treating e.g. diabetes, eczematous dermatitis, urticaria or vasculitis -
Matches	437;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX	
Db			PS	Claim 4: Page 81-82; 105pp: English.
QY	1	MILLIARCFLVILASSLIVCPGLACGPGRGKRRHPKKLPLAKYQFIPNVAEKTIGAS 60	CC	The present sequence represents a hedgehog (Shh) polypeptide. Hedgehog gene products and signal transduction pathways involving hedgehog are involved in the maturation of T lymphocytes. The specification describes a method for modulating immune function, by administration of a hedgehog or patched (ptc) polypeptide, agonists or antagonists. The method is used to treat disorders affecting the regulation of lymphocytes, particularly maturation and/or activation of T lymphocytes. It is used to treat bacterial or viral infection, diabetes, nutritional deficiencies, graft rejection or other hyperacute response such as kidney, heat, lung, bone marrow, spleen or cornea transplant or autoimmune disorders such as multiple sclerosis, psoriasis or atopic dermatitis. The method is used to treat inflammatory, proliferative and hyperproliferative diseases, as well as cutaneous manifestations of immunological disorders such as eczematous dermatitis, urticaria, vasculitis and scleroderma.
Db	61	GRYEKTRNSENSEKELETPNYNPDIKFDEENTGADRMTQRCKDKLNALISWMNQWPG 120	CC	
QY	121	VRLVATEGKEDGDGHSEESLHYEGRAVDITTSBDRSKYGMALARLAVEAGFDWVYESKA 180	CC	
QY	121	VRLVATEGKEDGDGHSEESLHYEGRAVDITTSBDRSKYGMALARLAVEAGFDWVYESKA 180	CC	
Db	181	HICCSYKAENSYAAKSGGCFPGSIVHLRQGGTFLVKDLPGRVLAADDQGRLYSDFL 240	CC	
Db	181	HICCSYKAENSYAAKSGGCFPGSIVHLRQGGTFLVKDLPGRVLAADDQGRLYSDFL 240	CC	
QY	241	TFLDRDEGAKKVVFYVTELERERLLTAHLLVAPHNDSGPTGPGPSALFASRVPGOR 300	CC	
Db	241	TFLDRDEGAKKVVFYVTELERERLLTAHLLVAPHNDSGPTGPGPSALFASRVPGOR 300	CC	
QY	301	VVVAERGGDRRLPAVHSVTLREEEAGAYAPLTAHTGTLINVLASCAYIEEHSAW 360	CC	
Db	301	VVVAERGGDRRLPAVHSVTLREEEAGAYAPLTAHTGTLINVLASCAYIEEHSAW 360	CC	
QY	361	RAFAPEFLAHALLAALAPARDGGGGSIPIAQOSATEARGAEPTAGIHWYSQQLYHIGTW 420	CC	
Db	361	RAFAPEFLAHALLAALAPARDGGGGSIPIAQOSATEARGAEPTAGIHWYSQQLYHIGTW 420	CC	
QY	421	LLDSETMHPGMVAVSS 437	CC	
Db	421	LLDSETMHPGMVAVSS 437	CC	
RESULT	12		XX	Sequence 437 AA:
AAB84672			Query Match	100.0%: Score 2289; DB 22; Length 437;
ID	AAB84672	standard; Protein; 437 AA.	Best Local Similarity	100.0%; Pred. No. 9.4e-226;
AC	AAB84672;		Matches	Mismatches 0; Indels 0; Gaps 0;
XX			Db	1
DT	17-SEP-2001	(first entry)	QY	MILLIARCFLVILASSLIVCPGLACGPGRGKRRHPKKLPLAKYQFIPNVAEKTIGAS 60
DE	Amino acid sequence of a mouse hedgehog (Shh) polypeptide.		Db	61
XX	Shh gene; hedgehog gene; T lymphocyte; patched gene; infection; diabetes; nutritional deficiency; graft rejection; hyperacute response; cornea transplant; autoimmune disorder; multiple sclerosis; psoriasis; atopic dermatitis; inflammatory disease; proliferative disease; hyperproliferative disease; eczematous dermatitis; urticaria; vasculitis; scleroderma.		QY	GRYEKTRNSENSEKELETPNYNPDIKFDEENTGADRMTQRCKDKLNALISWMNQWPG 120
OS			Db	61
XX			QY	VRLVATEGKEDGDGHSEESLHYEGRAVDITTSBDRSKYGMALARLAVEAGFDWVYESKA 180
PN			Db	181
W0200140438-A2.			QY	HICCSYKAENSYAAKSGGCFPGSIVHLRQGGTFLVKDLPGRVLAADDQGRLYSDFL 240
XX			Db	181
PD	07-JUN-2001.		QY	TFLDRDEGAKKVVFYVTELERERLLTAHLLVAPHNDSGPTGPGPSALFASRVPGOR 300
XX			Db	241
PF	30-NOV-2000; 2000W0-US32590.		QY	TFLDRDEGAKKVVFYVTELERERLLTAHLLVAPHNDSGPTGPGPSALFASRVPGOR 300
XX			Db	301
PR	30-NOV-1999; 990S-0168112.		QY	VVVAERGGDRRLPAVHSVTLREEEAGAYAPLTAHTGTLINVLASCAYIEEHSAW 360
XX			Db	361
PA	(CURI-) CURIS INC.		QY	RAFAPEFLAHALLAALAPARDGGGGSIPIAQOSATEARGAEPTAGIHWYSQQLYHIGTW 420
PI			Db	361
XX	Crompton T;		QY	LLDSETMHPGMVAVSS 437
DR	WPI: 2001-441484/-7.		Db	421
DR	N-PSDB; AAH28449.		RESULT	13
XX			AAB04685	
PA			ID	AAB04685 standard; Protein; 437 AA..
XX			AC	AAE04685;
XX			XX	04-SEP-2001 (first entry)
DE	Mouse sonic hedgehog (Shh) protein.		XX	
XX	Mouse; hedgehog protein; nootropic; neuroprotective; anticonvulsant; cyclostatic; therapy; Alzheimer's disease; Parkinson's disease; injury;		KW	

KW Huntington's chorea; amyotrophic lateral sclerosis; multiple sclerosis;
KW nervous system aging; neurodegenerative disease; immunological disease;
KW malignant glioma; medulloblastoma; neuroectodermal tumour; cancer;
KW extracellular signalling protein.
XX OS Mus sp.
XX PN WO200134654-A1.
XX PD 17-MAY-2001.
XX PR 02-NOV-2000; 2000WO-US30405.
XX PR 05-NOV-1999; 99US-0164025.
PA (BIOJ) BIOPEN INC.
XX PT Strauch K;
XX WPI; 2001-329075/34.
DR N-PSDB; AAD08032.
XX PT Novel isolated hedgehog fusion polypeptide useful for treating
PT neurological conditions such as Alzheimer's disease, Parkinson's
PT disease, Huntington's chorea, amyotrophic lateral sclerosis, and
XX multiple sclerosis - disclosure; Page 115-116; 178PP; English.
PS The present invention relates to hedgehog fusion proteins. Hedgehog
CC proteins are a family of extracellular signalling proteins that regulate
CC various aspects of embryonic development both in vertebrates and in
CC invertebrates. Hedgehog fusion protein is useful for the prophylaxis or
CC treatment of any condition or disease state for which a hedgehog or
CC patched protein constituent is efficacious and in the diagnosis or
CC specimens and for diagnostic purposes in non-physiological systems or
CC Hedgehog fusion protein is useful for treating neurological conditions
CC due to injury, aging of nervous system, including Alzheimer's disease,
CC chronic neurodegenerative diseases of the nervous system, including
CC Parkinson's disease, Huntington's chorea, amyotrophic lateral sclerosis,
CC and chronic immunological diseases of nervous system including multiple
CC sclerosis and malignant gliomas, medulloblastomas, neuroectodermal
CC tumours and to specifically target medical therapies against cancers and
CC tumours which express the receptor for the protein. The present sequence
XX is mouse sonic hedgehog (Shh) protein.
SQ Sequence 437 AA;

Query Match 100.0%; Score 2299; DB 22; Length 437;
Best Local Similarity 100.0%; Pred. No. 9.4e-226; Length 437;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLILARCFLVILLASLLVCPGLACGPGFRGRHRPKPLTPLAYKQFIPNVAEKTGAS 60
Dy 1 MLLILARCFLVILLASLLVCPGLACGPGFRGRHRPKLTPLAYKQFIPNVAEKTGAS 60
Oy 61 GRYEGKTKTRNSERKEELTPNYNPDLIKRDEENITGADRMLTORCKDKNIALISMNMQWPG 120
Dy 61 GRYEGKTKTRNSERKEELTPNYNPDLIKRDEENITGADRMLTORCKDKNIALISMNMQWPG 120
Oy 121 VRLRVTEGWDGDGHSEESLAVHGRADITSDRDRSKYGMALARVEAGDHWYYESKA 180
Dy 121 VRLRVTEGWDGDGHSEESLAVHGRADITSDRDRSKYGMALARVEAGDHWYYESKA 180
Oy 181 RIIHCYSKAENSAVAKSGGCOPGSATVHLEGGTIVKVKDLPGRDRFLAODQGRLLYSDFL 240
Dy 181 HIHSVSKAENSAVAKSGGCOPGSATVHLEGGTIVKVKDLPGRDRFLAODQGRLLYSDFL 240
Oy 241 TFLDRDEGAKKVYVIELEPREPLLTAHLFLVAPINDSGPMPGPALFAASRVPRQOR 300
Dy 241 TFLDRDEGAKKVYVIELEPREPLLTAHLFLVAPINDSGPMPGPALFAASRVPRQOR 300
CC 241 TFLDRDEGAKKVYVIELEPREPLLTAHLFLVAPINDSGPMPGPALFAASRVPRQOR 300
CC

QY 301 VYVVAERGDRRLPAVHVSVLREECAYAPLTAGCILINWVASCYVIEERSHAH 360
Db 301 VYVVAERGDRRLPAVHVSVLREECAYAPLTAGCILINWVASCYVIEERSHAH 360
XX 361 RAFAPRLAHLAALAPARTDGCGGCSIPAQSATGARGAEPTAGHWSOLLYHIGWT 420
Db 361 RAFAPRLAHLAALAPARTDGCGGCSIPAQSATGARGAEPTAGHWSOLLYHIGWT 420
QY 421 LDSETMHPGLMAVKSS 437
Db 421 LDSETMHPGLMAVKSS 437

RESULT 14**AAE05375****ID****AAE05375****standard****Protein****437 AA.****XX****AC****AAE05375;****XX****DT****12-SEP-2001****(first entry)****XX****DE****Mouse Sonic hedgehog protein.****XX****OS****Mus sp.****XX****FH****Key****Peptide****Location/Qualifiers****1..24****/label= Signal_peptide****25..437****/label= Mature_Shh_protein****XX****PN****US6261786-B1.****XX****PD****17-JUL-2001.****XX****PF****02-JUL-1996;****XX****PR****30-DEC-1993;****XX****PR****14-DEC-1994;****XX****PR****04-MAY-1995;****XX****PR****05-JUN-1995;****XX****PR****05-JUN-1995;****XX****PA****(IMCR) IMPERIAL CANCER RESEARCH TECHNOLOGY LTD.****XX****PA****(HARD) HARVARD COLLEGE.****XX****PI****Mario V, Tabin CJ, Ingham PW, McMahon AP;****XX****DR****WPI; 2001-440859/47.****XX****N-PSDB; AAD0149.****XX****PS****Claim 2; Fig 5A; 127PP; English.****XX****PT**

PN	US6165747-A.
XX	
PD	
XX	26-DEC-2000.
PP	
05-JUN-1995;	95US-0460900.
PR	
XX	30-DEC-1993; 93US-0176427.
PR	14-DEC-1994; 94US-0356060.
PR	04-MAY-1995; 95US-0435093.
PA	'HARD) HARVARD COLLEGE, IMPERIAL CANCER RES TECHNOLOGY LTD.
PA	(IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
XX	
PI	Ingham PW, McMahon AP, Tabin CJ, Marti-gorostiza E, Bumcrot DA;
XX	
DR	WPI: 2001-079847/09.
DR	N-PSDB; AAC87077.
XX	
PT	Poly nucleotides encoding hedgehog proteins, useful for treating
PT	diseases of nervous system such as Alzheimer's disease, Parkinson's
PT	disease, Huntington's chorea, amyotrophic lateral sclerosis, multiple
PT	sclerosis -
XX	
PS	Claim 10: Columns 143-146: 119pp; English.
CC	
CC	The present sequence represents a hedgehog related-protein. The
CC	specification describes a sonic hedgehog protein (Shh), a desert
CC	hedgehog protein (Dhh), and an indian hedgehog protein (Ihh). The
CC	hedgehog poly nucleotides are useful in diagnostic, in antisense
CC	therapy and in therapeutic assays for detecting and treating disorders
CC	involving, e.g., aberrant expression of vertebrate hedgehog homologue.
CC	Hedgehog polypeptides are useful therapeutically to enhance survival
CC	of neurons and other neuron cells and in treating neurological
CC	conditions deriving from acute, subacute, or chronic injury to the
CC	nervous system, including traumatic injury, chemical injury, vascular
CC	injury and deficits (such as the ischemia resulting from stroke),
CC	together with infectious/inflammatory and induced-induced injury, aging
CC	of the nervous system including Alzheimer's disease, chronic
CC	neurodegenerative diseases of the nervous system, including Parkinson's
CC	disease, Huntington's chorea, amyotrophic lateral sclerosis,
CC	spinocerebellar degenerations, and chronic immunological diseases of
CC	the nervous system or affecting the nervous system, including multiple
CC	sclerosis.
XX	
SQ	Sequence 437 AA;
Query	Match 100.0%; score 2289; DB 22; Length 437;
Best Local Similarity 100.0%; Pred. No. 9.4e-226;	
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
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Db	1 MLLIARCLFLVILASSLLVCPGLACGGPGRGKGRRKRPKKLPLAKYQFIPNWAERTLGAS 60
OY	61 GRYECKITRANSEREFELTPNNPNDIFKDENTGADRLLTMRDKLNALAISVMNOWPG 120
Db	61 GRYECKITRANSEREFELTPNNPNDIFKDENTGADRLLTMRDKLNALAISVMNOWPG 120
OY	121 VRLRITEGWEDBGHISESLHVEGRAVIDITSDRDRSKYGMRLARAVEAGEDDWVYESKA 180
Db	121 VRLRITEGWEDBGHISESLHVEGRAVIDITSDRDRSKYGMRLARAVEAGEDDWVYESKA 180
OY	181 HIIHCSVKAENSAVAKSGGCFPGSATVHLLEOGGTKLVKLDLPGDRVIAADDDGGRLLYSDFL 240
Db	181 HIIHCSVKAENSAVAKSGGCFPGSATVHLLEOGGTKLVKLDLPGDRVIAADDDGGRLLYSDFL 240
OY	241 TFLDRDEGAKKVYVVIETLPERRLLTAAHLFVAPHDNSGPTPGPSALEFASRVPGQR 300
Db	241 TFLDRDEGAKKVYVVIETLPERRLLTAAHLFVAPHDNSGPTPGPSALEFASRVPGQR 300
OY	301 VVVAERGDRLLPAHVSHTREEAGAYAPLTAHTGILINRYLASCYAVIEBSWAH 360

Db 301 VYVAERGGDRILLPAAVHSVTLREERAGAYAPLTAHGTILINRVLASCYAVIEHESWAH
Qy 361 RAFAPERLAHALLAALAPARIDGGGGSIAPAQSATEARGAEPTAGIHWSOLLYHIGTN 360
Db 361 RAFAPERLAHALLAALAPARIDGGGGSIAPAQSATEARGAEPTAGIHWSOLLYHIGTN 420
Qy 421 LLDSETMHPGMVKSS 437
Db 421 LLDSETMHPGMVKSS 437

Search completed: February 20, 2003, 10:10:18
Job time : 32.7046 secs

		GenCore version 5.1.3
copyright (c) 1993 - 2003	Compugen Ltd.	
run on:	February 20, 2003, 10:08:38 ; Search time 11.4398 Seconds	
protein - protein search, using sw model	(without alignments) 1123.956 Million cell updates/sec	
title: perfect score: 2289	US-09-827-110A-13	
sequence: BLOSM62	1 MILLARCLFLVILASSLIVC...GATWLDSSETMHPGLGMAYKSS 437	
scoring table: GapOp 10.0 , Gapext 0.5		
searched:	262574 seqs, 29422922 residues	
total number of hits satisfying chosen parameters:	262574	
Minimum DB seq length: 0		
Maximum DB seq length: 2000000000		
post-processing: Minimum Match 0%		
Maximum Match 100%		
Listing first 45 summaries		
Issued_Patents_AA:*		
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2: /cgn2_6/pctodata/1/1aa/6A_COMB.pep:*		
3: /cgn2_6/pctodata/1/1aa/6B_COMB.pep:*		
4: /cgn2_6/pctodata/1/1aa/PCRTUS_COMB.pep:*		
5: /cgn2_6/pctodata/1/1aa/backfiles1.pep:*		
6: /cgn2_6/pctodata/1/1aa/backfiles1.pep:*		
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		
SUMMARIES		
RESULT 1		
US-08-176-427B-8		
; Sequence 8, Application US/08176427B		
Patent No. 5789543		
GENERAL INFORMATION:		
APPLICANT: Ingham, Phillip W.		
APPLICANT: McMahon, Andrew P.		
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing		
TITLE OF INVENTION: Proteins and Uses Related Thereto		
NUMBER OF SEQUENCES: 33		
CORRESPONDENCE ADDRESS:		
ADDRESSEE: LAHIVE & COCKFIELD		
STREET: 60 State Street		
CITY: Boston		
STATE: MA		
COUNTRY: USA		
ZIP: 02109		
COMPUTER READABLE FORM:		
MEDIUM TYPE: FLOPPY DISK		
COMPUTER: IBM PC Compatible		
OPERATING SYSTEM: PC-DOS/MS-DOS		
SOFTWARE: ASCII(text)		
CURRENT APPLICATION DATA:		
APPLICATION NUMBER: US/08/176,427B		
FILING DATE: 30-DEC-1993		
CLASSIFICATION: 435		
ATTORNEY/AGENT INFORMATION:		
NAME: Vincent, Matthew P.		
REFERENCE/DOCKET NUMBER: HMT-006		
TELECOMMUNICATION INFORMATION:		
TELEPHONE: (617) 227-7400		
TELEFAX: (617) 227-5941		
INFORMATION FOR SEQ ID NO: 8:		
SEQUENCE CHARACTERISTICS:		
LENGTH: 437 amino acids		
TYPE: amino acid		
TOPOLOGY: linear		
MOLECULE TYPE: protein		
US-08-176-427B-8		
Query Match	100.0%	Score 2289; DB 1;
Best Local Similarity	100.0%	Length 437;
Matches 437; Conservative	0;	Mismatches 0;
Sequence 1, Appl	0;	Indels 0;
Sequence 2, Appl	0;	Gaps 0;
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Sequence 4, Appl		
Sequence 5, Appl		
Sequence 6, Appl		
Sequence 7, Appl		
Sequence 8, Appl		
Sequence 9, Appl		
Sequence 10, Appl		
Sequence 11, Appl		
Sequence 12, Appl		
Sequence 13, Appl		
Sequence 14, Appl		
Sequence 15, Appl		
Sequence 16, Appl		
Sequence 17, Appl		
Sequence 18, Appl		
Sequence 19, Appl		
Sequence 20, Appl		
Sequence 21, Appl		
Sequence 22, Appl		
Sequence 23, Appl		
Sequence 24, Appl		
Sequence 25, Appl		
Sequence 26, Appl		
Sequence 27, Appl		
QY	1	1 MILLARCLFLVILASSLIVCPLAGPGRGEGKRRHPRKLTPLAYKOFIPNVAEKTIGAS 60
Db	1	1 MILLARCLFLVILASSLIVCPLAGPGRGEGKRRHPRKLTPLAYKOFIPNVAEKTIGAS 60

QY 61 GRYEGKTRNSERFKELTTPNYNPDLIFKDEENTGADRMLTORCKDKNLAISVMQWPG
 ||||| VRLRVTEGWDENGHSEESLHYEGRADITTSDRDSKYGMARLAVEAGFDWVYESKA 120
 Db 61 GRYEGKTRNSERFKELTTPNYNPDLIFKDEENTGADRMLTORCKDKNLAISVMQWPG
 ||||| VRLRVTEGWDENGHSEESLHYEGRADITTSDRDSKYGMARLAVEAGFDWVYESKA 180
 Qy 181 HHCCKVAENSAAKSGGCFFPSAVHLEOGGTKLVKDRPGRDVLAAADDQGRLLYSPL 240
 Db 181 HHCCKVAENSAAKSGGCFFPSAVHLEOGGTKLVKDRPGRDVLAAADDQGRLLYSPL 240
 Qy 241 TFLDRDEGAKKVYVIELTEPRERLLTAALHLFVAPHDGSGTPGPSALFAASRVRGQR 300
 Db 241 TFLDRDEGAKKVYVIELTEPRERLLTAALHLFVAPHDGSGTPGPSALFAASRVRGQR 300
 Qy 301 VVVAERGGDRRLPAHVSHVREEEAGAVPLTAIGTILINRVLASCYAVIEEWSAH 360
 Db 301 VVVAERGGDRRLPAHVSHVREEEAGAVPLTAIGTILINRVLASCYAVIEEWSAH 360
 Qy 361 RAFAFPRLAHALLAALAPARTDGGGSIPAQSATEARGAEPTAGIHWSQLVHIGTW 420
 Db 361 RAFAFPRLAHALLAALAPARTDGGGSIPAQSATEARGAEPTAGIHWSQLVHIGTW 420
 Qy 421 LLDSETMHPGLGMAVKSS 437
 Db 421 LLDSETMHPGLGMAVKSS 437

RESULT 2
 ADDRESS: LAHNE & COCKFIELD
 STREET: 60 State Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII{text}
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/356, 060A
 FILING DATE: 14-DEC-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/176, 427
 FILING DATE: 30-DEC-1993

ATTORNEY/AGENT INFORMATION:
 NAME: Vincent, Matthew P.
 REGISTRATION NUMBER: 36,709
 REFERENCE/DOCKET NUMBER: HMT-006CP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 227-5941
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 437 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Protein

US-08-356-060A-11

; Sequence 11, Application US/08356060A
; Patent No. 584079

GENERAL INFORMATION:
; APPLICANT: Ingham, Phillip W.
; APPLICANT: McMahon, Andrew P.
; APPLICANT: Tabin, Clifford J.
; TITLE OF INVENTION: Proteins and Uses Related Thereto
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:

STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII{text}
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356, 060A
FILING DATE: 14-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/176, 427
FILING DATE: 30-DEC-1993

ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMT-006CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein

US-08-356-060A-11

Query Match
Best Local Similarity 100.0%; Score 2280; DB 2; Length 437;
Matches 437; Conservative 100.0%; Freq. No. 2, 7e-249;
; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MULIARCFHVLLVSLVPGLAGCPGPGKRRHKPKLTPLAYKQIPNVAEKTGAS 60
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Db 61 GRYEGKTRNSERFKELTTPNYNPDLIFKDEENTGADRMLTORCKDKNLAISVMQWPG 120
Qy 121 VRLRVTEGWDENGHSEESLHYEGRADITTSDRDSKYGMARLAVEAGFDWVYESKA 180
Db 121 VRLRVTEGWDENGHSEESLHYEGRADITTSDRDSKYGMARLAVEAGFDWVYESKA 180
Qy 181 HHCCKVAENSAAKSGGCFFPSAVHLEOGGTKLVKDRPGRDVLAAADDQGRLLYSPL 240
Db 181 HHCCKVAENSAAKSGGCFFPSAVHLEOGGTKLVKDRPGRDVLAAADDQGRLLYSPL 240
Qy 241 TFLDRDEGAKKVYVIELTEPRERLLTAALHLFVAPHDGSGTPGPSALFAASRVRGQR 300
Db 241 TFLDRDEGAKKVYVIELTEPRERLLTAALHLFVAPHDGSGTPGPSALFAASRVRGQR 300
Qy 301 VVVAERGGDRRLPAHVSHVREEEAGAVPLTAIGTILINRVLASCYAVIEEWSAH 360
Db 301 VVVAERGGDRRLPAHVSHVREEEAGAVPLTAIGTILINRVLASCYAVIEEWSAH 360
Qy 361 RAFAFPRLAHALLAALAPARTDGGGSIPAQSATEARGAEPTAGIHWSQLVHIGTW 420
Db 361 RAFAFPRLAHALLAALAPARTDGGGSIPAQSATEARGAEPTAGIHWSQLVHIGTW 420
Qy 421 LLDSETMHPGLGMAVKSS 437
Db 421 LLDSETMHPGLGMAVKSS 437

RESULT 3
US-08-460-900C-11

; Sequence 11, Application US/08460900C
; Patent No. 6165747

GENERAL INFORMATION:
; APPLICANT: Ingham, Phillip W.
; APPLICANT: McMahon, Andrew P.
; APPLICANT: Tabin, Clifford J.
; APPLICANT: Bumercot, David A.
; APPLICANT: Marti-Gorostiza, Elisa
; TITLE OF INVENTION: Proteins and Uses Related Thereto
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HONG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460, 900C
FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/435, 093
FILING DATE: 4-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/356, 060
FILING DATE: 14-DEC-1994
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/176,427
 FILING DATE: 30-DEC-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Vincent, Matthew P.
 REFERENCE/DOCKET NUMBER: HMV-006.05
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 832-7000
 TELEFAX: (617) 832-7000
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 437 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ; US-08-460-900C-11

Query Match 100.0%; Score 2289; DB 4; Length 437;
 Best Local Similarity 100.0%; Pred. No. 2.7e-249; Mismatches 0; Indels 0; Gaps 0;
 Matches 437; Conservatism 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MLLIARCEVLILASSLVLCPGLACGGPGRGKRRHKPKLTPLAYKOFIPNVAEKTLAS 60
 Db 1 MLLIARCEVLILASSLVLCPGLACGGPGRGKRRHKPKLTPLAYKOFIPNVAEKTLAS 60
 Qy 61 GRYECKITRNSERKELTPNYPDIFKDEENTGADRMLTORCKDKLNALAISMQNPG 120
 Db 61 GRYECKITRNSERKELTPNYPDIFKDEENTGADRMLTORCKDKLNALAISMQNPG 120
 Qy 121 VRLRVTEGKEDGHISEESLHYEGRAVDTTSDDRSKYGMLARLAVEAGFDWVYYESKA 180
 Db 121 VRLRVTEGKEDGHISEESLHYEGRAVDTTSDDRSKYGMLARLAVEAGFDWVYYESKA 180
 Qy 181 HICSYKAENSAVAKSGGCFFPGSATVHLSQGGTKLVKDLRPGDRVLAADDQGRILYDFL 240
 Db 181 HICSYKAENSAVAKSGGCFFPGSATVHLSQGGTKLVKDLRPGDRVLAADDQGRILYDFL 240
 Qy 301 VVVAERGGDRRLPAAVSIVTLEBEEAGAYAPITAHGTILINRVLASCYAVIEHSWAH 360
 Db 301 VVVAERGGDRRLPAAVSIVTLEBEEAGAYAPITAHGTILINRVLASCYAVIEHSWAH 360
 Qy 361 RAFAPFRLLAHALLALAPARTDGCGGSIPAQSATEARGAEPTAGIHWSQOLYHIGTW 420
 Db 361 RAFAPFRLLAHALLALAPARTDGCGGSIPAQSATEARGAEPTAGIHWSQOLYHIGTW 420
 Qy 421 LLDSETMHPLGMAYKSS 437
 Db 421 LLDSETMHPLGMAYKSS 437

RESULT 4
 US-08-509H-11
 Sequence 11, Application US/08674509B
 Patent No. 6261786
 GENERAL INFORMATION:
 APPLICANT: Ingham, Phillip W.
 APPLICANT: McMahon, Andrew P.
 APPLICANT: Tabin, Clifford J.
 APPLICANT: Marigo, Valeria
 TITLE OF INVENTION: SCREENING ASSAYS FOR HEDGEHOG AGONISTS
 NUMBER OF SEQUENCES: 48
 CORRESPONDENCE ADDRESS:
 ADDRESSE: FOLEY, HONG & EUOT LLP
 STREET: One Post Office Square
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109-2170

COMPUTER READABLE FORM:
 COMPUTER TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/674,509B
 FILING DATE: 02-JUL-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/460,900
 FILING DATE: 05-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Vincent, Matthew P.
 REGISTRATION NUMBER: 36,709
 RESEQUENCING/DOCKET NUMBER: HMV-006.06
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-832-7000
 TELEFAX: 617-832-7000
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 437 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ; US-08-674-509B-11

Query Match 100.0%; Score 2289; DB 4; Length 437;
 Best Local Similarity 100.0%; Pred. No. 2.7e-249; Mismatches 0; Indels 0; Gaps 0;
 Matches 437; Conservatism 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MLLIARCEVLILASSLVLCPGLACGGPGRGKRRHKPKLTPLAYKOFIPNVAEKTLAS 60
 Db 1 MLLIARCEVLILASSLVLCPGLACGGPGRGKRRHKPKLTPLAYKOFIPNVAEKTLAS 60
 Qy 61 GRYECKITRNSERKELTPNYPDIFKDEENTGADRMLTORCKDKLNALAISMQNPG 120
 Db 61 GRYECKITRNSERKELTPNYPDIFKDEENTGADRMLTORCKDKLNALAISMQNPG 120
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 Db 121 VRLRVTEGKEDGHISEESLHYEGRAVDTTSDDRSKYGMLARLAVEAGFDWVYYESKA 180
 Qy 181 HICSYKAENSAVAKSGGCFFPGSATVHLSQGGTKLVKDLRPGDRVLAADDQGRILYDFL 240
 Db 181 HICSYKAENSAVAKSGGCFFPGSATVHLSQGGTKLVKDLRPGDRVLAADDQGRILYDFL 240
 Qy 301 VVVAERGGDRRLPAAVSIVTLEBEEAGAYAPITAHGTILINRVLASCYAVIEHSWAH 360
 Db 301 VVVAERGGDRRLPAAVSIVTLEBEEAGAYAPITAHGTILINRVLASCYAVIEHSWAH 360
 Qy 361 RAFAPFRLLAHALLALAPARTDGCGGSIPAQSATEARGAEPTAGIHWSQOLYHIGTW 420
 Db 361 RAFAPFRLLAHALLALAPARTDGCGGSIPAQSATEARGAEPTAGIHWSQOLYHIGTW 420
 Qy 421 LLDSETMHPLGMAYKSS 437
 Db 421 LLDSETMHPLGMAYKSS 437

RESULT 5
 US-08-954-698-11
 Sequence 11, Application US/08954698
 Patent No. 6271363
 GENERAL INFORMATION:
 APPLICANT: Ingham, Phillip W.
 APPLICANT: McMahon, Andrew P.
 APPLICANT: Tabin, Clifford J.
 TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing

TITLE OF INVENTION: Proteins and Uses Related Thereto
 NUMBER OF SEQUENCES: 48
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FOLEY, HOAG & ELIOT LLP
 STREET: One Post Office Square
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109-2170

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/954,698
 FILING DATE: 20-OCT-1997
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/462,386
 FILING DATE: 05-JUN-1995
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/435,093
 FILING DATE: 04-MAY-1995
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/356,060
 FILING DATE: 14-DEC-1994
 APPLICATION NUMBER: US 08/176,427
 FILING DATE: 30-DEC-1993

ATTORNEY/AGENT INFORMATION:
 NAME: Vincent, Matthew P.
 REFERENCE/DOCKET NUMBER: 36,709

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-832-7000
 TELEX/FAX: 617-832-7000

INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 437 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-354-698-11

Query Match
 Best Local Similarity 100.0%; Score 2289; DB 4;
 Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MULLARCFVLASSILVCPGLACGPGRGKRRHPPKLTPLAKQFIPNVAEKTGAS 60

Db 1 MULLARCFVLASSILVCPGLACGPGRGKRRHPPKLTPLAKQFIPNVAEKTGAS 60

Qy 61 GRYEKITRNSERKEELTPNYPNDIKFDENTGADRMLTQRCOKDNLALISTMNQPG 120

Db 61 GRYEKITRNSERKEELTPNYPNDIKFDENTGADRMLTQRCOKDNLALISTMNQPG 120

Qy 121 VRLRTPEGEDEDGHSEESLHYEGRADVDTTSDDRSKYGMALARLAVEAGEDWYYESKA 180

Db 121 VRLRTPEGEDEDGHSEESLHYEGRADVDTTSDDRSKYGMALARLAVEAGEDWYYESKA 180

Qy 181 HINGSKVAKENSAVAKSGCGFPGSATVHLEOGGPKLVKOLRPDDRLLAADDQGRILYSDL 240

Db 181 HINGSKVAKENSAVAKSGCGFPGSATVHLEOGGPKLVKOLRPDDRLLAADDQGRILYSDL 240

Qy 241 TFLDRDEGAKKFVVIETLEPERRLLTAHHLFVAPHNDSCPTPGPSALASRVRPQR 300

Db 241 TFLDRDEGAKKFVVIETLEPERRLLTAHHLFVAPHNDSCPTPGPSALASRVRPQR 300

Qy 301 VVVAERGGDRRLPAHVSTLREEAGAYAPLTAHGTLTILNRYLASCYAVIENSHWAH 360

Db 301 VVVAERGGDRRLPAHVSTLREEAGAYAPLTAHGTLTILNRYLASCYAVIENSHWAH 360

Qy 361 RAFAFRLAHALLAALAPARTDGGGGSPAAQSATEARGAEPTAGIHWYSQQLYHIGW 420

RESULT 6
 US-08-957-874-11
 Sequence 11, Application US/08957874
 Patent No. 6384192
 GENERAL INFORMATION:
 APPLICANT: Ingham, Phillip W.
 APPLICANT: McMahon, Andrew P.
 APPLICANT: Tabin, Clifford J.

TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
 NUMBER OF SEQUENCES: 47
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FOLEY, HOAG & ELIOT LLP
 STREET: One Post Office Square
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII(text)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/957,874
 FILING DATE: 20-OCT-1997
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/462,386
 FILING DATE: 5-JUNE-1995
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/435,093
 FILING DATE: 4-MAY-1995
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/356,060
 FILING DATE: 14-DEC-1994
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/176,427
 FILING DATE: 30-DEC-1993

ATTORNEY/AGENT INFORMATION:
 NAME: Vincent, Matthew P.
 REFERENCE/DOCKET NUMBER: 36,709

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 832-7000
 TELEX/FAX: (617) 832-7000

INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 437 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-957-874-11

Query Match
 Best Local Similarity 100.0%; Score 2289; DB 4;
 Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MULLARCFVLASSILVCPGLACGPGRGKRRHPPKLTPLAKQFIPNVAEKTGAS 60

Db 1 MULLARCFVLASSILVCPGLACGPGRGKRRHPPKLTPLAKQFIPNVAEKTGAS 60

Qy 61 GRYEKITRNSERKEELTPNYPNDIKFDENTGADRMLTQRCOKDNLALISTMNQPG 120

Db 61 GRYEKITRNSERKEELTPNYPNDIKFDENTGADRMLTQRCOKDNLALISTMNQPG 120

Qy 121 VRLRTPEGEDEDGHSEESLHYEGRADVDTTSDDRSKYGMALARLAVEAGEDWYYESKA 180

Db 121 VRLRTPEGEDEDGHSEESLHYEGRADVDTTSDDRSKYGMALARLAVEAGEDWYYESKA 180

Qy 181 HINGSKVAKENSAVAKSGCGFPGSATVHLEOGGPKLVKOLRPDDRLLAADDQGRILYSDL 240

Db 181 HINGSKVAKENSAVAKSGCGFPGSATVHLEOGGPKLVKOLRPDDRLLAADDQGRILYSDL 240

Qy 241 TFLDRDEGAKKFVVIETLEPERRLLTAHHLFVAPHNDSCPTPGPSALASRVRPQR 300

Db 241 TFLDRDEGAKKFVVIETLEPERRLLTAHHLFVAPHNDSCPTPGPSALASRVRPQR 300

Qy 301 VVVAERGGDRRLPAHVSTLREEAGAYAPLTAHGTLTILNRYLASCYAVIENSHWAH 360

Db 301 VVVAERGGDRRLPAHVSTLREEAGAYAPLTAHGTLTILNRYLASCYAVIENSHWAH 360

Qy 361 RAFAFRLAHALLAALAPARTDGGGGSPAAQSATEARGAEPTAGIHWYSQQLYHIGW 420

Db 361 RAFAFRLAHALLAALAPARTDGGGGSPAAQSATEARGAEPTAGIHWYSQQLYHIGW 420
 Qy 421 LDSETHPLGMAVSS 437
 Db 421 LDSETHPLGMAVSS 437

```

Qy 121. VRRLVTEGSDWDEGHHSSESLHYEGRADVDTTSDRRSKYGMLARLAVEAGDFDWYYESKA 180
Db 121. VRLVTEGSDWDEGHHSSESLHYEGRADVDTTSDRRSKYGMLARLAVEAGDFDWYYESKA 180
Qy 181. HIRCSVKAEVNSVAAKSGGFFPSATVHLEOGGTKLVLDLRPGDRVLADDQGRLLYDFL 240
Db 181. HIRCSVKAEVNSVAAKSGGFFPSATVHLEOGGTKLVLDLRPGDRVLADDQGRLLYDFL 240
Qy 241. TFLDRDEGAKKVVIETLEPRERLLTAAHLLFVAPHNDSGPTGPSALFAASVRPQR 300
Db 241. TFLDRDEGAKKVVIETLEPRERLLTAAHLLFVAPHNDSGPTGPSALFAASVRPQR 300
Qy 361. RAFAFPFLAHALLAALAPARTDGGGSITAAQSATEARGAEPTAGIHWYSQOLYHGTW 420
Db 361. RAFAFPFLAHALLAALAPARTDGGGSITAAQSATEARGAEPTAGIHWYSQOLYHGTW 420
Qy 421. LLSETMHDLMGVKSS 437
Db 421. LLSETMHDLMGVKSS 437

RESULT 7
US-09-325-256-20
; Sequence 20, Application US/09325256
; Patent No. 644493
; GENERAL INFORMATION:
; APPLICANT: PEPPSKY, R. BLAKE
; APPLICANT: BAKER, DARREN P.
; APPLICANT: WEN, DINGT
; APPLICANT: WILLIAMS, KEVIN P.
; APPLICANT: GARGER, ELLEN A.
; APPLICANT: TAYLOR, FREDERICK R.
; APPLICANT: GALBES, ALPHONSE
; APPLICANT: PORER, JEFFREY
TITLE OF INVENTION: HYDROPHOBICALLY-MODIFIED PROTEIN COMPOSITIONS AND
FILE OF INVENTION: METHODS
CURRENT APPLICATION NUMBER: US/09/325, 256
CURRENT FILING DATE: 1999-06-03
PRIOR APPLICATION NUMBER: 60/099, 800
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/078, 935
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/089, 685
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/067, 423
PRIOR FILING DATE: 1997-12-03
PRIOR APPLICATION NUMBER: PCT/US98/25676
PRIOR FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 20
LENGTH: 437
TYPE: PRT
ORGANISM: Murine sp.

US-09-325-256-20

Query Match 100.0%; score 2289; DB 4; Length 437;
Best Local Similarity 100.0%; Pred. No. 2.7e-249; Indels 0; Gaps
Matches 437; Conservative 0; Mismatches 0; Gaps
Qy 1 MLLIARCLFLVLLASSLLVCPGLACGPRGRGCKRRHKKLTLPLAYQKFIPNVAEKTGAS 60
Db 1 MLLIARCLFLVLLASSLLVCPGLACGPRGRGCKRRHKKLTLPLAYQKFIPNVAEKTGAS 60
Qy 61 GRYEGKTRNERSERFKELTPNPNPDTIFKDEENNGADRMTOCRDKDLNLAISVMNQPG 120
Db 61 GRYEGKTRNERSERFKELTPNPNPDTIFKDEENNGADRMTOCRDKDLNLAISVMNQPG 120

```

Qy	121. VRURVTEGSDDEGDGHSESELHYSERAVDTTSDRDRSKYGMALARAVEAGIDWVYESKA 180
Db	121. VRLRVTEGDEGDGHSESELHYSERAVDTTSDRDRSKYGMALARAVEAGIDWVYESKA 180
Qy	181. HILCSVKAEENSAKSGGEPGSATVHLROGGTKVJKDLPGDRVLAADDOGGRLYSDFL 240
Db	181. HIICSVKAEENSAKSGGEPGSATVHLROGGTKVJKDLPGDRVLAADDOGGRLYSDFL 240
Qy	241. TFLDRDEGAKKVVIETEPRELLTAAHLFVAPHNDSGPTGPSALAFASVRVRGQR 300
Db	241. TFLDRDEGAKKVVIETEPRELLTAAHLFVAPHNDSGPTGPSALAFASVRVRGQR 300
Qy	301. VYVAERGGDRRLPAVVISVTLEEAGAYAPLTAHTILNRLASCYAVIEEWSWAH 360
Db	301. VYVAERGGDRRLPAVVISVTLEEAGAYAPLTAHTILNRLASCYAVIEEWSWAH 360
Qy	361. RAFAPFRLLAHALLALPARTDGSGGSITPAQSATEARGAEPTAGIHWYQOLLYHIGTW 420
Db	361. RAFAPFRLLAHALLALPARTDGSGGSITPAQSATEARGAEPTAGIHWYQOLLYHIGTW 420
Qy	421. LLSETMHLGMYKSS 437
Db	421. LLSETMHLGMYKSS 437

QY	121	VLRVTVEGWEDGHSBESLIVELVEGRADITVSDRDRSKYGMALARLAVEAGFDWVYESKA	180
Db	121	VRLRVTEGWDWEDGHHSBESLHVGRADITTSDRDRSKYGMALARLAVEAGFDWVYESKA	180
QY	181	HIHCSYKAENSAVAKSGCGFCGSATVHLEQSGTKYKDRGCDVLAADDGCRULLSDFL	240
Db	181	HIHCSYKAENSAVAKSGCGFCGSATVHLEQSGTKYKDRGCDVLAADDGCRULLSDFL	240
QY	241	TFLDRBEGAKKVYVETLERERULITAHLFVAPHNDSGPTPGPSALFASRVRQCQ	300
Db	241	TFLDRBEGAKKVYVETLERERULITAHLFVAPHNDSGPTPGPSALFASRVRQCQ	300
QY	301	WVVAERGGDRLLPAVHVSYVLREEEAGAYAPLTAHTGTLINRVLASCYAYIEHSWAH	360
Db	301	WVVAERGGDRLLPAVHVSYVLREEEAGAYAPLTAHTGTLINRVLASCYAYIEHSWAH	360
QY	361	RAFAPERLHALAALAPARTOGGGGSIPAAQOSATERRGASEPTAGTHWSOLYHGTW	4200
Db	361	RAFAPERLHALAALAPARTOGGGGSIPAAQOSATERRGASEPTAGTHWSOLYHGTW	4200
OY	421	LIDSETWHPPLGAVKSS	437
Db	421	LIDSETWHPPLGAVKSS	437

Query Match 99.9%; Score 2286; DB 3; Length 437;
 Best Local Similarity 99.8%; Pred. No. 5.9e-249; Length 437;
 Matches 436; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MILLIARCFVLVTLASSILVCPOLACGGGRGFGKRRHKPKLTPLAYKQFIPNVAEKTIGAS
 Db 1 MILLIARCFVLVTLASSILVCPOLACGGGRGFGKRRHKPKLTPLAYKQFIPNVAEKTIGAS 60

QY 61 GRYEGKTRNRSERKELETPNYNPDIKFDEENTGADRMLTQRCKOKLNALISVNQPG
 Db 61 GRYEGKTRNRSERKELETPNYNPDIKFDEENTGADRMLTQRCKOKLNALISVNQPG 60

QY 121 VRLVTEGMDEDGHISEESLHYEGRADTTSDRDSKGMLARLAVEAGFDWVYESKA 180
 Db 121 VRLVTEGMDEDGHISEESLHYEGRADTTSDRDSKGMLARLAVEAGFDWVYESKA 180

QY 181 HHCSVKAENSAKSAGCGCFPSATVHLEQGTKLVKDLRPGDRVLAADDQGRILYSDFL 240
 Db 181 HHCSVKAENSAKSAGCGCFPSATVHLEQGTKLVKDLRPGDRVLAADDQGRILYSDFL 240

QY 241 TFLDRDEGAKKYVVIETLERPERLLTAHLFLVAPAHNDSCPTPGSALFASRVRPGR
 Db 241 TFLDRDEGAKKYVVIETLERPERLLTAHLFLVAPAHNDSCPTPGSALFASRVRPGR 300

QY 301 VVVAERGDRRLPAVHSVTREBEEAGAYAPLTAHGTLINRVLASCCYAVIEHSHWAH 360
 Db 301 VVVAERGDRRLPAVHSVTREBEEAGAYAPLTAHGTLINRVLASCCYAVIEHSHWAH 360

QY 361 RAFAPFLRHALAALAPARTDGGGGSIPIAQSATEARGAEPTAGIHWSOLLYHIGW 420
 Db 361 RAFAPFLRHALAALAPARTDGGGGSIPIAQSATEARGAEPTAGIHWSOLLYHIGW 420

QY 421 LLSETMHPGLMAVKSS 437
 Db 421 LLSETMHPGLMAVKSS 437

RESULT 9
 US-08-567-357A-20
 ; Sequence 20, Application US/08567357A
 ; GENERAL INFORMATION:
 ; APPLICANT: Beachy, Philip A.
 ; APPLICANT: Moon, Randall T.
 ; APPLICANT: Porter, Jeffrey A.
 ; TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES
 ; NUMBER OF SEQUENCES: 37
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson P.C.
 ; STREET: 4225 Executive Square, Suite 1400
 ; CITY: La Jolla
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92037

RESULT 10

US-08-729-743A-20

; Sequence 20, Application US/08729743A

; Patent No. 6214794

; GENERAL INFORMATION:

; APPLICANT: Beachy, Philip A.

; APPLICANT: Moon, Randall T.

; APPLICANT: Porter, Jeffrey A.

; TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES

; NUMBER OF SEQUENCES: 37

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 4225 Executive Square, Suite 1400

; CITY: La Jolla

; STATE: CA

; COUNTRY: USA

; ZIP: 92037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows 95

; SOFTWARE: FastSEQ for Windows

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/729,743A

; FILING DATE: 07-OCT-1996

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 08/567,357

; FILING DATE: 04-DEC-1995

; APPLICATION NUMBER: 08/7349,498

Query Match 99.9%; Score 2286; DB 4; Length 437;
 Best Local Similarity 99.8%; Pred. No. 5.9e-249; Length 437;
 Matches 436; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MILLIARCFVLVTLASSILVCPOLACGGGRGFGKRRHKPKLTPLAYKQFIPNVAEKTIGAS
 Db 1 MILLIARCFVLVTLASSILVCPOLACGGGRGFGKRRHKPKLTPLAYKQFIPNVAEKTIGAS 60

QY 61 GRYEGKTRNRSERKELETPNYNPDIKFDEENTGADRMLTQRCKOKLNALISVNQPG
 Db 61 GRYEGKTRNRSERKELETPNYNPDIKFDEENTGADRMLTQRCKOKLNALISVNQPG 60

QY 121 VRLVTEGMDEDGHISEESLHYEGRADTTSDRDSKGMLARLAVEAGFDWVYESKA 180
 Db 121 VRLVTEGMDEDGHISEESLHYEGRADTTSDRDSKGMLARLAVEAGFDWVYESKA 180

QY 181 HHCSVKAENSAKSAGCGCFPSATVHLEQGTKLVKDLRPGDRVLAADDQGRILYSDFL 240
 Db 181 HHCSVKAENSAKSAGCGCFPSATVHLEQGTKLVKDLRPGDRVLAADDQGRILYSDFL 240

QY 241 TFLDRDEGAKKYVVIETLERPERLLTAHLFLVAPAHNDSCPTPGSALFASRVRPGR
 Db 241 TFLDRDEGAKKYVVIETLERPERLLTAHLFLVAPAHNDSCPTPGSALFASRVRPGR 300

QY 301 VVVAERGDRRLPAVHSVTREBEEAGAYAPLTAHGTLINRVLASCCYAVIEHSHWAH 360
 Db 301 VVVAERGDRRLPAVHSVTREBEEAGAYAPLTAHGTLINRVLASCCYAVIEHSHWAH 360

QY 361 RAFAPFLRHALAALAPARTDGGGGSIPIAQSATEARGAEPTAGIHWSOLLYHIGW 420
 Db 361 RAFAPFLRHALAALAPARTDGGGGSIPIAQSATEARGAEPTAGIHWSOLLYHIGW 420

QY 421 LLSETMHPGLMAVKSS 437
 Db 421 LLSETMHPGLMAVKSS 437

RESULT 9
 US-08-567-357A-20
 ; Sequence 20, Application US/08567357A
 ; GENERAL INFORMATION:
 ; APPLICANT: Beachy, Philip A.
 ; APPLICANT: Moon, Randall T.
 ; APPLICANT: Porter, Jeffrey A.
 ; TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES
 ; NUMBER OF SEQUENCES: 37
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson P.C.
 ; STREET: 4225 Executive Square, Suite 1400
 ; CITY: La Jolla
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92037

RESULT 10

US-08-729-743A-20

; Sequence 20, Application US/08729743A

; Patent No. 6214794

; GENERAL INFORMATION:

; APPLICANT: Beachy, Philip A.

; APPLICANT: Moon, Randall T.

; APPLICANT: Porter, Jeffrey A.

; TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES

; NUMBER OF SEQUENCES: 37

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 4225 Executive Square, Suite 1400

; CITY: La Jolla

; STATE: CA

; COUNTRY: USA

; ZIP: 92037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows 95

; SOFTWARE: FastSEQ for Windows

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/729,743A

; FILING DATE: 07-OCT-1996

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 08/567,357

; FILING DATE: 04-DEC-1995

; APPLICATION NUMBER: 08/7349,498

Query Match 99.9%; Score 2286; DB 3; Length 437;
 Best Local Similarity 99.8%; Pred. No. 5.9e-249; Length 437;
 Matches 436; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MILLIARCFVLVTLASSILVCPOLACGGGRGFGKRRHKPKLTPLAYKQFIPNVAEKTIGAS
 Db 1 MILLIARCFVLVTLASSILVCPOLACGGGRGFGKRRHKPKLTPLAYKQFIPNVAEKTIGAS 60

QY 61 GRYEGKTRNRSERKELETPNYNPDIKFDEENTGADRMLTQRCKOKLNALISVNQPG
 Db 61 GRYEGKTRNRSERKELETPNYNPDIKFDEENTGADRMLTQRCKOKLNALISVNQPG 60

QY 121 VRLVTEGMDEDGHISEESLHYEGRADTTSDRDSKGMLARLAVEAGFDWVYESKA 180
 Db 121 VRLVTEGMDEDGHISEESLHYEGRADTTSDRDSKGMLARLAVEAGFDWVYESKA 180

QY 181 HHCSVKAENSAKSAGCGCFPSATVHLEQGTKLVKDLRPGDRVLAADDQGRILYSDFL 240
 Db 181 HHCSVKAENSAKSAGCGCFPSATVHLEQGTKLVKDLRPGDRVLAADDQGRILYSDFL 240

QY 241 TFLDRDEGAKKYVVIETLERPERLLTAHLFLVAPAHNDSCPTPGSALFASRVRPGR
 Db 241 TFLDRDEGAKKYVVIETLERPERLLTAHLFLVAPAHNDSCPTPGSALFASRVRPGR 300

QY 301 VVVAERGDRRLPAVHSVTREBEEAGAYAPLTAHGTLINRVLASCCYAVIEHSHWAH 360
 Db 301 VVVAERGDRRLPAVHSVTREBEEAGAYAPLTAHGTLINRVLASCCYAVIEHSHWAH 360

QY 361 RAFAPFLRHALAALAPARTDGGGGSIPIAQSATEARGAEPTAGIHWSOLLYHIGW 420
 Db 361 RAFAPFLRHALAALAPARTDGGGGSIPIAQSATEARGAEPTAGIHWSOLLYHIGW 420

QY 421 LLSETMHPGLMAVKSS 437
 Db 421 LLSETMHPGLMAVKSS 437

FILING DATE: 03-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: US/07265/099001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
; US-08-729-743A-20

Query Match 99.9%; Score 2286; DB 4; Length 437;
Best Local Similarity 99.8%; Pred. No. 5.9e-249;
Matches 436; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLIARCFIVLTLASSLLVCPGLACGPGRGKRRHKKLTPLAKQFTPNAEKTIGAS 60
Db 1 MLLIARCFIVLTLASSLLVCPGLACGPGRGKRRHKKLTPLAKQFTPNAEKTIGAS 60
Qy 61 GRYEGKTRNRSERFKELTPNPNPDIKFDEBTGADRMLTQRCKDLNALAISVNQWPG 120
Db 61 GRYEGKTRNRSERFKELTPNPNPDIKFDEBTGADRMLTQRCKDLNALAISVNQWPG 120
Qy 121 VRLRVTEGDEDGHSEESLHYEGRADITTSDRSKYGMALAVAGEFDWVYESKA 180
Db 121 VRLRVTEGDEDGHSEESLHYEGRADITTSDRSKYGMALAVAGEFDWVYESKA 180
Qy 181 HIHCsvkaensvaaksggcpgsatzvhleoggktlvkdrpgdrrylaaadqgrlyxSDL 240
Db 181 HIHCsvkaensvaaksggcpgsatzvhleoggktlvkdrpgdrrylaaadqgrlyxSDL 240
Qy 241 TFLDRDEGAKKVYVIETLERERLLTAHLFVAPHNDSGPTPGPSALFASRVRPQ 300
Db 241 TFLDRDEGAKKVYVIETLERERLLTAHLFVAPHNDSGPTPGPSALFASRVRPQ 300
Qy 301 VVVAERGGDRLLPAVHSVTLREBEEAGAYAPLTAHTGTLINRVLASCYAVIEBSWAH 360
Db 301 VVVAERGGDRLLPAVHSVTLREBEEAGAYAPLTAHTGTLINRVLASCYAVIEBSWAH 360
Qy 361 RAFAFRFLAHALLALAAPTDGGGGSIPAAQSATEARCAEPTAGIHWSQLYHIGTW 420
Db 361 RAFAFRFLAHALLALAAPTDGGGGSIPAAQSATEARCAEPTAGIHWSQLYHIGTW 420
Qy 421 LLDSSEMHPGMVKSS 437
Db 421 LLDSSEMHPGMVKSS 437

RESULT 11
US-09-057-860A-6
Sequence 6, Application US/09057860A
Patient No. 6277820

GENERAL INFORMATION:
APPLICANT: Armon Rosenthal
APPLICANT: Mary Hynes
APPLICANT: Wellan Ye
TITLE OF INVENTION: Method Of Dopaminergic And Serotonergic
TITLE OF INVENTION: Neuron Formation From Neuroprogenitor Cells
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

Query Match 99.9%; Score 2286; DB 4; Length 437;
Best Local Similarity 99.8%; Pred. No. 5.9e-249;
Matches 436; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLIARCFIVLTLASSLLVCPGLACGPGRGKRRHKKLTPLAKQFTPNAEKTIGAS 60
Db 1 MLLIARCFIVLTLASSLLVCPGLACGPGRGKRRHKKLTPLAKQFTPNAEKTIGAS 60
Qy 61 GRYEGKTRNRSERFKELTPNPNPDIKFDEBTGADRMLTQRCKDLNALAISVNQWPG 120
Db 61 GRYEGKTRNRSERFKELTPNPNPDIKFDEBTGADRMLTQRCKDLNALAISVNQWPG 120
Qy 121 VRLRVTEGDEDGHSEESLHYEGRADITTSDRSKYGMALAVAGEFDWVYESKA 180
Db 121 VRLRVTEGDEDGHSEESLHYEGRADITTSDRSKYGMALAVAGEFDWVYESKA 180
Qy 181 HIHCsvkaensvaaksggcpgsatzvhleoggktlvkdrpgdrrylaaadqgrlyxSDL 240
Db 181 HIHCsvkaensvaaksggcpgsatzvhleoggktlvkdrpgdrrylaaadqgrlyxSDL 240
Qy 241 TFLDRDEGAKKVYVIETLERERLLTAHLFVAPHNDSGPTPGPSALFASRVRPQ 300
Db 241 TFLDRDEGAKKVYVIETLERERLLTAHLFVAPHNDSGPTPGPSALFASRVRPQ 300
Qy 301 VVVAERGGDRLLPAVHSVTLREBEEAGAYAPLTAHTGTLINRVLASCYAVIEBSWAH 360
Db 301 VVVAERGGDRLLPAVHSVTLREBEEAGAYAPLTAHTGTLINRVLASCYAVIEBSWAH 360
Qy 361 RAFAFRFLAHALLALAAPTDGGGGSIPAAQSATEARCAEPTAGIHWSQLYHIGTW 420
Db 361 RAFAFRFLAHALLALAAPTDGGGGSIPAAQSATEARCAEPTAGIHWSQLYHIGTW 420
Qy 421 LLDSSEMHPGMVKSS 437
Db 421 LLDSSEMHPGMVKSS 437

RESULT 12
US-08-349-498-20
Sequence 20, Application US/08349498
Patient No. 6281332
GENERAL INFORMATION:
APPLICANT: Beachy, Philip A.
APPLICANT: Moon, Randall T.
TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: U.S.A.

ZIP: 92037 ; EARLIER APPLICATION NUMBER: US 60/091,884
 COMPUTER READABLE FORM: ; EARLIER FILING DATE: 1998-04-15
 MEDIUM TYPE: Floppy disk ; NUMBER OF SEQ ID NOS: 32
 OPERATING SYSTEM: PC-DOS/MS-DOS ; SEQ ID NO: 14
 SOFTWARE: PatentIn Release #1.0, Version #1.30 ; LENGTH: 437
 CURRENT APPLICATION DATA: ; TYPE: PRT
 APPLICATION NUMBER: US/08/349,498 ; ORGANISM: Mus musculus
 FILING DATE: 02-DEC-1994 ; US-09-293-505-14
 CLASSIFICATION: 530 ; ATTORNEY/AGENT INFORMATION:
 ATTORNEY/AGENT INFORMATION: NAME: Haile, Lisa A.
 REGISTRATION NUMBER: 38,347 ; REFERENCE/DOCKET NUMBER: 07265/043001
 TELECOMMUNICATION INFORMATION: ;
 TELEPHONE: 619/678-5070 ;
 TELEFAX: 619/678-5099 ;
 INFORMATION FOR SEQ ID NO: 20: ;
 SEQUENCE CHARACTERISTICS: LENGTH: 437 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ;
 US-08-349-498-20

Query Match 99.9%; Score 2286; DB 4; Length 437;
 Best Local Similarity 99.8%; Pred. No. 5, 9e-249; Matches 436; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Matches 436; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MULLARCFLVTLASSLIVCPCGAGCPGRGFGRRHPRKLPKTPAYQFIPNVAEKTIGAS 60
 Db 1 MULLARCFLVTLASSLIVCPCGAGCPGRGFGRRHPRKLPKTPAYQFIPNVAEKTIGAS 60
 Qy 61 GRYEGKTRNRSERKELTPNVNPDIFKDEENTGADRMLTORKDKLNALAIISVMQWPG 120
 Db 61 GRYEGKTRNRSERKELTPNVNPDIFKDEENTGADRMLTORKDKLNALAIISVMQWPG 120
 Qy 121 VRLRVTEGWDGDGHSEESLHYEGRAVDTTSDRRSKYGMLARAVEAGDWVYESKA 180
 Db 121 VRLRVTEGWDGDGHSEESLHYEGRAVDTTSDRRSKYGMLARAVEAGDWVYESKA 180
 Qy 181 HINCYSKAENSAVAKSGGGCFFPGSATVHLEOGGTKLVKDLRPGDVLAAADQGRLLYSDPL 240
 Db 181 HINCYSKAENSAVAKSGGGCFFPGSATVHLEOGGTKLVKDLRPGDVLAAADQGRLLYSDPL 240
 Qy 241 TELRDEGAKKVVFVIELEPRERLLTAAHLFVAPINDSGPPGPGSALFAASRVRPQQR 300
 Db 241 TELRDEGAKKVVFVIELEPRERLLTAAHLFVAPINDSGPPGPGSALFAASRVRPQQR 300
 Qy 301 VVVAERGGDRRLPAAVHSVTLEEEREEAGAYPLTAHTGTLINRVLASCYAYIEEWSWAH 360
 Db 301 VVVAERGGDRRLPAAVHSVTLEEEREEAGAYPLTAHTGTLINRVLASCYAYIEEWSWAH 360
 Qy 361 RAFAFRLAHALAALAPARTDGGGSSIPAQOSATEARGAEPTAGIHWQSOLLYHIGTW 420
 Db 361 RAFAFRLAHALAALAPARTDGGGSSIPAQOSATEARGAEPTAGIHWQSOLLYHIGTW 420
 Qy 421 LIDSETHMPLGMVKSS 437
 Db 421 LIDSETHMPLGMVKSS 437

RESULT 14

PCT-US95-15463-20 ; Sequence 20, Application PC/TUS9515463
 ; GENERAL INFORMATION:
 ; APPLICANT: The Johns Hopkins University School of Medicine
 ; TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson P.C.
 ; STREET: 4225 Executive Square, Suite 1400
 ; CITY: La Jolla
 ; STATE: CA
 ; COUNTRY: U.S.A.
 ; ZIP: 92037

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-Dos/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PC/TUS95/15463
 FILING DATE: 01-DEC-1995
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Haile, Lisa A.
 REGISTRATION NUMBER: 38,347
 REFERENCE/DOCKET NUMBER: 07265/080W01

RESULT 13

US-09-293-505-14
 Sequence 14, Application US/09293505
 Patent No. 634857
 GENERAL INFORMATION:
 APPLICANT: de Savage, Frederic
 APPLICANT: Carpenter, David A.
 TITLE OF INVENTION: Patched-2
 FILE REFERENCE: P14051
 CURRENT APPLICATION NUMBER: US/09/293,505
 CURRENT FILING DATE: 1999-04-15

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619/678-5070
 TELEFAX: 619/678-5059

INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 437 amino acids
 TYPE: amino acid
 TOPOLGY: linear
 MOLECULE TYPE: protein

PCT-US95-15463-20

Query Match 99.9%; Score 2286; DB 5; Length 437;

Best local similarity 99.8%; Pred. No. 5. 9e-249;
 Matches 436; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLIARCPFLVILLASLLVCPGLACGGPGRGKRRHPKKLTPLAYKOPTIPVAEKTIGAS 60
 Db 1 MLLIARCPFLVILLASLLVCPGLACGGPGRGKRRHPKKLTPLAYKOPTIPVAEKTIGAS 60

Qy 61 GRYEGKITRNSEERKELTPTNYPDIDIFKDEENTGADRMLTQRCKDLNALISTWMQPG 120
 Db 61 GRYEGKITRNSEERKELTPTNYPDIDIFKDEENTGADRMLTQRCKDLNALISTWMQPG 120

Qy 121 VRLRTGEKGDEDGHISEESLYHGRADVITTSDRDRSKYGMALARLAVEAGFDWVYESKA 180
 Db 121 VRLRTGEKGDEDGHISEESLYHGRADVITTSDRDRSKYGMALARLAVEAGFDWVYESKA 180

Qy 181 HICHSVKAENSAVAKSGCCFGPSATVHLBQGGTKLVKDLRPGDRVLADDQGRILYSPL 240
 Db 181 HICHSVKAENSAVAKSGCCFGPSATVHLBQGGTKLVKDLRPGDRVLADDQGRILYSPL 240

Qy 241 TFLDRDEGAKKVYVIETLERPERLLTAHLIVAPHNDSGPTPGPSALFAASVRPGQR 300
 Db 241 TFLDRDEGAKKVYVIETLERPERLLTAHLIVAPHNDSGPTPGPSALFAASVRPGQR 300

Qy 301 VVVAERGGDRRLPAAVHSTLREEEAGAYATPLAHTGTLINRVLASCYAVIEEWSWAH 360
 Db 301 VVVAERGGDRRLPAAVHSTLREEEAGAYATPLAHTGTLINRVLASCYAVIEEWSWAH 360

Qy 361 RAFAPFRLLAHALLALAPARTDGGGGSIFFAQOSATEARGAEPTAGIHWSQLYHIGW 420
 Db 361 RAFAPFRLLAHALLALAPARTDGGGGSIFFAQOSATEARGAEPTAGIHWSQLYHIGW 420

Qy 421 LLDSETMHPGMVKSS 437
 Db 421 LLDSETMHPGMVKSS 437

Qy 301 VVVAERGGDRRLPAAVHSTLREEEAGAYATPLAHTGTLINRVLASCYAVIEEWSWAH 360
 Db 301 VVVAERGGDRRLPAAVHSTLREEEAGAYATPLAHTGTLINRVLASCYAVIEEWSWAH 360

Qy 361 RAFAPFRLLAHALLALAPARTDGGGGSIFFAQOSATEARGAEPTAGIHWSQLYHIGW 420
 Db 361 RAFAPFRLLAHALLALAPARTDGGGGSIFFAQOSATEARGAEPTAGIHWSQLYHIGW 420

Qy 421 LLDSETMHPGMVKSS 437
 Db 421 LLDSETMHPGMVKSS 437

RESULT 15

PCT-US95-15923-20
 Sequence 20, Application PC/TUS9515923

GENERAL INFORMATION:
 APPLICANT: The Johns Hopkins University School of Medicine, et al.

TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES
 NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.
 STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla
 STATE: CA
 COUNTRY: U.S.A.

ZIP: 92037
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT-US95-15923
 FILING DATE: 04-DEC-1995

CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Haile, Lisa A.

REGISTRATION NUMBER: 38,347
 REFERENCE/DOCKET NUMBER: 07265/043W01

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619/678-5070
 TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 437 amino acids
 TYPE: amino acid
 MOLECULE TYPE: protein

PCT-US95-15923-20

Query Match 99.9%; Score 2286; DB 5; Length 437;

Best local similarity 99.8%; Pred. No. 5. 9e-249;
 Matches 436; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLIARCPFLVILLASLLVCPGLACGGPGRGKRRHPKKLTPLAYKOPTIPVAEKTIGAS 60
 Db 1 MLLIARCPFLVILLASLLVCPGLACGGPGRGKRRHPKKLTPLAYKOPTIPVAEKTIGAS 60

Qy 61 GRYEGKITRNSEERKELTPTNYPDIDIFKDEENTGADRMLTQRCKDLNALISTWMQPG 120
 Db 61 GRYEGKITRNSEERKELTPTNYPDIDIFKDEENTGADRMLTQRCKDLNALISTWMQPG 120

Qy 121 VRLRTGEKGDEDGHISEESLYHGRADVITTSDRDRSKYGMALARLAVEAGFDWVYESKA 180
 Db 121 VRLRTGEKGDEDGHISEESLYHGRADVITTSDRDRSKYGMALARLAVEAGFDWVYESKA 180

Qy 181 HICHSVKAENSAVAKSGCCFGPSATVHLBQGGTKLVKDLRPGDRVLADDQGRILYSPL 240
 Db 181 HICHSVKAENSAVAKSGCCFGPSATVHLBQGGTKLVKDLRPGDRVLADDQGRILYSPL 240

Qy 241 TFLDRDEGAKKVYVIETLERPERLLTAHLIVAPHNDSGPTPGPSALFAASVRPGQR 300
 Db 241 TFLDRDEGAKKVYVIETLERPERLLTAHLIVAPHNDSGPTPGPSALFAASVRPGQR 300

Qy 301 VVVAERGGDRRLPAAVHSTLREEEAGAYATPLAHTGTLINRVLASCYAVIEEWSWAH 360
 Db 301 VVVAERGGDRRLPAAVHSTLREEEAGAYATPLAHTGTLINRVLASCYAVIEEWSWAH 360

Qy 361 RAFAPFRLLAHALLALAPARTDGGGGSIFFAQOSATEARGAEPTAGIHWSQLYHIGW 420
 Db 361 RAFAPFRLLAHALLALAPARTDGGGGSIFFAQOSATEARGAEPTAGIHWSQLYHIGW 420

Qy 421 LLDSETMHPGMVKSS 437
 Db 421 LLDSETMHPGMVKSS 437

Qy 301 VVVAERGGDRRLPAAVHSTLREEEAGAYATPLAHTGTLINRVLASCYAVIEEWSWAH 360
 Db 301 VVVAERGGDRRLPAAVHSTLREEEAGAYATPLAHTGTLINRVLASCYAVIEEWSWAH 360

Qy 361 RAFAPFRLLAHALLALAPARTDGGGGSIFFAQOSATEARGAEPTAGIHWSQLYHIGW 420
 Db 361 RAFAPFRLLAHALLALAPARTDGGGGSIFFAQOSATEARGAEPTAGIHWSQLYHIGW 420

Qy 421 LLDSETMHPGMVKSS 437
 Db 421 LLDSETMHPGMVKSS 437

Search completed: February 20, 2003, 10:14:11
 Job time : 12.4398 secs

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OM protein - protein search, using sw model.

Run on: February 20, 2003, 10:08:18 ; Search time 14.3815 Seconds
(without alignments)
2921.176 Million cell updates/sec

Title: US-09-827-110a-13

Perfect score: 2289
Sequence: 1 MLLIARCLFLVILASSLLV... GTWILDSETMHPLGMVKSS 437

Scoring table: BLASTME2
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73;*
1: pir1;*
2: pir2;*
3: pir3;*
4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	2286	99.9	437	2 A49425	Sonic hedgehog protein precursor - mouse
2	2200	98.1	437	2 B53193	C;Species: Mus musculus (house mouse) C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 10-Dec-1999 C;Accession: A49425 R;Schelard, Y.; Epstein, D.J.; St-Jacques, B.; Shen, L.; Mohler, J.; McMahon, J.A.; M
3	1788	78.1	425	2 A49424	Cell 75, 1417-1430, 1993
4	1525	66.6	444	2 S56765	A;Title: Sonic hedgehog, a member of a family of putative signaling molecules, is imp
5	1517	66.3	418	2 A53193	A;Reference number: A49425; MUID: 94094334; PMID: 791661
6	1458	63.7	415	2 A49426	A;Accession: A49425 A;Status: preliminary; nucleic acid sequence not shown
7	1219	53.3	396	2 B49425	A;Molecule type: mRNA
8	1033	45.6	336	2 C49425	A;Residues: 1-437 <ECH>
9	894	47.1	471	2 A46020	A;Cross-references: GB:X76290 A;Note: authors translation is shown for the codon TCC at position 436
10	452	19.7	94	2 G02135	C;Genetics: A;Gene: Shh C;Superfamily: sonic hedgehog protein
11	170	7.4	615	2 T2950	Query Match 99.9%; Score 2286; DB 2; Length 437; Best Local Similarity 99.9%; Pred. No. 7.2e-177; Matches 436; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
12	153	6.7	1207	2 T2754	Db 1 MLLIARCLFLVILASSLLVCPGLACGPGRRGGRRPKLTPLAYKPIPNAAKTIGAS 60
13	148	6.5	1226	2 T24045	QY 1 MLLIARCLFLVILASSLLVCPGLACGPGRRGGRRPKLTPLAYKPIPNAAKTIGAS 60
14	146	6.4	481	2 T27975	Db 1 GRYEKGTRNNSERKELPPNYPNIDIFKEENGDADMTQRDKDNALATSVMNQPG 120
15	140	5.5	629	2 T19563	QY 121 VRLRVTEGDEGHHSERSESLHYGRADVITTSDRDRSKYGMALARLAYEAGFDVYVYESKA 180
16	130	5.7	868	2 T2281	Db 121 VRLRVTEGDEGHHSERSESLHYGRADVITTSDRDRSKYGMALARLAYEAGFDVYVYESKA 180
17	128	5.6	1021	2 T23252	Db 181 HICSVKNSVAKSQGCCFPGSATVHLEQGGTKLVKDRPGRDVLADDQRLYSDFL 240
18	127	5.5	484	2 T3452	QY 241 TFLDRDEGAKKVYVIETLEPRERLLTAAHLFLVAPHNDSGPTPGPSALFASRVRCQR 300
19	118	5.2	598	2 T42070	Db 241 TFLDRDEGAKKVYVIETLEPRERLLTAAHLFLVAPHNDSGPTPGPSALFASRVRCQR 300
20	117	5.1	1407	2 T28702	QY 301 VVVAERGGDRRLPAAVHVSIVTREEEAGAYAQLTAHGCTILINRVLASCYAYTEHWAH 360
21	108	4.7	481	2 T27975	Db 301 VVVAERGGDRRLPAAVHVSIVTREEEAGAYAQLTAHGCTILINRVLASCYAYTEHWAH 360
22	107	4.7	672	2 T36083	QY 361 RAFAPFLHALLAALAPARTDGGSISPAQOSATERGAEPAGTHWSOLYHGTW 420
23	105	4.6	1324	2 T14070	Db 361 RAFAPFLHALLAALAPARTDGGSISPAQOSATERGAEPAGTHWSOLYHGTW 420
24	102	4.5	484	2 T80719	snc protein [Impor
25	101	4.4	482	2 E70554	Db 301 VVVAERGGDRRLPAAVHVSIVTREEEAGAYAQLTAHGCTILINRVLASCYAYTEHWAH 360
26	100	4.4	863	2 H84177	QY 361 RAFAPFLHALLAALAPARTDGGSISPAQOSATERGAEPAGTHWSOLYHGTW 420
27	99	4.4	930	2 T35180	hypothetical protein
28	100	4.4	831	2 H84369	MCM / cell division
29	4.4	1147	2 D87295	probable glycosyl	

ALIGNMENTS

hypothetical protein ABC transporter, A bacula gene protein [protein-Pi] urid hypothetical protein thyroid hormone receptor tyrosyl-tRNA synth retrovirus-related copper resistance probable exoribonuclease probable outer membrane C-erbB beta p probable anthranilic acid propionyl-CoA carb

Query Match 66.3%; Score 1517; DB 2; Length 418;
 Best Local Similarity 67.7%; Pred. No. 9.6e-115; Matches 299; Conservative 46; Mismatches 78; Indels 18; Gaps 5;
 Matches 294; Conservative 47; Mismatches 75; Indels 18; Gaps 3;

C;Species: Brachydanio rerio (zebra fish)
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 10-Dec-1999
 C;Accession: A53193
 R;Roelink, H.; Augburger, A.; Heemskerk, J.; Korzh, V.; Norlin, S.; Ruiz I Altaba, A.; Cell 76, 761-775, 1994
 A;Title: Floor plate and motor neuron induction by vhh-1, a vertebrate homolog of hedgehog genes
 A;Reference number: A53193; MUID:94170375; PMID:8124714
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-418 <ROE>
 A;Cross-references: GB:L27585; NID:9452159; PID:9452160
 C;Superfamily: sonic hedgehog protein

Query Match 63.7%; Score 1458; DB 2; Length 415;
 Best Local Similarity 67.1%; Pred. No. 5.6e-110; Matches 289; Conservative 46; Mismatches 78; Indels 18; Gaps 5;
 Matches 289; Conservative 46; Mismatches 78; Indels 18; Gaps 5;

QY 4 LLARCFVLVLLSLVPGLAGCPGRGFGKRRHPPKKTPLAYQKFIPNVAEKTIGASRY 63
 Db 3 LLTRVLVLLSLTLLSVLVSGLACCPGRGFGKRRHPPKKTPLAYQKFIPNVAEKTIGASRY 62

QY 64 EGKTRNSRERKELETPNNDIFKEEETGABLMRCKDKNLALISVMNQWPGRV 123
 Db 63 EGKTRNSRERKELETPNNDIFKEEETGABLMRCKDKNLALISVMNQWPGRV 122

QY 124 RVTEGWDDEGHHRFEELSHVEGRAVDITSDRSKSYGTLRNLAVEAGDWVYESKAHII 183
 Db 123 RVTEGWDDEGHHRFEELSHVEGRAVDITSDRSKSYGTLRNLAVEAGDWVYESKAHII 182

QY 184 CSVKAENSAAKSGCCFPSSATVILEQSGTCKVLDRPDRVLADDGCRLLSDFPL 243
 Db 183 CSVKAENSAAKSGCCFPSSALVSLQDGQKAVDKLNPDGVKLADSAQNLVFSDFIMFT 242

QY 244 DRDEGAKKVYVLTLEPERLRLTAAHLFVAPHNDSGGPTGPSALFAASRVPGQRVY 303
 Db 243 DRDSTTRRYVYVLTQEPVKITLAHILFVL-DNSTEDLHTWTAASSVRQKVN 301

QY 304 VAERGDDRLLPAAWHSTLREERAGAYAPLTAGTILINRVLASCYAVIEENSWAHRAF 363
 Db 302 VDSSGQLSIVIORITYI--EGORGSEPVTHGTIVDRLILASCYAVIEDOGLAHAF 357

QY 364 APFRLAHALAALAPARTDGGGGSIPAAQSATEARGAEPTAGIHWSOLLYHIGTWLID 423
 Db 358 APARLYYYVSSFLSP-KIPAVG---PMRLYNRRGSTGTPG----SCHQMGTWLID 404

QY 424 SETMPHPGMV 434
 Db 405 SNMLHPLGMSV 415

RESULT 7
 B4425
 Desert hedgehog protein precursor - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 10-Dec-1999
 C;Accession: B49425
 R;Echelard, Y.; Epstein, D.J.; St-Jacques, B.; Shen, L.; Mohler, J.; McMahon, J.A.; Cell 75, 1417-1430, 1993
 A;Title: Sonic hedgehog, a member of a family of putative signaling molecules, is imp
 A;Reference number: A49425; MUID:94094334; PMID:7916661
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-396 <ECH>

QY 181 HHCSYKAENSAAKSGCCFPSSATVILEQSGTCKVLDRPDRVLADDGCRLLSDFL 240
 Db 181 HHCSYKAENSAAKSGCCFPSSATVILEQSGTCKVLDRPDRVLADDGCRLLSDFL 240

QY 241 TFLDRDEGAKKVYVLTLEPERLRLTAAHLFVAPHNDSGGPSALFAASRVGRQV 300
 Db 241 MFIDQERDVKKFVYIET--SORKIRITAHLFVQTKVNG-TRSFKSVFASNQIQLD 297

QY 301 VVWAERGGDRLLPAAWHSTLREERAGAYAPLTAGTILINRVLASCYAVIEENSWAHRAF 363
 Db 298 iYTADPK--TMTLKA KVKEKVLD-EEDIGAYA P LTAHGTVWIDQVLA SCYAVIEENSWAHRAF 357

QY 361 RAFAFPLLAHALAALAPARTDGGGGSIPAAQSATEARGAEPTAGIHWSOLLYHIGTWLID 423
 Db 355 LAFAFPLRGMSLSSYIWP-RDSSPSSGLOPHHQVDLQSHHQVDLQSHHQVDLQSHHQLEG 413

QY 407 IHWSOLLYHIGTWLIDSETMPLGMAVKSS 437
 Db 414 IHWSOLLYQIQTGWLDSNSLHPIGMATKSS 444

A;Cross-references: GB:X76292; NID:9443941; PID:CAA53924.1; PID:9443942
 C;Genetics:
 A;Gene: Dhh
 C;Superfamily: sonic hedgehog protein

Query Match 53.3%; Score 1219; DB 2; Length 396;
 Best Local Similarity 58.7%; Pred. No. 1.1e-90; Indels 40; Gaps 12;
 Matches 249; Conservative 55; Mismatches 80; InDelS 40; Gaps 12;

Qy 4 LLARCFVLVILLASLLVCPGLACGPG-RG-PGKRRPKK-LTPPLAYKOFINTVAEKTILGASC 61
 Db 7 LIPCCCLIALALS--AQSCGORGPGVRRVRVKOLVPLIKQFVEMPEITLGASG 61

Qy 122 RLRTYEGWDEGHISEESEHLYEGRAVDTTSDRRSKGMLARIAVEAGFDWVYTESKAH 181
 Db 122 RLRTYEGWDEGHISEESEHLYEGRAVDTTSDRRSKGMLARIAVEAGFDWVYTESKAH 181

Qy 182 IHCSYKAENSAVAAAGGGCFFPSATVHLECGGTTKVKDLRPGDRYLAADDODDGRYLSDFL 241
 Db 182 IHVSYKAENSLAVRAGCFFPSATVHLECGGTTKVKDLRPGDRYLAADDODDGRYLSDFL 241

Qy 242 FLDLDRDEGAKKVYFYIETLEPRERLITAHLFVAPAHNDSGPTGP--SALFASRVRPG 298
 Db 242 FLDLDRDQRASFAVAVETERPRPKLILTPHLVFAA---RGPAAPGDFAPVFARRLAG 297

Qy 299 QRVVVAERGGDRRLPAWHSVLRREEAGAVPLANTGTLILNRLVASCYVIEHSH 358
 Db 298 DSVLA--PGGD-AQCPARVARY-REAAVGVPFLTAHGTLVNDVLAASCYAVLEHSH 352

Qy 359 AHRAPAPFLAHIALALAPARTOGGGSIAPAQSATEARGAAPTGTWHYSQQQLYHTG 418
 Db 353 AHRAPAPFLAHIALALAPARTOGGGSIAPAQSATEARGAAPTGTWHYSQQQLYHTG 418

Oy 419 TWL1 422
 Db 392 EELM 395

RESULT 8

C4925 Indian hedgehog protein - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 06-Jan-1995 #sequence_change 11-Jan-2000
 C;Accession: C49425
 R;Ebelard, Y.; Epstein, D.J.; St-Jacques, B.; Shen, L.; Mohler, J.; McMahon, J.A.; McMahon, Cell, 75, 1417-1430, 1993
 A;Title: Sonic hedgehog, a member of a family of putative signaling molecules, is implicated in the development of the nervous system
 A;Reference number: A49425; MUID:94094334; PMID:7916661
 A;Accession: C49425
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-336 <ECH>
 A;Cross-references: GB:X76291
 C;Superfamily: sonic hedgehog protein

Query Match 45.6%; Score 1043; DB 2; Length 336;
 Best Local Similarity 58.7%; Pred. No. 1.5e-76; Indels 32; Gaps 5;

Matches 21; Conservative 38; Mismatches 80; InDelS 32; Gaps 5;

Qy 72 ERFFELTPWNPDPDIFKOBENTGADRMLTQCRDKLNALAISTMWNQPGVRLATEGDE 131
 Db 1 ERFELTPWNPDPDIFKOBENTGADRMLTQCRDKLNALAISTMWNQPGVRLATEGDE 60

Qy 132 DGHHSSEESLHYEGRAVDTTSDRRSKGMLARIAVEAGFDWVYYESKAHICSVKAENS 191
 Db 61 DGHHSSEESLHYEGRAVDTTSDRRSKGMLARIAVEAGFDWVYYESKAHICSVKSFSHS 120

Qy 192 VAAAGGGCPGSGATVHLSQGGTKLVKDRPGLVLAADQGRLLYSDLTFRDEGAKK 251
 Db 192 VAAAGGGCPGSGATVHLSQGGTKLVKDRPGLVLAADQGRLLYSDLTFRDEGAKK 251

RESULT 9

A46400 segment polarity protein hedgehog - fruit fly (*Drosophila melanogaster*)
 C;Species: Drosophila melanogaster
 C;Accession: A46400; JN0501; A4380
 R;Tabata, T.; Eaton, S.; Kornberg, T.B.
 Genes Dev, 6, 2635-2645, 1992
 A;Title: The *Drosophila* hedgehog gene is expressed specifically in posterior compartment
 A;Reference number: A46400; MUID:94040725; PMID:134074
 A;Accession: A46400
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-471 <TAB>
 A;Cross-references: GB:S66384; NID:9435848; PID:9435849
 A;Experimental source: Oregon-R
 A;Note: sequence extracted from NCBI backbone (NCBIN:138996, NCBIP:138997)
 R;Tashiro, S.; Michile, T.; Higashijima, S.; Zeno, S.; Ishimaru, S.; Takahashi, F.;
 Gene 124, 183-189, 1993
 A;Title: Structure and expression of hedgehog, a *Drosophila* segment-polarity gene required for dorsal appendage formation
 A;Reference number: JN0501; MUID:93165922; PMID:816882
 A;Accession: JN0501
 A;Molecule type: DNA
 A;Residues: 1-471 <TAB>
 A;Cross references: GB:L05404
 A;Note: It is uncertain whether Met-1 or Met-51 is the initiator
 R;Note: intron positions were determined from partial DNA sequence
 R;Lee, J.J.; von Kessler, D.P.; Parks, S.; Beachy, P.A.
 A;Title: Secretion and localized transcription suggest a role in positional signaling
 A;Reference number: A43480; MUID:93008241; PMID:1394430
 A;Accession: A43480
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: DNA
 A;Residues: 1-471 <TAB>
 A;Cross references: GB:L02793; NID:9157609; PID:9157610
 A;Note: sequence extracted from NCBI backbone (NCBIP:115418)
 C;Comment: This protein is required for cell-cell communication.
 C;Genetics:

A;Gene: hh
 A;Cross-references: FlyBase:FBgn004644
 C;Superfamily: sonic hedgehog protein
 C;Keywords: transmembrane protein
 F;62-82/Domain: transmembrane #status predicted <TMM>

Query Match 39.1%; Score 894; DB 2; Length 471;
 Best Local Similarity 46.8%; Pred. No. 2.5e-64; Indels 22; Gaps 9;
 Matches 197; Conservative 62; Mismatches 140;

Qy 10 LVIYLASSLIVCPGLACPGPGRGFKKRHKPKLQPLAKOFIPWAEKTLGAGSRGEYKTR 69
 Db 70 LLIYLVPMVSPAHSCPGPGFLGLRHR-ARNLYPLVLTQKOTIPNLSEYNTNSAQPLEGVIRR 128

QY 70 NSERKFELPPNPYDILFKEEINGADRLMTORCKDKLNLATISLVMNKNOWPGVRLRVTEGW 129
A; Molcule type: DNA
A; Residues: :1-615 <NHA>
A; Cross-references: EMBL:U88183; PIDN:AAB52656.1; GSPDB:GN00028; CESP:ZK377.1
A; Experimental source: strain Bristol N2; clone ZK377
C; Genetics:
A; Gene: CESP:ZK377.1
A; Map position: X
A; Introns: 46/1; 70/3; 157/2; 176/1; 245/2; 314/3; 402/3; 499/2
QY 190 NSVAAKSGCCFGPSATVHLEQGGTKLVLDLRPLADDGGRLLSDFLTLDRDEGA 249
A; Cross-references:
C; Species: Caenorhabditis elegans
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C; Accession: T29550
Db 129 DSPFKDLPVNPNRDLFPRDEEGTGDADMKSCKKEKLNVLYASVMNWPGLRVLVTEW 188
Db 130 DEGCHSEPSLHGEGRAVITATSDRQSYKGMLARAVEAGFDWVYESSAHICHSVKE 189
Db 189 DEYHGGESLHGEGRAVITATSDRQSYKGMLARAVEAGFDWVYSSRRHICSVKD 248
Db 250 KKVIVVIELPERERLLTAHLIF-KHNDGSPTRPFSALASRVSFQRVYVALEG 308
Db 249 SSISSHVHCFCPTPESTALLESGVRKPLGELSIDGRVLSTMQAVSSEVLFMDNLQ 308
QY 309 GDRRLPAVHHSV-TLREEEAGAYAPLTHGTILINRVLASCYAVIEEHWAHRAFAPR 367
Db 363 GELR-PQVVKVSVRSK-GVVAFLREGTIVVNSVYASCAVINSQSLSAHGLAFR 418
QY 368 LAHALAALAPARIDGGGGSIPAQSITEARAEPTAGIHWYSQQLYHIGTMILDSTM 427
Db 419 LLSTLEAWL-PAKEQ-----LHSSPKVVSQSQONQHWNALYKVKDYLPOSWR 469
QY 428 H 428
Db 470 H 470

RESULT 10
G02735
desert hedgehog - human (fragment)
C; Species: Homo sapiens (man)
C; Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 11-Jan-2000
C; Accession: G02735
R; Drummond, I.A.
Submitted to the EMBL Data Library, June 1996
A; Reference number: H01643
A; accession: G02735
A; Status: preliminary; translated from GB/EMBL/DDJB
A; Residues: 1-94 <DRU>
A; Cross-references: EMBL:U59748; NID:91401271; PID:91401272
A; Gene: hdhh
A; Genes:
C; Superfamily: sonic hedgehog protein

Query Match 19.7%; Score 452; DB 2; Length 94;
Best Local Similarity 85.1%; Pred. No. 1.5e-29; 2; Indels 0; Gaps 0;
Matches 80; Conservative 12; Mismatches 2;

QY 85 IIFKDEENITGADRILMTOQCKDKUNALATISLVMNQPGVRLRVTEGWDEODHHSEBSLHYBG 144
Db 1 IIFKDEENITGADRILMTOQCKDKUNALATISLVMNQPGVRLRVTEGWDEODHHSEBSLHYBG 60
Db 61 RAIDITTSRDRNRYGLLARLAVEGFDWVYGS 94

RESULT 11
T29550
hypothetical protein ZK377.1 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C; Accession: T29550
R; Nhan, M.; Hawkins, J.
A; Description: The sequence of the EMBL data library, February 1997
A; Reference number: Z20639
A; accession: T29550
A; Status: preliminary; translated from GB/EMBL/DDJB

Query Match 6.7%; Score 153.5%; DB 2; Length 1207;
Best Local Similarity 28.6%; Pred. No. 0.00063; 7; Indels 21; Gaps 8;
Matches 56; Conservative 32; Mismatches 87; Indels 21; Gaps 8;

QY 145 RAVDITTSRDRSKYGMRLARLAVEGFDWVYGS 178
Db 1 IIFKDEENITGADRILMTOQCKDKUNALATISLVMNQPGVRLRVTEGWDEODHHSEBSLHYBG 60
Db 61 RAIDITTSRDRNRYGLLARLAVEGFDWVYGS 94

Query Match 6.7%; Score 153.5%; DB 2; Length 1207;
Best Local Similarity 28.6%; Pred. No. 0.00063; 7; Indels 21; Gaps 8;
Matches 56; Conservative 32; Mismatches 87; Indels 21; Gaps 8;

QY 185 SYKAKENSAVAKSGG---CPFGSATVHLEQGGTKLVKDLRPGDRRLADDGGRLLSDF 239
Db 146 RAVDITTSRDRSKYGMRLARLAVEGFDWVYGS 178
Db 1 IIFKDEENITGADRILMTOQCKDKUNALATISLVMNQPGVRLRVTEGWDEODHHSEBSLHYBG 60
Db 61 RAIDITTSRDRNRYGLLARLAVEGFDWVYGS 94

Query Match 6.7%; Score 153.5%; DB 2; Length 1207;
Best Local Similarity 28.6%; Pred. No. 0.00063; 7; Indels 21; Gaps 8;
Matches 56; Conservative 32; Mismatches 87; Indels 21; Gaps 8;

QY 291 FASMRPGVRYVVAERSDRLIPPAVHSVTREEEAGAYAPLTHGTILINRVLASCY 350
Db 1001 EMFTIREPRTIRTNVWVLYIKSGR-KLSLTGRHLIPLVAECQSVEQTMMRDGDIVAMRESK 1059
Db 1060 YAERKAKRKGCVLSIDESG---EVIADETIVRG-RMTNVGIVYSPMTVEGSLIVDGLVLLSCF 1115

QY 351 AVIERSWAHRAFAF 366

Db 1116 SHLESHS-AHKLIEFD 1130

RESULT 13

T24045 hypothetical protein R08B4.1 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
R;White, S.
A;Reference number: Z19834
A;Accession: T24045
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1226 <WIL>
A;Cross-references: EMBL:Z68008; PIDN:CAA92000.1; GSPDB:GN00028; CESP:R08B4.1
A;Experimental source: clone R08B4
C;Genetics:
A;Gene: CESP:R08B4.1
A;Map position: X
A;Introns: 53/2; 113/1; 152/3; 204/3; 272/1; 354/1; 389/3; 714/3; 839/3; 879/1; 960/3; 1

Query Match 6.5%; Score 148; DB 2; Length 1226;
Matches 51; Conservative 39; Mismatches 66; Indels 34; Gaps 9;

Qy 190 NSVAAKSGGCFPGSATVHLQGGTKLVKDLRPGSRVLAADDQGRLLYSSFLTRDDEGA 249
Db 1012 SALVATAGCFSLDTWV-TPTGKRMQDIDGVLTADLE-KTYFTITLWHRPEK 1069

Qy 250 KKVIVVIEPLEPRERLLTA AHLF-----VAPHNSGPPGPSALAFASRV 296
Db 1070 VQEFLTMT-EYGMTRITSRHFMWNKCGKSVPQYIKMLPHD-----EAFTASDLE 1121

Qy 297 PGQRIVVVAERGGGRRLPAVHSVTLREBEEAGAYAPLTAHGTILINRVLASCYAVIEEH 356
Db 1122 VGDEV-WVWVKGKFRQ--QKIEIT-RSYRTGIGYSPLTNNGRILVNMLASCYSEIQQN 1176

Qy 357 S-----WAH 360

Db 1177 TLQTFFWAY 1186

RESULT 14

T27665 hypothetical protein ZK1037.10 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Accession: T27665
R;Basham, V.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z20401
A;Accession: T27665
A;Molecule type: DNA
A;Residues: 1-481 <WIL>
A;Cross-references: EMBL:Z81142; PIDN:CAB03509.1; GSPDB:GN00023; CESP:ZK1037.10
A;Experimental source: clone ZK1037
C;Genetics:
A;Gene: CESP:ZK1037.10
A;Map position: 5
A;Introns: 23/1; 111/3; 177/3; 207/2; 287/1; 381/3; 399/3; 417/1; 476/2; 528/3; 537/2

Query Match 6.1%; Score 140.5; DB 2; Length 629;
Matches 45; Conservative 31; Mismatches 72; Indels 17; Gaps 6;

Qy 199 CPGSATVHLQGGTKLVKDLRPGRVLAADDQGRLLYSSFLTRDDEGA 258
Db 421 CFPADEAVNVYEKVKRDALEVQDWQALHK-ETIVSPKVWLHRDP-EQEAEEVFL 478

Qy 259 LEPRERLLTA AHLF-----VAPHNSGPPGPSALAFASRVPSGQRYVVAERGGDR 311
Db 479 LENSESFTEKHKVFA TDQCNWKNLNDNNIPS-----TGKINIG:CFENNAOPENAS 531

Qy 312 RLPAVHSVTLREBEEAGAYAPLTAHGTILINRVLASCYAVIEEH 356
Db 532 KFQKVOILDIQ-RVYKRTGIVAPMTSLGHLLVNOHTSCHSEIDHH 575

Search completed: February 20, 2003, 10:13:34
Job time: 18.3815 secs

Db 369 ---FLEFSLNGEFTLTERKHLYVTECRONSELKISWEISAGKVNAGDCFVLAQSEA 425
Qy 309 GDRRLPAVHSVTLREBEEAGAYAPLTAHGTILINRVLASCYAVIEEH 356
Db 426 LTKYVLFELID-TKRVKKGIVAPMTSGQHLLVNUKHMCSIVDHH 471

RESULT 15

T19563 hypothetical protein C29F3.2 - *Caenorhabditis elegans*
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T19563; T23034
R;Matthews, L.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z19142
A;Accession: T19563
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-629 <WIL>
A;Cross-references: EMBL:Z81043; PIDN:CAA02804.1; GSPDB:GN00023; CESP:C29F3.2
A;Experimental source: clone C29F3
R;White, S.
submitted to the EMBL Data Library, June 1998
A;Reference number: Z19657
A;Accession: T23034
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-629 <WIL>
A;Cross-references: EMBL:AL023813; PIDN:CAA19424.1; GSPDB:GN00023; CESP:C29F3.2
A;Experimental source: clone H02K04
C;Genetics:
A;Gene: CESP:C29F3.2
A;Map position: 5
A;Introns: 23/1; 111/3; 177/3; 207/2; 287/1; 381/3; 399/3; 417/1; 476/2; 528/3; 537/2

Query Match 6.1%; Score 140.5; DB 2; Length 629;
Matches 45; Conservative 31; Mismatches 72; Indels 17; Gaps 6;

Qy 199 CPGSATVHLQGGTKLVKDLRPGRVLAADDQGRLLYSSFLTRDDEGA 258
Db 421 CFPADEAVNVYEKVKRDALEVQDWQALHK-ETIVSPKVWLHRDP-EQEAEEVFL 478

Qy 259 LEPRERLLTA AHLF-----VAPHNSGPPGPSALAFASRVPSGQRYVVAERGGDR 311
Db 479 LENSESFTEKHKVFA TDQCNWKNLNDNNIPS-----TGKINIG:CFENNAOPENAS 531

Qy 312 RLPAVHSVTLREBEEAGAYAPLTAHGTILINRVLASCYAVIEEH 356
Db 532 KFQKVOILDIQ-RVYKRTGIVAPMTSLGHLLVNOHTSCHSEIDHH 575

Search completed: February 20, 2003, 10:13:34
Job time: 18.3815 secs

Db 369 ---FLEFSLNGEFTLTERKHLYVTECRONSELKISWEISAGKVNAGDCFVLAQSEA 425
Qy 309 GDRRLPAVHSVTLREBEEAGAYAPLTAHGTILINRVLASCYAVIEEH 356
Db 426 LTKYVLFELID-TKRVKKGIVAPMTSGQHLLVNUKHMCSIVDHH 471

Query Match 6.4%; Score 146; DB 2; Length 481;
Best Local Similarity 25.6%; Pred. No. 0.0073;
Matches 43; Conservative 35; Mismatches 70; Indels 20; Gaps 5;

Qy 199 CFPSSATVHLQGGTKLVKDLRPGRVLAADDQGRLLYSSFLTRDDEGA 250
Db 314 CFPHDAVVNEYEKVKRMDLEIGDWVRLDENG-----EDUTLPVVKWLHRDPDEQAE 368

Qy 251 KVFWVIETLEPRERLLTA AHLFVAP--HNDSGGTPGPSALFASRVPGQRYVVAERG 308

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Gencore version 5.1.3

Run on: February 20, 2003, 10:07:32 ; Search time 13.409 Seconds
 (without alignments)
 1352.533 Million cell updates/sec

Title: Perfect score: US-09-827-110A-13

Sequence: 1 MLLIARCFLVILASSLLVNC..... GTWLLDSETMHPLGMKSS 437

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Swissprot,40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2386	99.9	437	1 SHH_MOUSE
2	2200	96.1	437	1 SHH_RAT
3	2065	90.2	462	1 SHH_HUMAN
4	1788	78.1	425	1 SHH_CHICK
5	1542.5	67.4	432	1 SHH_CINPY
6	1525.5	66.6	444	1 SHH_XENLA
7	1527	66.3	418	1 SHH_BRARE
8	1464	64.0	416	1 TWH_BRARE
9	1310	57.2	408	1 DHH_CHICK
10	1271.5	55.5	411	1 IHH_MOUSE
11	1268	55.4	411	1 IHH_XENLA
12	1267	55.4	409	1 IHH_BRARE
13	1228	53.6	412	1 HH_BRARE
14	1219	53.3	395	1 DHL_MOUSE
15	1217	53.2	396	1 DHH_HUMAN
16	1104.5	48.3	398	1 DHX2_XENLA
17	1098.5	48.0	396	1 DHX1_XENLA
18	894	39.1	471	1 HH_DROME
19	855.5	37.4	481	1 HH_DROHY
20	603	26.3	121	1 SHH_RASL
21	600	26.2	121	1 SHH_CARAU
22	600	26.2	121	1 SHH_PUNTE
23	599	26.2	121	1 SHH_RASHE
24	599	26.2	121	1 SHH_RASPA
25	598	26.1	121	1 SHH_TANAL
26	596	26.0	121	1 SHH_AMBH
27	595	26.0	121	1 SHH_DANAE
28	595	26.0	121	1 SHH_DANAK
29	595	26.0	121	1 SHH_DANER
30	595	26.0	121	1 SHH_DANFR
31	595	26.0	121	1 SHH_DANPA
32	595	26.0	121	1 SHH_DANPU
33	595	26.0	121	1 SHH_DEVDE

ALIGNMENTS

RESULT 1

ID SHH_MOUSE STANDARD; PRT; 437 AA.

AC Q02226; DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 10-OCT-2001 (Rel. 40, Last annotation update)

DE Sonic hedgehog protein precursor (SHH) (HHG-1).

OS SHH OR HHG1.

OC Mus musculus (Mouse).

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10990;

[1]

RN SEQUENCE FROM N.A.

RP STRAIN=C57BL/6J; TISSUE=Embryo;

RX MEDLINE=9404334; PubMed=916661;

RA Echeland Y., Epstein D.J., St Jacques B., Shen L., Mohler J., McMahon J.A., McMahon A.P., RT "Sonic hedgehog, a member of a family of putative signaling molecules, is implicated in the regulation of CNS polarity"; RL Cell 75:1417-1430(1993).

RN [2]

RP REVISION TO 122.

RC STRAIN=C57BL/6J;

RA McMahon A.P.; RT Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.

RL [3]

RA SEQURENCE FROM N.A. AND AUTOPROTEOLYTIC CLEAVAGE.

RX MEDLINE=9525697; PubMed=7720571; RA Chang D.T., Lopez A., von Kessler D.P., Chiang C., Simandl B.K., Zhao R., Seidin M.F., Fallon J.F., Beachy P.A.; RT "Products, genetic linkage and limb patterning activity of a murine hedgehog gene"; RL Development 120:3339-3353(1994).

[4]

RA FUNCTION, AND AUTOPROTEOLYTIC CLEAVAGE.

RX MEDLINE=95254654; PubMed=7736596; RA Reinkin H., Porter J.A., Chiang C., Tanabe Y., Chang D.T., Beachy P.A., Jessell T.M.; RT "Floor plate and motor neuron induction by different concentrations of the amino-terminal cleavage product of sonic hedgehog autoproteolysis"; RT Cell 81:445-455(1995). Cell 81:445-455(1995). [5]

X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 34-195.

RX MEDLINE=96059744; Published=77329; RA Hall T.M.T., Porter J.A., Beachy P.A., Leahy D.J.; RT "A Potential catalytic site revealed by the 1.7-A crystal structure of the amino-terminal signalling domain of Sonic hedgehog.";

RT Nature 378:212-216(1995).

RL -1- FUNCTION: BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH, PTC REPRESSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO. ALSO REGULATES ANOTHER TARGET, THE GLI ONCOGENE. INTERCELLULAR SIGNAL ESSENTIAL FOR A

		Best Local Similarity 99.8%; Pred. No. 3e-176; Matches 436; Conservative 1; Mismatches 0; Indels 0; Gaps 0;					
CC	VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT: SIGNAL PRODUCED BY THE NOTOCHORD THAT INDUCES VENTRAL CELL FATE IN THE NEURAL TUBE AND SOMITES, AND THE POLARIZING SIGNAL FOR PATTERNING OF THE ANTERIOR-POSTERIOR AXIS OF THE DEVELOPING LIMB BUD. DISPLAYS BOTH FLOOR PLATE-AND MOTOR NEURON-INDUCING ACTIVITY. THE THRESHOLD CONCENTRATION OF N-PRODUCT REQUIRED FOR MOTOR NEURON INDUCTION IS 5-FOLD LOWER THAN THAT REQUIRED FOR FLOOR PLATE INDUCTION (BY SIMILARITY).	-1 - SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURFACE. THIS IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).	Qy 1 MLLIARCTEVILASSLIVCPGLACPGSGFGGRHRPKLTPLAYQFIPNVAEKTIGAS Db 1 MLLIARCTEVILASSLIVCPGLACPGSGFGGRHRPKLTPLAYQFIPNVAEKTIGAS				
CC	-1 - TISSUE SPECIFICITY: EXPRESSED IN A NUMBER OF EMBRYONIC TISSUES INCLUDING THE NOTOCHORD, VENTRAL NEURAL TUBE, FLOOR PLATE, LUNG BUD, ZONE OF POLARIZING ACTIVITY AND POSTERIOR DISTAL MESENCHYME OF LIMBS. IN THE ADULT, EXPRESSED IN LUNG AND NEURAL RETINA.	-1 - DEVELOPMENTAL STAGE: FIRST DEFECTABLE DURING GASTRULATION.	Qy 121 VLRVTEGEGEDGHISEESEHHYEGRAVDTTSDRDSKYGMLARLAVERAGFDWVYESKA Db 121 VKLRVTEGEGEDGHISEESEHHYEGRAVDTTSDRDSKYGMLARLAVERAGFDWVYESKA				
CC	-1 - INDUCTION: BY RETINOID ACID.	-1 - PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N- TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE C-PRODUCT HAS NO SIGNALING ACTIVITY.	Qy 181 HIRGSVKAENSVAAKSQGCGFPGSATVHQBGGTKLVKDLRPGDVLADDGRLYSDFL Db 181 HIRGSVKAENSVAAKSQGCGFPGSATVHQBGGTKLVKDLRPGDVLADDGRLYSDFL				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - CC European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ CC or send an email to license@isb-sib.ch).	CC	EMBL: X71290; CAA55922.1; -. PDB: 1VHH; 29-JAN-96. MEROPS: C46.002; -. MGD: MG1:98297; Shh. DR InterPro: IPR00320; HH_signal. DR InterPro: IPR001767; Hedgehog_hint. DR InterPro: IPR003586; Hedgehog_hhNC. DR InterPro: IPR002203; Intein. DR InterPro: IPR001657; SonicHH. DR Pfam: PF01079; Hint; 1. DR PRINTS; PR00632; SONICHHog. DR probom; PD003042; HH_signal; 1. DR SMART; SM00305; HintC; 1. DR PROSITE; PS50817; INTEIN_N_TER; 1. DR KW developmental protein; Autocatalytic cleavage; Hydrolase; Protease; KW Signal; Lipoprotein; Palmitate; 3D-structure. FT SIGNAL 1 24 POTENTIAL. FT CHAIN 25 437 SONIC HEDGEHOG PROTEIN. FT CHAIN 25 198 SONIC HEDGEHOG PROTEIN N-PRODUCT. FT SITE 199 437 SONIC HEDGEHOG PROTEIN C-PRODUCT. FT SITE 198 244 244 CLEAVAGE ("AUTO-") (BY SIMILARITY). INVOLVED IN CHOLESTEROL TRANSFER (BY SIMILARITY). INVOLVED IN AUTO-CLEAVAGE (BY SIMILARITY). FT ACT_SITE 271 271 ESSENTIAL FOR AUTO-CLEAVAGE (BY SIMILARITY). INVOLVED IN CHOLESTEROL (BY SIMILARITY). FT BINDING 198 198 POLY-GLY. FT DOMAIN 383 387 LIPID 25 25 PALMITATE (BY SIMILARITY). SEQUENCE 437 AA; 4773 MW; DDBB72R08E7B60EF CRC64; Query Match 99.9%; Score 2266; DB 1; Length 437;	CC	CC	CC	CC
RESULT 2							
SHH_RAT	SHH_RAT	STANDARD:	PRT: 437 AA.				
MRDPS	C46.002	AC: 063673;					
DR	MGD: MG1:98297	DT: 15-JUL-1999 (Rel. 38, created)					
DR	InterPro: IPR00320	DT: 15-JUL-1999 (Rel. 38, last sequence update)					
DR	InterPro: IPR001767	DT: 16-OCT-2001 (Rel. 40, last annotation update)					
DR	InterPro: IPR003586	DE: Sonic hedgehog protein precursor (SHH).					
DR	InterPro: IPR002203	GN: SHH OR VHH-1.					
DR	InterPro: IPR001657	OS: Rattus norvegicus (Rat).					
DR	Pfam: PF01079	OC: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.					
DR	PRINTS; PR00632	OX: NCBI-TaxID=10116;					
DR	probom; PD003042	RN: [1] SEQUENCE FROM N.A.					
DR	SMART; SM00305	RP: STRAIN=Sprague-Dawley; TISSUE=Embryonic floor plate;					
DR	PROSITE; PS50817	RX: MEDLINE=9417035; PubMed=812474;					
DR	KW	RA: Roeilik H., Augsburger A., Heemskerk J., Korzh V., Norlin S., Ruiz I Altaba A., Tanabe Y., Placzek M., Edlund T., Jessell T.M., Dodd J.;					
FT	SIGNAL	RT: "Floor plate and motor neuron induction by vhh-1, a vertebrate homolog of hedgehog expressed by the notochord";					
FT	CHAIN	RT: Cell 76:761-775(1994).					
FT	CHAIN	CC: -1 - FUNCTION: Binds to the Patched (Ptc) receptor, which functions in association with Smoothened (Smo), to activate the transcription of target genes. In the absence of Shh, Ptc represses the constitutive signaling activity of Smo. Also regulates another target, the gli oncogene. Intercellular signal essential for a variety of patterning events during development: signal produced by the notochord that induces ventral cell fate in the neural tube and somites, and the polarizing signal for patterning of the anterior-posterior axis of the developing limb bud. Displays both floor plate and motor neuron-inducing activity. The threshold concentration of N-product required for motor neuron induction is 5-fold lower than that required for floor plate induction (by similarity).					
FT	SITE	CC: -1 - SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE					

CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).

TISSUE SPECIFICITY: EXPRESSED IN THE NODE, NOTOCHORD, FLOOR PLATE, AND POSTERIOR LIMB BUD MESENCHYME.

PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N- TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).

SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.

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RES

181	RHCSVKAENSAKGGCPGATVHLEGGTKLYKDLRFGDRVLAAODGEGLISDPL	240
181	RIHCSVKAENSAKGGCPGATVHLEGGTKLYKDLRFGDRVLAAODGEGLISDPL	240
241	TFLDRDEGAKKVYTYTTELPRERLLTAHHLFVAPRHNDSGPTPGSALFASRVRCQR	300
241	TFLDRDEGAKKVYTYTTELPRERLLTAHHLFVAPRHNDSGPTPGSPLFASRVRCQR	300
301	VYVVAERGGDRRLPAVHSVTREREAGAYAAPTHTGLINRVLASCYAYTEEHWAH	360
301	VYVVAERGGDRRLPAVHSVTREREAGAYAAPTHTGLINRVLASCYAYTEEHWAH	360
361	RAFAFPFLATAALLAALAPARDGGGGSIPAQOSAERVEARGEPTAGTHWYSOLYHGTW	420
361	RAFAFPFLATAALLAALAPARDGGGGSIPAQOSAERVEARGEPTAGTHWYSOLYHGTW	420
421	LLDSBTMHPGMVKSS	437
421	LLDSBTMHPGMVKSS	437

RP VARIANT HPE ARG-31; GLY-117 AND ARG-117.
 RX MEDLINE=97051937; PubMed=8896572;
 RA Roessler E., Belloni E., Gaudenz K., Jay P., Berta P., Scherer S.W.,
 RA Tsui L.-C., Muenke M.;
 RT "Mutations in the human Sonic hedgehog gene cause holoprosencephaly.";
 RL Nat. Genet. 14:357-360(1996).
 RN [7]
 RP VARIANT HPE ARG-31; GLY-117; ARG-117; GLU-224; THR-226 AND THR-383.
 RX MEDLINE=9027056; PubMed=9302262;
 RA Roessler E., Belloni E., Gaudenz K., Vargas F., Scherer S.W.,
 RT "Mutations in the C-terminal domain of Sonic hedgehog cause
 holoprosencephaly.";
 RL Mol. Genet. 6:1847-1853(1997).
 RN [8]
 RP MEDLINE=9331775; PubMed=10441331;
 RX Oent S., Atti-Batich T., Blayau M., Mathieu M., Aug J.,
 RA Deleuze de A.L., Galli J.Y., Le Marec B., Munich A., David V.,
 RA Vekemans M.;
 RT "Expression of the Sonic hedgehog (SHH) gene during early human
 holoprosencephaly and phenotypic expression of new mutations causing
 RT holoprosencephaly.";
 RL Hum. Mol. Genet. 8:1693-1699(1999).
 RN [9]
 RP VARIANT HPE V-88; K-115; R-236; 263-R-A-269 DEL; D-290; A-424 AND
 L-436.
 RX MEDLINE=20025757; PubMed=10556296;
 RA Ranni L., Ming J.E., Bocian M., Steinhaus K., Bianchi D.W.,
 RA Die-Smulders C., Giannotti A., Imaizumi K., Jones K.L., Campo M.D.,
 RA Martin R.A., Meinecke P., Pierpont M.E.M., Robin N.H., Young I.D.,
 RA Reissler E., Muenke M.;
 RT "The mutational spectrum of the sonic hedgehog gene in
 holoprosencephaly: SHH mutations cause a significant proportion of
 RT autosomal dominant holoprosencephaly.";
 RL Hum. Mol. Genet. 8:2479-2488(1999).
 CC -1- FUNCTION: BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN
 CC ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE TRANSCRIPTION
 CC OF TARGET GENES. IN THE ABSENCE OF SHH, PTC REPRESSES THE
 CC CONSTITUTIVE SIGNALING ACTIVITY OF SMO. ALSO REGULATES ANOTHER
 CC VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT: SIGNAL PRODUCED
 BY THE NOTOCORD THAT INDUCES VENTRAL CELL FATE IN THE NEURAL TUBE
 AND SOMITES, AND THE POLARIZING SIGNAL FOR PATTERNING OF THE
 ANTERIOR-POSTERIOR AXIS OF THE DEVELOPING LIMB BUD. DISPLAYS BOTH
 FLOOR PLATE AND MOTOR NEURON-INDUCING ACTIVITY. THE THRESHOLD
 CONCENTRATION OF N-PRODUCT REQUIRED FOR MOTOR NEURON INDUCTION IS
 5-FOLD LOWER THAN THAT REQUIRED FOR FLOOR PLATE INDUCTION (BY
 SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE
 CC CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE
 CC CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM
 CC TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN FETAL INTESTINE, LIVER, LUNG, AND
 CC KIDNEY. NOT EXPRESSED IN ADULT TISSUES.
 CC -1- PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY
 CC AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN
 CC THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF
 CC A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N-
 CC TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS
 TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION
 CC OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE
 CC ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE
 CC C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).
 CC -1- DISEASE: DEFECTS IN SHH ARE THE CAUSE OF HOLOPROSENCEPHALY (HPE).
 CC HPE IS A CLINICALLY VARIABLE AND GENETICALLY HETEROGENEOUS
 CC MALFORMATION IN WHICH THE DEVELOPING FOREBRAIN FAILS TO CORRECTLY
 CC SEPARATE INTO RIGHT AND LEFT HEMISPHERES. IN THE MOST SEVERE FORM
 CC (ALOBAR HPE), THERE IS NO INTERHEMISPERMIC FISSURE, A SINGLE BRAIN
 CC VENTRICLE IS PRESENT. HPE IS ASSOCIATED WITH SEVERAL DISTINCT
 CC FACIES AND PHENOTYPIC VARIABILITY. IN THE MOST EXTREME CASES,
 CC ANOPHTHALMIA OR CYCLOPSA IS EVIDENT ALONG WITH A CONGENITAL
 CC ABSENCE OF THE MATURE NOSE. THE LESS SEVERE FORM FEATURES FACIAL
 CC

CC DYSMORPHIA CHARACTERIZED BY OCULAR HYPERTELORISM, DEFECTS OF THE
 CC UPPER LIP AND/OR NOSE, AND ABSENCE OF THE OLFACTORY NERVES OR
 CC CORPUS CALLOSUM. THE MAJORITY OF HPE CASES ARE APPARENTLY
 CC SPORADIC, ALTHOUGH CLEAR EXAMPLES OF AUTOSOMAL DOMINANT (AD)
 CC INHERITANCE HAVE BEEN DESCRIBED. INTERESTINGLY, UP TO 30% OF
 CC OBLIGATE CARRIERS OF HPE GENE IN AD PEDIGREES ARE CLINICALLY
 CC UNAFFECTED.

CC -1- SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.

CC -1- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="http://www.infobiolegen.fr/services/chromcancer/genes/SHHID378.html".

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 CC or send an email to license@isb-sib.ch).

CC DR MMW; L38518; AA62179_1;
 CC DR EMBL; AC002484; RAB67604_1; -.
 CC DR HSSP; 062226; IVHH.
 CC DR MEROPS; C46_002; -.
 CC DR PRODOM; PD003042; HH_signal; 1.
 CC DR SMART; SM00306; HintN; 1.
 CC DR PROSITE; PS50817; INTRIN_N-TER; 1.
 CC KW Developmental protein; Autocatalytic cleavage; Hydrolase; Protease;
 CC KW Signal; Lipoprotein; Palmitate; Disease mutation; Holoprosencephaly.
 FT SIGNAL 1 23
 FT CHAIN 24 462
 FT CHAIN 24 197 SONIC HEDGEHOG PROTEIN N-PRODUCT.
 FT CHAIN 198 462 SONIC HEDGEHOG PROTEIN C-PRODUCT.
 FT SITE 197 198 CLEAVAGE (AUTO-) (BY SIMILARITY).
 FT SITE 243 243 INVOLVED IN CHOLESTEROL TRANSFER (BY
 FT SITE 267 267 SIMILARITY).
 FT ACT_SITE 270 270 INVOLVED IN AUTO-CLEAVAGE (BY
 FT BINDING 197 197 ESSENTIAL FOR AUTO-CLEAVAGE (BY
 FT DOMAIN 407 411 SIMILARITY).
 FT LIPID 24 24 INVOLVED IN CHOLESTEROL TRANSFER (BY
 FT VARIANT 31 31 SIMILARITY).
 FT FTid=VAR_003619
 FT D->V (IN HPE; FAMILIAL).
 FT /FTid=VAR_009163
 FT O->H (IN HPE; SPORADIC).
 FT FTid=VAR_009164
 FT N->K (IN HPE; FAMILIAL).
 FT /FTid=VAR_009165
 FT W->G (IN HPE).
 FT /FTid=VAR_003620
 FT W->R (IN HPE).
 FT FTid=VAR_003621
 FT E->Q (IN HPE; FAMILIAL).
 FT /FTid=VAR_009166
 FT D->N (IN HPE; FAMILIAL).
 FT /FTid=VAR_009167
 FT V->E (IN HPE).
 FT /FTid=VAR_009168

FT	VARIANT	226	226	A -> T (IN HPE; FAMILIAL). /FTID=VAR_009169; S -> R (IN HPE; FAMILIAL).
FT	VARIANT	236	236	/FTID=VAR_009170. MISSING (IN HPE; SPORADIC).
FT	VARIANT	263	269	Qy 2 LILARCLFLVILASSLIVCPGLACGPGNGFGKRRHKKLTPLAYQFIPNVAEKTGAS 90.2%; Score 205; DB 1; Length 462; Best Local Similarity 87.2%; Pred. No 1.9e-158; Matches 403; Conservative 9; Mismatches 24; Indels 26; Gaps 3;
RL				Db 1 MLLARCLFLVILASSLIVCPGLACGPGNGFGKRRHKKLTPLAYQFIPNVAEKTGAS 60 1 MLLARCLFLVILASSLIVCPGLACGPGNGFGKRRHKKLTPLAYQFIPNVAEKTGAS 60
Qy				Qy 62 RYEGKIKTRNSERKELTNPYNNPDIKFKEENTGADRMTQRCIDKLNALAISMNQPGV 61 : : : : : : : : : : : : : 61 RYEGKIKTRNSERKELTNPYNNPDIKFKEENTGADRMTQRCIDKLNALAISMNQPGV 120
Qy				Qy 122 RLRYTEGEGEDGHSEESUYECRAVDITTSDDRSKYGMLARLAVAGFDWYYESRAH 181 121 KLRVTEGMDEDGHSEESUYECRAVDITTSDDRSKYGMLARLAVAGFDWYYESRAH 180
Qy				Qy 182 IHCSVKAENSAVAKSGGCPGSGATVHLBQGGTKLVKDLSPGDVRVLAADDQGRILYSDLT 241 : : : : : : : : : : : : : 241 FLORDGAKKVVFVIEPRELILTAHHLEVAPND-----SGPTPG 286
Db				Db 181 IHCSVKAENSAVAKSGGCPGSGATVHLBQGGTKLVKDLSPGDVRVLAADDQGRILYSDLT 240 : : : : : : : : : : : : 287 PSALFAFSRVRPGORYVVAERGDRRLPAAVVISVTLBEEAAYAPTAHGTLINRTL 346
Qy				Qy 301 PRALFAFSRVRPGORYVVAERGDRRLPAAVVISVTLBEEAAYAPTAHGTLINRTL 360
Qy				Qy 347 ASYAVIIEBHSWAHRAFPLRHALLAALAPRTD-----GGGGSP-AMOSA 395 : : : : : : : : : : Db 361 ASYAVIIEBHSWAHRAFPLRHALLAALAPRTD-----GGGGSP-AMOSA 420
Qy				Qy 396 TERGAEPAGIHWYSQOLYHIGTWLSETMMPRLGMAVKSS 437 : : : : : : : : Db 421 ADPAGAGATAGIHWYSQOLYQIWMLLDEALHPLGMAVKSS 462
RESULT 4				
SHH_CHICK	STANDARD:	PRT;	425 AA.	
ID	SHH_CHICK			
AC	Q91035;			
DT	15-JUL-1999 (Rel. 38, created)			
DT	15-JUL-1999 (Rel. 38, last sequence update)			
DT	16-OCT-2001 (Rel. 40, last annotation update)			
DR	Sonic hedgehog protein precursor (SHH).			
GN	SHH.			
OS	Gallus gallus (Chicken).			
OC	Eutaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauvia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.			
OC	NCBL_TaxID=9031;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Emb bud;			
RX	MEDLINE94094333; PubMed=829518;			
RA	Riddle R.D., Laufer E., Tabin C.;			
RT	"Sonic hedgehog mediates the polarizing activity of the zpa."			
RL	Cell 75:1401-1416(1993).			
[2]				
RP	FUNCTION AND AUTOPROTEOLYTIC CLEAVAGE.			
RX	MEDLINE9525654; PubMed=776596;			
RA	Roelink H., Porter J.A., Chiang C., Tanabe Y., Chang D.T., Beachy P.A., Jessell T.M.;			
RT	*Floor plate and motor neuron induction by different concentrations of the amino-terminal cleavage product of sonic hedgehog autoproteolysis";			
RT	autoprolysis";			
RL	Cell 81:445-455(1995).			
CC	-1- FUNCTION: BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH, PTC REPRESSIONS THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO ALSO REGULATES ANOTHER TARGET, THE GLI ONCOGENE. INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT: SIGNAL PRODUCED BY THE NOTOCHORD THAT INDUCES VENTRAL CELL FATE IN THE NEURAL TUBE AND SOMITES, AND THE POLARIZING SIGNAL FOR PATTERNING OF THE ANTERIOR-POSTERIOR AXIS OF THE DEVELOPING LIMB BUD. DISPLAYS BOTH FLOOR PLATE-AND MOTOR NEURON-INDUCING ACTIVITY. THE THRESHOLD CONCENTRATION OF N-PRODUCT REQUIRED FOR MOTOR NEURON INDUCTION IS 5-FOLD LOWER THAN THAT REQUIRED FOR FLOOR PLATE INDUCTION.			
CC	-1- SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).			
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN THE POSTERIOR LIMB BUD MESENCHYME, THE HENSEN'S NODE, THE NOTOCHORD, AND THE FLOOR PLATE OF THE NEURAL TUBE.			
CC	-1- DEVELOPMENTAL STAGE: FIRST DETECTABLE AT STAGE 17 DURING THE INITIATION OF LIMB BUD FORMATION. FROM THAT POINT ONWARDS, THE EXPRESSION PATTERN EXACTLY MATCHES THE LOCATION OF THE ZONE OF POLARIZING ACTIVITY (ZPA).			
CC	-1- INDUCTION: BY RETINOIC ACID.			
CC	-1- PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N- TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG RANGE SIGNALING, WHEREAS THE C-PRODUCT HAS NO SIGNALING ACTIVITY.			
CC	-1- SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.			
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CC	... DR EMBL: L28099 AAAT2428.1; DR HSSE; 062226; IVRR. DR MEROPS: C46.001; - DR Interpro: IPR000320; HH_signal. DR Interpro: IPR001767; Hedgehog_hint. DR Interpro: IPR003586; Hedgehog_hintCC. DR Interpro: IPR003587; Hedgehog_hintC. DR Interpro: IPR002203; Intein. DR Interpro: IPR001657; SonichH. DR Pfam: PF01079; Hint; 1. DR Pfam: PF01085; HH_signal; 1. DR PRINTS: PR000322; SONICHOG. DR PRODOM: PD000142; HH_signal; 1. DR SMART: SM00305; HintCC; 1. DR SMART: SM00306; HintN; 1. DR PROSITE: PS50817; INTERN_N_TER; 1. KW Developmental protein; Autocatalytic cleavage; Hydrolase; Protease; KW Signal; Lipoprotein; Palmitate. KW SIGNAL 1 POTENTIAL. FT CHAIN 27 425 SONIC HEDGEHOG PROTEIN. FT CHAIN 27 200 SONIC HEDGEHOG PROTEIN N-PRODUCT. FT CHAIN 201 425 SONIC HEDGEHOG PROTEIN C-PRODUCT. FT SITE 200 201 CLEAVAGE (AUTO-) (PROBABLE). FT SITE 246 246 INVOLVED IN CHOLESTEROL TRANSFER (BY SIMILARITY). FT SITE 270 270 INVOLVED IN AUTO-CLEAVAGE (BY SIMILARITY). FT ACT_SITE 273 273 ESSENTIAL FOR AUTO-CLEAVAGE (BY SIMILARITY). FT BINDING 200 200 CHOLESTEROL (BY SIMILARITY).			

FT DOMAIN	390	393	POLY-THR.
FT LIPID	27	27	PALMATE (BY SIMILARITY).
FT SEQUENCE	425 AA;	46474 MW;	DA9627443D4A0173 CRC64;
CC			TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).
CC			- I - INDUCTION: ACTIVATED BY ACTIVIN, BASIC FIBROBLAST GROWTH FACTOR
CC			(BFGF) AND FORK HEAD
CC			- II - PFM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N- TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).
CC			- III - SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.
CC			-----
QY 2 LLLLARCFVLILLASSILVCPGLACCPGRRGKRRPKKLTPLAYQFIPNVAEKTIGASG 61			This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation of the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
Db 4 MLLTRLILVGFCIALLVSGLTCGPGRGKRRPKKLTPLAYQFIPNVAEKTIGASG 63			-----
QY 62 RYEKTRNNSERKELTNPNNPDIKFDEENTGADRMLTQRCKOKNLNALAISVNQWPGV 121			DR HSSP; D63339; BAA09657.1; -.
Db 64 RYEKTRNNSERKELTNPNNPDIKFDEENTGADRMLTQRCKOKNLNALAISVNQWPGV 123			DR MEROPS; CA6_002; -.
QY 122 RLRLVTEGWDDEGHHSBESLHVEGRAVDITTSDRDRSKYGMARLAVAEQGDWVYESKAH 181			DR InterPro; IPR00320; HH.signal.
Db 182 IHCSYKAENSAVAKSGGCCPGSATVHLEGGTKVLKDPLSPGDRVLAADQGRLLYSDFLT 241			DR InterPro; IPR001767; Hedgehog_hint.
Db 184 IHCSYKAENSAVAKSGGCCPGSATVHLEGGTKVLKDPLSPGDRVLAADQGRLLYSDFLT 243			DR InterPro; IPR003586; Hedgehog_hintC.
QY 242 FLDRDGGAKKVYVETLEPERRLLTAAMLLFWAP-HNDS--GPTPGPSALASRVRP 297			DR InterPro; IPR002203; Intein.
Db 244 FLDRDGGAKKVYVETLEPERRLLTAAMLLFWAP-HNDS--GPTPGPSALASRVRP 302			DR InterPro; IPR001657; SonICHH.
QY 298 GORVVVVAERGGDRRLPLPAVHSVLRREEAGAVAPLTAGHTLNLNRVIALSCVYIEEH 357			DR Pfam; PF01079; Hint; 1.
Db 303 GORVVVLGE--GGQQLPASVHSVSLREEAAGVAPLTOGTTLNLNRVIALSCVYIEEH 360			DR Pfam; PF01082; SonICHOG.
Qy 358 WAHRARAPFLAHALLAALAPARTDGGGSIPQAQSATERGARGPTAGTHWYSONLYHI 417			DR ProDom; PD003042; HH_signal; 1.
Db 361 WAHRARAPFLAHALLAALAPARTDGGGSIPQAQSATERGARGPTAGTHWYSONLYHI 405			DR SMART; SM00306; HinC; 1.
Qy 418 GTWLIDSETMPHPLGAVKSS 437			DR SMART; SM00306; HinN; 1.
Db 406 GSWVLDGDLAHLPLGAVPAS 425			DR PSS0017; INFEIN_N-TER; 1.
RESULT 5			DR Developmental_protein; Autocatalytic cleavage; Hydrolase; Protease; Signal; Lipoprotein; Palmitate.
SHH_CNPY STANDARD; PRT: 432 AA.			FT SIGNAL 1 26 POTENTIAL.
ID SHH_CNPY			FT CHAIN 27 432 SONIC_HEDGEHOG_PROTEIN_N-PRODUCT.
AC 090385;			FT CHAIN 201 432 SONIC_HEDGEHOG_PROTEIN_C-PRODUCT.
DT 15-JUL-1999 (Rel. 38, Created)			FT SITE 200 201 CLEAVAGE (AUTO-) (BY SIMILARITY).
DT 15-JUL-1999 (Rel. 38, Last sequence update)			FT SITE 268 268 INVOLVED IN AUTO-CLEAVAGE (BY SIMILARITY).
DT 16-OCT-2001 (Rel. 40, Last annotation update)			DE Sonic hedgehog protein precursor (SHH).
DE Sonic hedgehog protein precursor (SHH).			FT ACT_SITE 271 271 ESSENTIAL FOR AUTO-CLEAVAGE (BY SIMILARITY).
SHH			FT BINDING 200 200 CHOLESTEROL (BY SIMILARITY).
CNops Pyrrhogaster (Japanese common newt).			FT LIPID 27 27 PALMATE (BY SIMILARITY).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			FT SEQUENCE 432 AA; 47847 MW; B455C7E46CB85A8 CRC64;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.			QY Query Match 67.4%; Score 1542.5; DB 1; Length 432; Best Local Similarity 70.2%; Pred. No. 1.7e-16; Indels 27; Gaps 7; Matches 313; Conservative 32; Mismatches 74; Indels 27; Gaps 7;
OX NCBI_TaxID=8330;			Db 4 MLLRVLILVGFCIALLVSGLTCGPGRGKRRPKKLTPLAYQFIPNVAEKTIGASG 63
RN [1] SEQUENCE FROM N.A.			QY 62 RYEKTRNNSERKELTNPNNPDIKFDEENTGADRMLTQRCKOKNLNALAISVNQWPGV 121
RC TISSUE=Embryo;			Db 64 RYEKTRNNSERKELTNPNNPDIKFDEENTGADRMLTQRCKOKNLNALAISVNQWPGV 123
RX MEDLINE=9613634; PubMed=8573168;			QY 122 RLRLVTEGWDDEGHHSBESLHVEGRAVDITTSDRDRSKYGMARLAVAEQGDWVYESKAH 181
RA Takabatake T., Takemoto T.C., Inoue K., Ogawa M., Takeshima K.;			Db 124 KLRLVTEGWDDEGHHSBESLHVEGRAVDITTSDRDRSKYGMARLAVAEQGDWVYESKAH 183
RT "Activation of two Cnops genes, fork head and sonic hedgehog, in animal cap explants.",			CC 182 IHCSYKAENSAVAKSGGCCPGSATVHLEGGTKVLKDPLSPGDRVLAADQGRLLYSDFLT 241
RT Biophys. Res. Commun. 218:395-401(1996).			CC 184 IHCSYKAENSAVAKSGGCCPGSATVALEQVRIKPVKDLRPGDRVLAADQGRLLYSDFLT 243
RT - FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT AND METAMORPHOSIS. INVOLVED IN LIMB FORMATION, PATTERNING OF THE CENTRAL NERVOUS SYSTEM AND VENTRAL SOMITE DIFFERENTIATION. INDUCES ECTOIC CEMENT GLAND FORMATION IN EMBRYOS. BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SMO, PTC REPRESSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO (BY SIMILARITY).			
CC - SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE			

Qy 242 FLDRDEGAKKVVFVIELEPRELLTAHLIEVA--PHNDSG-----PTPGPSALF 291
 : : : | : ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 244 FMDKEETVVKYFVIET--SREVRLPAHLFLFGQAIPIGNQNSGGDERSVFGAFMSMF 301
 Qy 292 ASIVRPGORVYVVAERGDDRILPAAVHSVTREEEAGAYAPITLAHGTLINNVASCYA 351
 ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 302 ASSVRAGHRVLYDREG--RGLREATVERVYL-EATGAYAIFTANGTVWIDVLASCYA 358
 Qy 352 VTEKSHWAHRAFYPPFLRHALLALAPARTDGGSSTPAQASATEARGAEPTAGIHWYS 411
 ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 359 VTEKSHWAHRAFYPPFLRHALLALAPARTDGGSSTPAQASATEARGAEPTAGIHWYS 406
 Qy 412 QLYHIGWLDSSETMHLGMAYKSS 437
 :: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 407 EILYRIGTWWLQEDTIPHLGMAAKSS 432

RESULT 6

SHH_XENLA STANDARD; PRT: 444 AA.

ID SHH_XENLA STANDARD; PRT: 444 AA.

AC Q93000; 091894; [1]

DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Sonic hedgehog protein precursor (x-SHH) (VHH-1).

GN SHH.

OS Xenopus laevis (African clawed frog).

OC Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Xenopoda; Xenophidae; Xenopidae; Pipidae;

OC NCBI_TAXID=8355;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Intestine;

RX MEDLINE=9535169; PubMed=7630736;

RT Stolow M.A., Shi Y.-B.;
 RT "Xenopus sonic hedgehog as a potential morphogen during embryogenesis and thyroid hormone-dependent metamorphosis.";
 RL Nucleic Acids Res. 23:2555-2562(1995).
 RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Embryo;

RX MEDLINE=95401852; PubMed=7671800;

RA Ecker S.C., McGrew L.L., Lal C.J., Lee J.J., von Kessler D.P., Moon R.T., Beachy P.A.;

RT "Distinct expression and shared activities of members of the hedgehog gene family of *Xenopus laevis*".
 Development 121:2337-2347(1995).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Notochord;

RX MEDLINE=9608338; PubMed=7551564;

RA Ruiz I, Altaba A., Jessell T.M., Roelink H.;
 RT "Restrictions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";
 RL Mol. Cell. Neurosci. 6:106-121(1995).

CC -1- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT AND METAMORPHOSIS. INVOLVED IN LIMB FORMATION, PATTERNING OF THE CENTRAL NERVOUS SYSTEM AND VENTRAL SOMITE DIFFERENTIATION. INDUCES ECTOPIC CEMENT GLAND FORMATION IN EMBRYOS. BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH, PTC REPRESSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).

CC -1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN NOTOCHORD AND NEURAL FLOOR PLATE DURING EMBRYOGENESIS. IN TADPOLE, HIGH EXPRESSION IS OBSERVED IN PANCREAS/STOMACH, MODERATE EXPRESSION IN TAIL, AND LOW EXPRESSION IN INTESTINE, BRAIN, AND HIND LIMB.

CC -1- EXPRESSION IN INTESTINE, BRAIN, AND HIND LIMB.
 CC FIRST PEAK OF EXPRESSION AROUND TADPOLE HATCHING (STAGES 33-40).
 CC HIGH EXPRESSION OBSERVED IN INTESTINE AT THE CLIMAX OF MORPHOGENESIS (STAGES 60-62) WHEN INTESTINE EPITHELIAL UNDERGOES INDUCTION: BY THYROID HORMONE.

CC -1- PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N-Terminal fragment (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.

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CC DR EMBL; L39213; AAC42227.1; -

CC DR EMBL; U26314; AAA85162.1; -

CC DR EMBL; L35248; AAA49981.1; -

CC DR HSSP; 082226; IVRH.

CC DR MEROPS; C46.002; -

CC DR InterPro; IPR000330; HH_signal.

CC DR InterPro; IPR01167; Hedgehog_hint.

CC DR InterPro; IPR03596; Hedgehog_hintC.

CC DR InterPro; IPR03597; Hedgehog_hintN.

CC DR InterPro; IPR02203; Intein.

CC DR InterPro; IPR01657; Sonichh.

CC DR Pfam; PF01079; Hint_1.

CC DR Pfam; PF01082; HH_signal_1.

CC DR PRINTS; PR00332; SONICHHOG.

CC DR PRODOM; PD00302; HH_signal_1.

CC DR SMART; SM00305; HintC; 1.

CC DR SMART; SM00306; HintN; 1.

CC DR PROSITE; PS50817; INTEIN_N_TER; 1.

CC KW Developmental protein; Auto-catalytic cleavage; Hydrolase; Protease; Signal; Lipoprotein; Palmitate; Repeat.

FT SIGNAL 1 24 POTENTIAL.

FT CHAIN 25 444 SONIC HEDGEHOG PROTEIN.

FT CHAIN 25 198 SONIC HEDGEHOG PROTEIN N-PRODUCT.

FT CHAIN 199 444 SONIC HEDGEHOG PROTEIN C-PRODUCT.

FT SITE 198 199 CLEAVAGE (AUTO-) (BY SIMILARITY).

FT SITE 266 266 INVOLVED IN AUTO-CLEAVAGE (BY SIMILARITY).

FT ACT_SITE 269 269 ESSENTIAL FOR AUTO-CLEAVAGE (BY SIMILARITY).

FT DOMAIN 386 409 3 X 8 AA TANDEM REPEATS OF Q-V-D-L-Q-S-H-

FT REPEAT 386 393 1.

FT REPEAT 394 401 2.

FT REPEAT 403 409 3.

FT BINDING 198 198 CHOLESTEROL (BY SIMILARITY).

FT LIPID 25 25 PALMITATE (BY SIMILARITY).

FT CONFLICT 5 9 TQSL-> NSNLW (IN REF. 3).

FT CONFLICT 302 319 DPKNITKAVKVERDLE-> ESDQHDLEGGRKWRRLIR (IN REF. 3).

FT CONFLICT 432 432 N > S (IN REF. 3).

FT SEQUENCE 444 AA; 49453 MR; 73B4E4932FA2EFF2 CRC64;

Query Match 66.6%; Score 1535.5; DB 1; Length 444;
 Best Local Similarity 67.4%; Pred. No. 4e-115;
 Matches 304; Conservative 38; Mismatches 88; Indels 21; Gaps 6;

OY 1 MLLLARCFLVILLASSILVCPGLACGPGRGFRGKRRRHPKKLPLAYKOFIPVAKTLGAS 60

DR PRODOM: PD003042; HH_signal; 1.
 DR SMART; SM0305; HintC; 1.
 DR SMRT; SM0306; HintN; 1.
 DR PROSITE: PS50817; INTEIN_N_TER; 1.
 KW Developmental Protein; Autocatalytic cleavage; Hydrolase; Protease;
 KW Signal; Lipoprotein; Palmitate.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 418 SONIC_HEDGEHOG PROTEIN.
 FT CHAIN 24 197 SONIC_HEDGEHOG PROTEIN_N-PRODUCT.
 FT CHAIN 198 418 SONIC_HEDGEHOG PROTEIN_C-PRODUCT.
 FT CLEAVAGE (AUTO-).
 FT SITE 197 198 CLEAVAGE (AUTO-).
 FT SITE 243 243 INVOLVED IN CHOLESTEROL TRANSFER (BY
 FT INVOLVED IN CHOLESTEROL (BY SIMILARITY).
 FT SITE 267 267 INVOLVED IN AUTO-CLEAVAGE (BY
 FT ACT_SITE 270 270 INVOLVED IN SIMILARITY).
 FT BINDING 197 197 INVOLVED IN SIMILARITY).
 FT LIPID 24 24 PALMITATE (BY SIMILARITY).
 SQ SEQUENCE 418 AA; 46402 MW; CR000AFFD2F5795 CRC64;

Query Match 66.3%; Score 1517; DB 1; Length 418;
Best Local Similarity 67.7%; Pred. No. 1.8e-14; Mismatches 75; Indels 18; Gaps 3;

Qy 4 LLARCFVYLASSILVCPOLACCGPGCGKRRPKLTPLAYQFIPVNAEKLIGASRY 63
 ||| | | | : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 3 LLTRVLVLLSLLTSLUVSGLACCGPGCGYGRRRPKLTPLAYQFIPVNAEKLIGASRY 62

Qy 64 EGKTRNNSERKFELTPNNPNDITFKDEENTGADRLLMTORCKDKLNLALISVMNQPGVRL 123
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 63 EGKTRNNSERKFELTPNNPNDITFKDEENTGADRLLMTORCKDKLNLALISVMNQPGVRL 122
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 124 RVTRGWDDEGHHSIISLVEBESLAVEGRAVDTTSDRDKSKYMLARLAVEAGRDWVYIESKAH 183
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 123 RVEBGWDEGHHSIISLVEBESLHVGEGRADITTSDRDKSKYIGTLSLRAVEAGDWVYIESKAH 182
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Qy 184 CSYKAENSAVAKSGCGFCGSATVHLEQGKTKLDRPGDRVIAADDQGRLLYSDFLTF 243
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 183 CSYKAENSAVAKSGCGFCGSALVSIQDGQKAYRDLNPQGDKVLAADSAGNLVPSDFMFT 242

Qy 244 DRDBGAKKVVIVTLEPERLILTAHLFVAPHNDSCPTGPQPSALEFASRVPQQRIV 303
 ||| ||| : ||| ||| ||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 243 DRDSSTTRPVYVFLTQEPVKITLTAAHFLV-DNSDELDHTAAVASSVRAQOKMV 301
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Qy 304 VAERKGDRLLPAVAVHSLTREBEGAYAPLTHGHTILNRVASCYAVIEEWSWAHRF 363
 ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 302 VDDSGQLKSVIVQRIFT---EDEGSGSAPVTGHTIVDRIEASCYAVIEDGLAHAF 357
 ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Qy 364 APFRLLAHALLAALAPARTGGGGSIPAQSATEARGAEPTAGIHWMSOLLYHIGTWILD 423
 ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 358 APARLYYYVVSFFLP-----ONSSRSNATLQOEGVHWSRLYQMGWTILD 404

Qy 424 SEMPHPLGHAVKSS 437
 ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 405 SMUHLPLGMVSNS 418

RESULT 8
TWHH_BRARE STANDARD; PRT; 416 AA.

ID 09019; Rel. 38; created)
 DT 15-JUL-1999 (Rel. 38; last sequence update)
 DT 16-OCT-2001 (Rel. 40; last annotation update)
 DE T199y-winkle hedgehog protein precursor (TWHH).

GN TWHH.
 OS Brachydanio rerio (zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophys; Cypriniformes;
 OC Cyprinidae; Danio.
 RN NCBI_TAXID=7955;

RQ SEQUENCE FROM N.A., AND AUTOPROPOLYTIC CLEAVAGE.
 RC TISSUE-Embryo;
 RX MEDLINE-96014264; PubMed=7583153;
 RA Ekier S.C., Ungar A.R., Greenstein P., von Kessler D.P.,
 RA Porter J.A., Moon R.T., Beachy P.A.;
 RT "Patterning activities of vertebrate hedgehog proteins in the
 developing eye and brain.";
 RL Curt. Biol. 5:944-955(1995).
 CC -I- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF
 PATTERNING EVENTS DURING DEVELOPMENT. INVOLVED IN DORSO-VENTRAL
 PATTERNING OF THE BRAIN AND IN EARLY PATTERNING OF THE DEVELOPING
 EYES.
 CC -I- SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE
 CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE
 CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM
 TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).
 CC -I- TISSUE SPECIFICITY: EXPRESSED IN THE VENTRAL MIDLINE OF THE NEURAL
 TUBE AND BRAIN. IN THE DEVELOPING BRAIN, EXPRESSION OCCURS IN
 DOMAINS THAT INCLUDE A DISCRETE REGION IN THE FLOOR OF THE
 Diencephalon. NOT DETECTED IN THE NOTOCHORD OR DEVELOPING FIN BUD.
 CC -I- PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROPOLYTIC ACTIVITY
 AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN
 THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF
 A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NNEWLY GENERATED N-
 TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS
 TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION
 OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE
 ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE
 C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).
 CC -I- SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.
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 or send an email to license@isb-sib.ch).
 CC -----
 DR HSPP; Q6226; VHHL.
 DR MEROPS; C46_001; --.
 DR ZFPN; ZDP-GENE-980526-41; twhh.
 DR InterPro; IPR000320; HH_signal.
 DR InterPro; IPR01167; Hedgehog_hintC.
 DR InterPro; IPR03586; Hedgehog_hintC.
 DR InterPro; IPR03587; Hedgehog_hintN.
 DR InterPro; IPR01657; Sonichh.
 DR Pfam; PRO1079; Hint; 1.
 DR Pfam; PRO1085; HH_signal; 1.
 DR PRINTS; PR00532; SONICHOG.
 DR PRODOM; PD003042; HH_signal; 1.
 DR SMART; SM0305; HintC; 1.
 DR SMART; SM0306; HintN; 1.
 KW Developmental Protein; Autocatalytic cleavage; Hydrolase; Protease;
 KW Signal; Lipoprotein; Palmitate.
 FT SIGNAL 1 26 POTENTIAL.
 FT CHAIN 27 416 TIGY-WINKLE_HEDGEHOG PROTEIN_N-PRODUCT.
 FT CHAIN 200 416 TIGY-WINKLE_HEDGEHOG PROTEIN_C-PRODUCT.
 FT SITE 270 270 INVOLVED IN AUTO-CLEAVAGE (BY
 FT ACT_SITE 273 273 ESSENTIAL FOR AUTO-CLEAVAGE (BY
 FT BINDING 200 200 SIMILARITY).
 FT LIPID 27 27 CHOLESTEROL (BY SIMILARITY).
 SQ SEQUENCE 416 AA; 46576 MW; 61BC2218305CEFE59 CRC64;

Query Match 64.0%; Score 1464; DB 1; Length 416;
Best Local Similarity 66.7%; Pred. No. 3.2e-10; Mismatches 64; Indels 36; Gaps 6;

Matches 287; Conservative 43; Mismatches 64; Indels 36; Gaps 6;

[1]

QY	359 AHRKFAPFLAHLAALAPARTDGGGGSIKPAQSATEARGAEPGAGIHWYSQOLYLNG 418	CC	use by non-profit institutions as long as its content is in no way
-	: : : : : : : : : : : : : : : : : : : :	CC	modified and this statement is not removed. Usage by and for commercial
Db	AQMWFWRFLRYLHSIL-----GG--PGVQG-----DGHWYSGLLYRLG 389	CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/)
Oy	419 TWLDSETMHPIC 431	CC	or send an email to license@isb-sib.ch).
Db	390 RMLLPDPDFHPLG 402	DR	EMBL; AB018076; BAA33523.2; JOINED.
		DR	EMBL; AB010022; BAA33523.2; JOINED.
		DR	EMBL; AB01075; BAA33523.2; JOINED.
		DR	EMBL; L38517; AAG62178.1; .
		DR	HSSP; 062226; IVHH.
		DR	MEROPS; C4.003; .
		DR	Genew; HGNC; 9556; IHH.
		DR	MIM; 600726; .
		DR	InterPro; IPR000320; HH_Signal.
		DR	InterPro; IPR01767; Hedgehog_hint.
		DR	InterPro; IPR03586; Hedgehog_hintC.
		DR	InterPro; IPR00507; Hedgehog_hintN.
		DR	InterPro; IPR02203; Intein.
		DR	Pfam; PF01079; Hint; 1.
		DR	Pfam; PF01085; Hs_Signal; 1.
		DR	SMART; SM00305; HintC; 1.
		DR	SMART; SM00306; HintN; 1.
		DR	PROSITE; FS50817; INTEIN_N-TER; 1.
		KW	Developmental protein; Autocatalytic cleavage; Hydrolase; Protease;
		FT	SIGNAL; Lipoprotein; Palmitate.
		FT	POTENTIAL.
		FT	INDIAN HEDGEHOG PROTEIN.
		FT	INDIAN HEDGEHOG PROTEIN N-PRODUCT.
		FT	INDIAN HEDGEHOG PROTEIN C-PRODUCT.
		FT	CLEAVAGE (AUTO-) (BY SIMILARITY).
		FT	INVOLVED IN CHOLESTEROL TRANSFER (BY SIMILARITY).
		FT	INVOLVED IN AUTO-CLEAVAGE (BY SIMILARITY).
		FT	ESSENTIAL FOR AUTO-CLEAVAGE (BY SIMILARITY).
		FT	CHOLESTEROL (BY SIMILARITY).
		FT	PALMITATE (BY SIMILARITY).
		FT	D -> R (IN REF. 2).
		FT	L -> F (IN REF. 2).
		FT	CONFLICT
		FT	349 309 A -> V (IN REF. 2).
		SO	SEQUENCE
		SO	411 AA; 45188 MW; 14C90436C344DEA CRC64;
		Query Match	55.5%; Score 1271.5; DB 1; Length 411;
		Best Local Similarity	60.6%; Pred. No. 9.4e-95;
		Matches	260; Conservative 40; Mismatches 92; Indels 37; Gaps 8;
		Db	13 CLVILL--LLVPAAWCGCPGRVGNSRRPKLTPLAYKOPTNAYKTGASGRVEG 65
		Qy	8 CFLVILASSLLVCPGL-ACGGPGAGFG-KRRHPPKLTPLAYKOPTNAYKTGASGRVEG 65
		Db	70 KIARRSERKELTNYNPNDIFKDEENTGADRMTORCKDKLNALATSWMNQPGVLRV 125
		Qy	66 KITVNRSEERKELTNYNPNDIFKDEENTGADRMTORCKDKLNALATSWMNQPGVLRV 125
		Db	70 KIARRSERKELTNYNPNDIFKDEENTGADRMTORCKDKLNALATSWMNQPGVLRV 129
		Qy	126 TEGMDEDGHSESLHYFGRAVLITSDRDSKYGMLARRLAVEGFDWVYYESKAHCS 185
		Db	130 TEGMDEDGHSESLHYFGRAVLITSDRDSKYGMLARRLAVEGFDWVYYESKAHCS 189
		Qy	186 VKAENSAVAKSGGGPPGSGATVHLEQGGTKLVKVLDRPGDRVLAADDQGRLLSYSDLFTFLDR 245
		Db	190 VKSBSHAASKTGCFCPAGAQVRLESQARVALSAVRGDRVLAGEDGSDPTFSVLLIDR 249
		Qy	246 DEGAKKVVFVIELEPRERLPLPAHLFVAPHINDSGPTPGPSALFASRVPGCVYWA 305
		Db	250 EPHRLAQVIEQDPPRPLPAHLFETA-DNHTEPARFRATFASHVQEQVLYAG 308
		Qy	306 ERGCDRRLPAAVHSVTLREEAGAYAPLTAHGTLTILNRYASCYVIEEHSHWARAFP 365
		Db	309 APG---LQPARYAAVS-THALGAYAQLPKTGHSTLQVVEDWVASCFAAVADHHLAQAFWP 363
		Qy	365 FRLAHALLALAPARTDGGGGSIKPAQSATEARGA_EPTAGIHWYSQOLYHGTWILDS 424

RESULTS 10

IHH_HUMAN STANDARD: PRT: 411 AA.

ID IHH_HUMAN

AC Q1623; O43322; DR 15-JUL-1999 (Rel. 38, created)

DT 15-JUN-2002 (Rel. 41, last sequence update)

DE Indian hedgehog protein precursor (IHH) (HIG-2).

GN IHH.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homino.

OX NCBI_TAXID=9606;

RN SEQUENCE FROM N.A.

RA Tate G., Kishimoto K., Mitsuya T.;

RT "Expression of Sonic hedgehog and its receptor Patched/Smoothered in human cancer cell lines and embryonic organs.",

RL J. Biochem. Mol. Biol. Biophys. 4:27-34(2000).

RP SEQUENCE OF 100-411 FROM N.A.

RC TISSUE=Petal lung;

RX MEDLINE=96070431; PubMed=7509746;

RA Marigo V., Roberts D.J., Lee S.M.K., Tsukurov O., Levi T.,

RA Gabier J.M., Epstein D.J., Gilbert D.J., Copeland N.G., Seidman C.E., Jenkins N.A., Seidman J.G., McMahon A.P., Tabin C.,

RT "Cloning, expression, and chromosomal location of SHH and IHH: two human homologues of the Drosophila segment polarity gene hedgehog.",

RL Genomics 28:44-51(1995).

RN [3]

RP SEQUENCE OF 124-172 FROM N.A.

RX MEDLINE=9523997; PubMed=7720571;

RA Chang D.T., Lopez A., von Kessler D.P., Chiang C., Simandl B.K., Zhao R., Seldin M.F., Fallon J.F., Beachy P.A.;

RT Products genetic linkage and limb patterning activity of a murine hedgehog gene.",

RL Development 120:3339-3353(1994).

-1- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT. BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IMPLICATED IN ENDCHONDRAL OSSIFICATION: MAY REGULATE THE BALANCE BETWEEN GROWTH AND OSSIFICATION OF THE DEVELOPING BONES. INDUCES THE EXPRESSION OF PARATHYROID HORMONE-RELATED PROTEIN (PTHrP) (BY SIMILARITY).

-1- SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).

-1- TISSUE SPECIFICITY: EXPRESSED IN EMBRYONIC LUNG, AND IN ADULT KIDNEY AND LIVER.

-1- PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N-TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).

-1- SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.

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	364	LRLHSL--	DB	--AWGSWTPGEGVHWYPOOLYLGRLLIEE 398
QY	425	ETMHPGLMA 433		
Db	399	GSRPHPLMS 407		
RESULT 11				
INH_MOUSE				
ID INH_MOUSE STANDARD; PRT; 411 AA.				
AC F97812; 061724; PRT; 411 AA.				
DT 15-JUL-1999 (Rel. 38, Created)				
DT 15-JUL-1999 (Rel. 38, Last sequence update)				
DT 16-OCT-2001 (Rel. 40, Last annotation update)				
DE Indian hedgehog protein precursor (IHH) (HHG-2).				
GN INH.				
OS Mus musculus (Mouse).				
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;				
OC Mammalia; Eutheria; Rodentia; Sciuropnathi; Muridae; Murinae; Mus.				
OX NCBI_TAXID=10090;				
RN [1] SEQUENCE FROM N.A., AND AUTOPROTEOLYTIC CLEAVAGE.				
RC STRAIN=CD-1; TISSUE=Kidney;				
RX MEDLINE-97256802; PubMed=9079674;				
RA Valentini R.P., Brookhiser W.T., Park J., Yang T., Briggs J.,				
RA Dressler G., Holman L.B.,				
RT "Post-translational processing and renal expression of mouse Indian hedgehog.";				
RL J. Biol. Chem. 272:8466-8473(1997).				
RN [2] SEQUENCE OF 76-411 FROM N.A.				
RC STRAIN=NC57BL/6J; TISSUE=Embryo;				
RX MEDLINE-94030434; PubMed=7316661;				
RA Schaefer D.J., St Jacques B., Shen L., Mohler J.,				
RA McMahon J.A., McMahon A.P.;				
RT "Sonic hedgehog, a member of a family of putative signaling molecules, is implicated in the regulation of CNS polarity.";				
RL Cell 75:1417-1430(1993).				
RN [3] REVISIONS.				
RC STRAIN=NC57BL/6J;				
RA St. Jacques B.;				
RL Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.				
RN [4] SEQUENCE OF 124-172 FROM N.A.				
RX MEDLINE=95256997; PubMed=7720571;				
RA Chang D.T., Lopez A., von Kessler D.P., Chiang C., Simandl B.K.,				
RA Zhao R., Seldin M.F., Fallon J.F., Beachy P.A.;				
RT "Proteins, genetic linkage and limb patterning activity of a murine hedgehog gene.";				
RL Development 120:3339-3353(1994).				
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CC -1- PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN				
CC INH_MOUSE				
CC ID INH_MOUSE STANDARD; PRT; 411 AA.				
CC AC F97812; 061724; PRT; 411 AA.				
CC DT 15-JUL-1999 (Rel. 38, Created)				
CC DT 15-JUL-1999 (Rel. 38, Last sequence update)				
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)				
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CC OC Mammalia; Eutheria; Rodentia; Sciuropnathi; Muridae; Murinae; Mus.				
CC OX NCBI_TAXID=10090;				
CC RN [1] SEQUENCE FROM N.A., AND AUTOPROTEOLYTIC CLEAVAGE.				
CC RC STRAIN=CD-1; TISSUE=Kidney;				
CC RX MEDLINE-97256802; PubMed=9079674;				
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CC RN [2] SEQUENCE OF 76-411 FROM N.A.				
CC RC STRAIN=NC57BL/6J; TISSUE=Embryo;				
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Db 252 NLRLAQFOVITQDPPRRLAATPAHLFLIA-DNHTPEAAHFRATEASHVQPOQYVILSGVP 310 DR MEROPS; C46 UPW; -.

Qy 308 GGDRRLIPAVHSVTREEEAGAYAPITAHTGTLINRVLASCYAVTEBHSWAHRAFPR 367 DR InterPro; IPR000320; HH_Signal.

Db 311 G---LQPARPAVS THVALGSYAPLTRGTLVVEDVASCFAAVADHLLAQAFWPLR 365 DR InterPro; IPR003586; Hedgehog_hintC.

Qy 368 LAHALAALAPARTDGGGSIPIAQSAATEARGA-BPTAGIHWYDOLYHGTWILSET 426 DR InterPro; IPR003587; Hedgehog_hintN.

Db 366 LFPSL-----AWGWTPEGVHWPOMLYRLGRILLEEST 400 DR Pfam; PRO1079; Hint; 1.

Qy 427 MHPGLMA 433 DR Pfam; PRO0632; SONICHHOG.

Db 401 EHPGLMS 407 DR Prints; PR003042; HH_Signal; 1.

DR Prodrom; DD003042; HH_Signal; 1.

DR SMART; SMO0306; HintC; 1.

DR SMART; SMO0305; HintN; 1.

KW Developmental protein; Autocatalytic cleavage; Hydrolase; Protease; KW Signal; Lipoprotein; Palmitate.

FT SIGNAL 1 23 POTENTIAL.

FT CHAIN 24 409 INDIAN HEDGEHOG PROTEIN.

FT CHAIN 24 197 INDIAN HEDGEHOG PROTEIN N-PRODUCT.

FT CHAIN 198 409 INDIAN HEDGEHOG PROTEIN C-PRODUCT.

FT SITE 197 198 CLEAVAGE (AUTO-) (BY SIMILARITY).

FT SITE 267 267 INVOLVED IN AUTO-CLEAVAGE (BY SIMILARITY).

FT ACT_SITE 270 270 ESSENTIAL FOR AUTO-CLEAVAGE (BY SIMILARITY).

FT BINDING 197 197 CHOLESTEROL (BY SIMILARITY).

FT DOMAIN 32 35 POLY-ARG.

FT LIPID 24 24 PALMITATE (BY SIMILARITY).

FT SEQUENCE 409 AA; 45591 MW; 6FB263367FB98627 CRC64;

Query Match 55.4%; Score 1267; DB 1; Length 409; Best Local Similarity 59.9%; Pred. No. 2.1e-94; Matches 257; Conservative 49; Mismatches 95; Indels 28; Gaps 6

RC TISSUE-Embryo; Qy 5 LARCFPLVILASSLILVCPSL-ACGPGFGKRRHKPKLTPLAYQFIPWAKTLGASRY 63

RC MEDLINE-95A01852; PubMed-7671800; Db 3 LPKVWLICCAAILLSGAVRGEGPGRVGRRPTKLSPLKQFSNPVPEKTLGASRY 62

RA Ecker S.C., McGrew L.L., Lal C.-J., Lee J.J., von Kessler D.P.,

RA Moon R.T., Beachy P.A.,

RT "Distinct expression and shared activities of members of the hedgehog gene family of *Xenopus laevis*.";

RL Development 121:2337-2347(1995).

CC - FUNCTION: SIGNAL INVOLVED IN THE EARLY INDUCTION AND PATTERNING OF ANTERODORSAL ECTODERM, NERVOUS SYSTEM AND SOMITES. INDUCES ECTOPIC CANTERGLOM FORMATION IN EMBRYOS.

CC - SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURFACE. HEDGEHOG PROTEIN IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).

-1- DEVELOPMENTAL STAGE: DETECTABLE WITHIN THE EARLY GASTRULA. AT STAGE 14 NEURULA, HIGH EXPRESSION IN NEURODCTODERM. EXPRESSED THROUGHOUT THE NEURAL PLATE AND SUBSEQUENTLY IN BOTH THE NERVOUS SYSTEM AND IN THE DERMATOME OF SOMITES.

-1- INDUCTION: BY ACTIVIN.

-1- PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY IN A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N- TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.

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CC EMBL; U26404; AAA85165.1; -.

CC DR EMBSP; O62226; 1MVH.

Db 243 DHSPKKEEMQIKTQDPHRRLFLTPAHILFVS-DNSTPASEFQAVFASSVRPGQVIL 301

Db 304 VAIRGGDRLIPAVHSVTREEEAGAYAPITAHTGTLINRVLASCYAVTEBHSWAHRAF 363

Db 302 SNVVG---LIPAKVRSN-TQNYGATAQIPTQHTLVDDVVSCFALVQORLADVY 356

Qy 364 APRLAHALAALAPARTDGGGSIPIAQSAATEARGA-BPTAGIHWYDOLYHGTWIL 423

Db 357 WPLRVLYNL-----GILAGTQPSQ-----MGIHWISKALYHLGRILH 395

Qy 424 SETMHPLGM 432

Db 396 GNEFHPLGI 404

RESULT 13

TH_BRACE ID TH_BRACE STANDARD; PRT; 412 AA.

AC Q98862; DT 15-JUL-1999 (Rel. 38, Created)

CC DT 15-JUL-1999 (Rel. 38, Last sequence update)

CC DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Indian hedgehog protein precursor (IHH) (Schidag hedgehog protein).

FT	CHAIN	198	412	INDIAN HEDGEHOG PROTEIN C-PRODUCT.
FT	SITE	197	198	CLEAVAGE "AUTO" (BY SIMILARITY).
FT	SITE	246	246	INVOLVED IN CHOLESTEROL TRANSFER (BY SIMILARITY).
FT	SITE	246	246	SIMILARITY.
FT	SITE	269	269	INVOLVED IN AUTO-CLEAVAGE (BY SIMILARITY).
FT	ACT_SITE	272	272	ESSENTIAL FOR AUTO-CLEAVAGE (BY SIMILARITY).
FT	BINDING	197	197	CHOLESTEROL (BY SIMILARITY).
FT	LIPID	24	24	PALMITATE (BY SIMILARITY).
FT	CONFFLICT	121	121	R -> K (IN REF. 2).
FT	SEQUENCE	412 AA:	45746 MW:	21d43f052a278ca1 c1c64;
RN	SEQUENCE FROM N.A.			
RP	SEQUENCE OF 113-170 FROM N.A.			
RC	TISSUE=MUSCLE;			
RX	MEDLINE=96310864; PubMed=8664485;			
RA	Currie P.D., Ingham P.W.;			
RA	Zardoya R., Abouheif E., Meyer A.;			
RT	"Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species closely related to the zebrafish";			
RT	In zebrafish,"; Nature 382:452-455 (1996).			
RL	Nature 382:452-455 (1996).			
[2]				
RN	SEQUENCE OF 113-170 FROM N.A.			
RP	SEQUENCE OF 113-170 FROM N.A.			
RX	MEDLINE=97075114; PubMed=8917540;			
RA	Zardoya R., Abouheif E., Meyer A.;			
RT	"Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species closely related to the zebrafish";			
RT	In zebrafish,"; Nature 382:452-455 (1996).			
CC	-1- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT. SIGNAL PRODUCED BY THE NOTOCHORD THAT INDUCES SOMITE PATTERNING AND MUSCLE PIIONEER DIFFERENTIATION.			
CC	-1- SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).			
CC	-1- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN THE NOTOCHORD.			
CC	-1- DEVELOPMENTAL STAGE: FIRST DETECTABLE AT THE MID-GASTRULA STAGE.			
CC	-1- DISAPPEARS AT THE END OF THE SOMITOGENESIS.			
CC	-1- PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N-TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).			
CC	-1- SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.			
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CC	RESULTS	14		
DR	DHH_MOUSE			
DR	ID			
DR	DHH_MOUSE			
DR	STANDARD;			
DR	PRT;			
DR	396 AA.			
DR	06188;			
DT	06188;			
DT	15-JUL-1999 (Rel. 38, Created)			
DT	15-JUL-1999 (Rel. 38, Last sequence update)			
DT	16-Oct-2001 (Rel. 40, Last annotation update)			
DE	Desert hedgehog protein precursor (DHH) (HMG-3).			
GN	DHH.			
OS	Mus musculus (Mouse);			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxId=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=129/Sv;			
RX	MEDLINE=94094334; PubMed=7916661;			
RA	Echelard Y., Epstein D.J., St Jacques B., Shen L., Mohler J., McMahon J.A., McMahon A.P.;			
RT	"Sonic hedgehog, a member of a family of putative signaling molecules that are implicated in the regulation of CNS polarity"; Cell 75:1417-1430 (1993).			
RL	[2]			
RN	SEQUENCE OF 120-168 FROM N.A.			
RP	SEQUENCE OF 120-168 FROM N.A.			
RT	MEDLINE=95235997; PubMed=7720571;			
RA	Chang D.T., Lopez A., von Kessler D.P., Chiang C., Simandl B.K., Zhao R., Seiden M.F., Fallon J.F., Beachy P.A.;			
FT	CHAIN	24	412	INDIAN HEDGEHOG PROTEIN N-PRODUCT.
FT	CHAIN	24	197	INDIAN HEDGEHOG PROTEIN N-PRODUCT.

RT "Products genetic linkage and limb patterning activity of a murine hedgehog gene." ;
 RT hedgehog gene. " ;
 RL Development 120:3139-3153 (1994).
 CC -1- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF
 CC PATTERNING EVENTS DURING DEVELOPMENT. MAY FUNCTION AS A
 CC SPERMATOCYTE SURVIVAL FACTOR IN THE TESTES. ESSENTIAL FOR TESTES
 CC DEVELOPMENT.
 CC -1- SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE
 CC CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE
 CC CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM
 CC TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ADULT TESTES. NOT EXPRESSED IN
 CC LIMB BUDS.
 CC -1- PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY
 CC AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN
 CC THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF
 CC A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N-
 CC TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS
 CC TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION
 CC OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE
 CC ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING. WHEREAS THE
 CC C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.
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 CC
 CC EMBL; X61629; CAAS53924_1; -. .
 DR HSSP; 062226; 1VHH.
 DR MEROPS; C46_004; -. .
 DR MGD; MGI_9489; DH.
 DR InterPro; IPR000320; HH_signal.
 DR InterPro; IPR0167; Hedgehog_hint.
 DR InterPro; IPR03586; Hedgehog_hintC.
 DR InterPro; IPR03587; Hedgehog_hintN.
 DR InterPro; IPR02203; Intein.
 DR InterPro; IPR00165; Sonichh.
 DR Pfam; PF01079; Hint; 1.
 DR PRINTS; PR0632; SONICHHOG.
 DR PRODOM; PD000042; HH_signal; 1.
 DR SMART; SM00305; HintC; 1.
 DR SMART; SM00306; HintN; 1.
 DR PROSITE; PS50817; INTERNTR; 1.
 KW Signal; Lipoprotein; Palmitate.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 396 DESERT HEDGEHOG PROTEIN.
 FT CHAIN 23 198 DESERT HEDGEHOG PROTEIN N-PRODUCT.
 FT SITE 199 396 DESERT HEDGEHOG PROTEIN C-PRODUCT.
 FT SITE 198 396 CLEAVAGE (AUTO-).
 FT SITE 244 244 INVOLVED IN CHOLESTEROL TRANSFER (BY
 FT SITE 268 268 INVOLVED IN AUTO-CLEAVAGE (BY
 FT ACT_SITE 271 271 ESSENTIAL FOR AUTO-CLEAVAGE (BY
 FT BINDING 198 198 SIMILARITY).
 FT LIPID 23 23 CHOLESTEROL (BY SIMILARITY).
 SQ SEQUENCE 396 AA; 43542 MW; AFEBE031BE930FDB CRC64;

Query Match 53.3%; Score 1219; DB 1; Length 396;
 Best Local Similarity 58.7%; Pred. No. 1.5e-90; Gaps 12;
 Matches 249; Conservative 55; Mismatches 80; Indels 40; QY 62 RYECKITRNSEERKEELTPNPINPDIFKDEENTGADRLMTRQCKDLKNAISVMNDPGV 121
 4 LLARCFLVTLASLILVCPLACGCRG-FGKRRIPKK-LTFLAYKQFIPNVAFKTGLGASG 61
 CC ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| 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:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

QY 62 RYECKITRNSEERKEELTPNPINPDIFKDEENTGADRLMTRQCKDLKNAISVMNDPGV 121
 Db 62 PAGCRVTRGSRERDRDVNNPNPIKDFEENGSDAHLTRCKVNLAIAVNMPGV 121
 CC 122 RLRLVTEGMDEDGHHAQDSILHYEGRALDITTSDRDRSKYGMMLARLAVENGFDWVYESRHN 181
 Db 182 IHOSVKAENSAVAKSGCCFFPGSATVHLEGGCGKLVKLUQDGRVLAADDGRULYSPLT 241
 Db 182 IHHSVKAENSLAVTRAGGERGKLRSELHRGDMVLAADAGRVPPTVLL 241
 QY 242 FLDRDEGAKKVVFVIELEPRERLLTAAHLLEVAPHINDSGTPGP--SALFAVRVPG 298
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 QY 299 QRYVVAEERGDRRLPLPAVHSVTLREERAGAYAPLTHAFTLNLINVLSCTAVIEHWS 358
 Db 298 DSVLA--FGGD-ALQPARYVARA-REEAVGFPALTAHGTLVNDVLASCTAVLESQW 352
 QY 359 AHRAFAPFLAHALLAALAPARDGGGGSPAPIQAOSATEARCAEPTAGHWSOLHHG 418
 Db 353 AHRAFAPFLAHLLA-LGALIP-----GGAV-----OPT-GMWHSRLIRLA 391
 QY 419 TWLL 422
 Db 392 EELM 395

RESULT 15
 DHU_HUMAN ID DHU_HUMAN STANDARD PRT; 396 AA.
 AC O43323; Q15794 Rel. 38, Created DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DE DT 15-JUN-2002 (Rel. 41, Last annotation update) Desert hedgehog protein precursor (DHU) (HhG-3).
 OS Homo sapiens (Human); Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; NCBI_TAXID=9606;
 RN [1] SEQUENCE FROM N.A.
 RA Tate G., Kishimoto K., Mitsuya T.;
 RT "Expression of Sonic hedgehog and its receptor Patched/Smoothened in human cancer cell lines and embryonic organs";
 RL J. Biochem. Mol. Biol. Biophys. 4:27-34(2000).
 RN SEQUENCE OF 85-178 FROM N.A.
 RC TISSUE=Kidney;
 RA Drummond I.A.;
 RT Human desert hedgehog. "
 RL Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
 RN [3] DISASE.
 RX Pubmed=11017805;
 RA Umehara F., Tate G., Ichio K., Yamaguchi N., Douchi T., Mitsuya T., Osame M.;
 RT "A novel mutation of desert hedgehog in a patient with 46,XY partial gonadal dysgenesis accompanied by minifascicular neuropathy"; Am. J. Hum. Genet. 67:1302-1305(2000).
 CC -1- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT. MAY FUNCTION AS A SPERMATOCYTE SURVIVAL FACTOR IN THE TESTES. ESSENTIAL FOR TESTES DEVELOPMENT.
 CC -1- SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).
 CC -1- PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN

Search completed: February 20, 2003, 10:12:39
Job time : 15.4009 secs

GenCore version 5.1.3
 Copyright (c) 1993 - 2003 Compugen Ltd.

Database : Published_Applications_AA;

GenCore version 5.1.3
copyright (c) 1993 - 2003 Compugen Ltd.

ALIGNMENTS

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Sequence 15, Appl
Sequence 15, Appl
Sequence 39, Appl
Sequence 15, App
Sequence 10, Appl
Sequence 10, Appl
Sequence 34, App
Sequence 10, App
Sequence 38, App
Sequence 14, Appl
Sequence 14, Appl
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Sequence 30, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 12, App
Sequence 11, Appl
Sequence 13, Appl

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; US-08-900-220C-13
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Best Local Similarity 100.0%; Pred. No. 1.2e-17;
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Db 181 HHCsvkAensvaAKSGCCPGSATVHLEGGTKLVKUDLRPGDVLADDGCRLLYSDFL 240
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Db 241 TFLDRDEGAKKYVYIETLERERLLTAHLFVAPHDGPPPSALEASRVRPGQR 300
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Db 301 VVVAERGDDRLLPAAVSHYLREEEAGAYAPLHTGTLINRVASCYAVIEHSWAH 360
Qy 361 RAFAPERLAHALALAAPARTDGGGGSIPAQSATEARGAEPTAGIHWYSOLLYHGTW 420
Db 361 RAFAPERLAHALALAAPARTDGGGGSIPAQSATEARGAEPTAGIHWYSOLLYHGTW 420
Qy 421 LLDSETMHPGMVKSS 437
Db 421 LLDSETMHPGMVKSS 437

RESULT 2

US-09-883-848A-13

; Sequence 13, Application US/0988384A

; GENERAL INFORMATION:

; APPLICANT: Ling, L.

; TITLE OF INVENTION: ANGIOGENESIS-MODULATING COMPOSITIONS AND USES

; FILE REFERENCE: CIBT-P01-119

; CURRENT APPLICATION NUMBER: US/09/883,848

; PRIORITY FILING DATE: 2001-06-18

; PRIORITY NUMBER: 60/211,919

; NUMBER OF SEQ ID NOS: 48

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO: 13

; LENGTH: 437

; TYPE: PRT

; ORGANISM: Mus musculus

; US-09-883-848A-13

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: Patentin Ver. 2.0

; LENGTH: 437

; TYPE: PRT

; ORGANISM: murine Shh

; US-09-151-999-13

; Sequence 13, Application US/09151999

; PATENT NO. US20020151460A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Elizabeth

; TITLE OF INVENTION: REGULATION OF EPITHELIAL TISSUE BY HEDGEHOG-LIKE

; FILE REFERENCE: ONY-031-02

; CURRENT APPLICATION NUMBER: US/09/151,999

; CURRENT FILING DATE: 1998-08-11

; EARLIER APPLICATION NUMBER: 08/955,552

; EARLIER FILING DATE: 1997-10-20

; SOFTWARE: Patentin Ver. 2.0

; LENGTH: 437

; TYPE: PRT

; ORGANISM: murine Shh

; US-09-151-999-13

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: Patentin Ver. 2.0

; LENGTH: 437

; TYPE: PRT

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; CURRENT APPLICATION NUMBER: US/09/151,999

; CURRENT FILING DATE: 1998-08-11

; EARLIER APPLICATION NUMBER: 08/955,552

; EARLIER FILING DATE: 1997-10-20

; SOFTWARE: Patentin Ver. 2.0

; LENGTH: 437

; TYPE: PRT

; ORGANISM: murine Shh

; US-09-151-999-13

; Sequence 13, Application US/09151999

; PATENT NO. US20020151460A1

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; EARLIER FILING DATE: 1997-10-20

; SOFTWARE: Patentin Ver. 2.0

; LENGTH: 437

; TYPE: PRT

; ORGANISM: murine Shh

; US-09-151-999-13

; Sequence 13, Application US/09151999

; PATENT NO. US20020151460A1

; GENERAL INFORMATION:

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; EARLIER APPLICATION NUMBER: 08/955,552

; EARLIER FILING DATE: 1997-10-20

; SOFTWARE: Patentin Ver. 2.0

; LENGTH: 437

; TYPE: PRT

; ORGANISM: murine Shh

; US-09-151-999-13

; Sequence 13, Application US/09151999

; PATENT NO. US20020151460A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Elizabeth

; TITLE OF INVENTION: REGULATION OF EPITHELIAL TISSUE BY HEDGEHOG-LIKE

; FILE REFERENCE: ONY-031-02

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; CURRENT FILING DATE: 1998-08-11

; EARLIER APPLICATION NUMBER: 08/955,552

; EARLIER FILING DATE: 1997-10-20

; SOFTWARE: Patentin Ver. 2.0

; LENGTH: 437

; TYPE: PRT

; ORGANISM: murine Shh

; US-09-151-999-13

; Sequence 13, Application US/09151999

; PATENT NO. US20020151460A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Elizabeth

; TITLE OF INVENTION: REGULATION OF EPITHELIAL TISSUE BY HEDGEHOG-LIKE

; FILE REFERENCE: ONY-031-02

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; CURRENT FILING DATE: 1998-08-11

; EARLIER APPLICATION NUMBER: 08/955,552

; EARLIER FILING DATE: 1997-10-20

; SOFTWARE: Patentin Ver. 2.0

; LENGTH: 437

; TYPE: PRT

; ORGANISM: murine Shh

; US-09-151-999-13

; Sequence 13, Application US/09151999

; PATENT NO. US20020151460A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Elizabeth

; TITLE OF INVENTION: REGULATION OF EPITHELIAL TISSUE BY HEDGEHOG-LIKE

; FILE REFERENCE: ONY-031-02

; CURRENT APPLICATION NUMBER: US/09/151,999

; CURRENT FILING DATE: 1998-08-11

; EARLIER APPLICATION NUMBER: 08/955,552

; EARLIER FILING DATE: 1997-10-20

; SOFTWARE: Patentin Ver. 2.0

; LENGTH: 437

; TYPE: PRT

; ORGANISM: murine Shh

; US-09-151-999-13

; Sequence 13, Application US/09151999

; PATENT NO. US20020151460A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Elizabeth

; TITLE OF INVENTION: REGULATION OF EPITHELIAL TISSUE BY HEDGEHOG-LIKE

; FILE REFERENCE: ONY-031-02

; CURRENT APPLICATION NUMBER: US/09/151,999

; CURRENT FILING DATE: 1998-08-11

; EARLIER APPLICATION NUMBER: 08/955,552

; EARLIER FILING DATE: 1997-10-20

; SOFTWARE: Patentin Ver. 2.0

; LENGTH: 437

; TYPE: PRT

; ORGANISM: murine Shh

; US-09-151-999-13

; Sequence 13, Application US/09151999

; PATENT NO. US20020151460A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Elizabeth

; TITLE OF INVENTION: REGULATION OF EPITHELIAL TISSUE BY HEDGEHOG-LIKE

; FILE REFERENCE: ONY-031-02

; CURRENT APPLICATION NUMBER: US/09/151,999

; CURRENT FILING DATE: 1998-08-11

; EARLIER APPLICATION NUMBER: 08/955,552

; EARLIER FILING DATE: 1997-10-20

; SOFTWARE: Patentin Ver. 2.0

; LENGTH: 437

; TYPE: PRT

; ORGANISM: murine Shh

; US-09-151-999-13

; Sequence 13, Application US/09151999

; PATENT NO. US20020151460A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Elizabeth

; TITLE OF INVENTION: REGULATION OF EPITHELIAL TISSUE BY HEDGEHOG-LIKE

; FILE REFERENCE: ONY-031-02

; CURRENT APPLICATION NUMBER: US/09/151,999

; CURRENT FILING DATE: 1998-08-11

; EARLIER APPLICATION NUMBER: 08/955,552

; EARLIER FILING DATE: 1997-10-20

; SOFTWARE: Patentin Ver. 2.0

; LENGTH: 437

; TYPE: PRT

; ORGANISM: murine Shh

; US-09-151-999-13

; Sequence 13, Application US/09151999

; PATENT NO. US20020151460A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Elizabeth

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; FILE REFERENCE: ONY-031-02

; CURRENT APPLICATION NUMBER: US/09/151,999

; CURRENT FILING DATE: 1998-08-11

; EARLIER APPLICATION NUMBER: 08/955,552

; EARLIER FILING DATE: 1997-10-20

; SOFTWARE: Patentin Ver. 2.0

; LENGTH: 437

; TYPE: PRT

; ORGANISM: murine Shh

; US-09-151-999-13

; Sequence 13, Application US/09151999

; PATENT NO. US20020151460A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Elizabeth

; TITLE OF INVENTION: REGULATION OF EPITHELIAL TISSUE BY HEDGEHOG-LIKE

; FILE REFERENCE: ONY-031-02

; CURRENT APPLICATION NUMBER: US/09/151,999

; CURRENT FILING DATE: 1998-08-11

; EARLIER APPLICATION NUMBER: 08/955,552

; EARLIER FILING DATE: 1997-10-20

; SOFTWARE: Patentin Ver. 2.0

; LENGTH: 437

; TYPE: PRT

; ORGANISM: murine Shh

; US-09-151-999-13

; Sequence 13, Application US/09151999

; PATENT NO. US20020151460A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Elizabeth

; TITLE OF INVENTION: REGULATION OF EPITHELIAL TISSUE BY HEDGEHOG-LIKE

; FILE REFERENCE: ONY-031-02

; CURRENT APPLICATION NUMBER: US/09/151,999

; CURRENT FILING DATE: 1998-08-11

; EARLIER APPLICATION NUMBER: 08/955,552

; EARLIER FILING DATE: 1997-10-20

; SOFTWARE: Patentin Ver. 2.0

; LENGTH: 437

; TYPE: PRT

; ORGANISM: murine Shh

; US-09-151-999-13

; Sequence 13, Application US/09151999

; PATENT NO. US20020151460A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Elizabeth

; TITLE OF INVENTION: REGULATION OF EPITHELIAL TISSUE BY HEDGEHOG-LIKE

; FILE REFERENCE: ONY-031-02

; CURRENT APPLICATION NUMBER: US/09/151,999

; CURRENT FILING DATE: 1998-08-11

; EARLIER APPLICATION NUMBER: 08/955,552

; EARLIER FILING DATE: 1997-10-20

; SOFTWARE: Patentin Ver. 2.0

; LENGTH: 437

; TYPE: PRT

; ORGANISM: murine Shh

; US-09-151-999-13

; Sequence 13, Application US/09151999

RESULT 4

US-09-990-046-14

; Sequence 14, Application US/09990046

; GENERAL INFORMATION:

; APPLICANT: de Savage, Frederick

; APPLICANT: Carpenter, David A.

; TITLE OF INVENTION: Patched-2

; FILE REFERENCE: P1405R1

; CURRENT APPLICATION NUMBER: US/09/990,046

; CURRENT FILING DATE: 2001-11-20

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/293,505

; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-15

; NUMBER OF SEQ ID NOS: 32

; SEQ ID NO: 14

; LENGTH: 437

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-990-046-14

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Best Local Similarity 99.8%; Pred. No. 2.3e-197; Matches 436; Conservative 1; Mismatches 0; Gaps 0;

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US-09-999-520A-1

; Sequence 1, Application US/09969520A

; Patent No. US2002177163A1

; GENERAL INFORMATION:

; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE

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US-10-013-310-1

; Sequence 1, Application US/10013310

; Publication No. US20020192216A1

; GENERAL INFORMATION:

; APPLICANT: Lamb, Jonathan Robert

; APPLICANT: Hoynes, Gerard Francis

; APPLICANT: Dallman, Margaret Jane

; TITLE OF INVENTION: Therapeutic Use

; FILE REFERENCE: 674525-2003

; CURRENT APPLICATION NUMBER: US/10/013, 310

; CURRENT FILING DATE: 2001-12-07

; PRIOR APPLICATION NUMBER: PCT/GB00/02191

; PRIOR FILING DATE: 2000-06-05

PRIOR APPLICATION NUMBER: UK 9913350.6

PRIOR FILING DATE: 1999-06-08

PRIOR APPLICATION NUMBER: UK 9921953.7

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin version 3.1

SEQ ID NO: 1

LENGTH: 437
; TYPE: PRT
; ORGANISM: House Mouse
US-10-013-310-1

Query Match 99.9%; Score 2286; DB 9; Length 437;
Best Local Similarity 99.8%; Pred. No. 2.3e-17;
Matches 436; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MLLLARCFVLVILLASLLVCPGLACGPGRGFRGRKRPKKLTPLAYKQFIPNVAEKTGAS 60
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Qy 301 VVVAERGGDRLLPAAVHSVTLRREEAGAYAPLTAGHTLIRNLASCYAVIEBSWAH 360
Db 301 VVVAERGGDRLLPAAVHSVTLRREEAGAYAPLTAGHTLIRNLASCYAVIEBSWAH 360
Qy 361 RAFAPFRLAHALAALAPARTDGCGGSIPAQSATEARGAETAGIHWYSOLLYHGTW 420
Db 361 RAFAPFRLAHALAALAPARTDGCGGSIPAQSATEARGAETAGIHWYSOLLYHGTW 420
Qy 421 LLDSETMHPGMVAKSS 437
Db 421 LLDSETMHPGMVAKSS 437
Qy 241 TFLDRDEGAKKVYETLERERLLTAHHLFVAPHNDSCPPGSALFASVVRPGQ 300
Db 241 TFLDRDEGAKKVYETLERERLLTAHHLFVAPHNDSCPPGSALFASVVRPGQ 300
Qy 301 VVVAERGGDRLLPAAVHSVTLRREEAGAYAPLTAGHTLIRNLASCYAVIEBSWAH 360
Db 301 VVVAERGGDRLLPAAVHSVTLRREEAGAYAPLTAGHTLIRNLASCYAVIEBSWAH 360
Qy 361 RAFAPFRLAHALAALAPARTDGCGGSIPAQSATEARGAETAGIHWYSOLLYHGTW 420
Db 361 RAFAPFRLAHALAALAPARTDGCGGSIPAQSATEARGAETAGIHWYSOLLYHGTW 420
Qy 421 LLDSETMHPGMVAKSS 437
Db 421 LLDSETMHPGMVAKSS 437

RESULT 7
US-09-733-634-16
; Sequence 16, Application US/09/733,634
; Publication No. US20030136461
; GENERAL INFORMATION:
; APPLICANT: Massachusetts General Hospital
; TITLE OF INVENTION: Method to stimulate Insulin production by pancreatic b-cells
; FILE REFERENCE: 1763/1240
; CURRENT APPLICATION NUMBER: US/09/733,634
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: US 60/170,282
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 16
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-733-634-16

Query Match 99.9%; Score 2286; DB 10; Length 437;
Best Local Similarity 99.9%; Pred. No. 2.3e-197;
Matches 436; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLLARCFVLVILLASLLVCPGLACGPGRGFRGRKRPKKLTPLAYKQFIPNVAEKTGAS 60
Db 1 MLLLARCFVLVILLASLLVCPGLACGPGRGFRGRKRPKKLTPLAYKQFIPNVAEKTGAS 60
Qy 61 GRYEGKITRNSERKELETPNNPDIFKDEENTGADRMLTQRCKDLNALAISVMNQPG 120
Db 61 GRYEGKITRNSERKELETPNNPDIFKDEENTGADRMLTQRCKDLNALAISVMNQPG 120
Qy 121 VRLRVTEGWDCHHSEESLSHYGRAVDTTSDRDRSKYGMALARLAVEAGFDWVYESKA 180
Db 121 VRLRVTEGWDCHHSEESLSHYGRAVDTTSDRDRSKYGMALARLAVEAGFDWVYESKA 180
Qy 181 HICSVKAENSAAKSGCFCPOSATVILEQGGTKLUVKDRLPQCDRVLAAADDQGRLLSDFL 240
Db 181 HICSVKAENSAAKSGCFCPOSATVILEQGGTKLUVKDRLPQCDRVLAAADDQGRLLSDFL 240
Qy 241 TFLDRBEGAKKVYETLERERLLTAHHLFVAPHNDSGPTGPSALFAASRYRPGQ 300
Db 241 TFLDRBEGAKKVYETLERERLLTAHHLFVAPHNDSGPTGPSALFAASRYRPGQ 300
Qy 301 VVVAERGGDRLLPAAVHSVTLRREEAGAYAPLTAGHTLIRNLASCYAVIEBSWAH 360
Db 301 VVVAERGGDRLLPAAVHSVTLRREEAGAYAPLTAGHTLIRNLASCYAVIEBSWAH 360
Qy 361 RAFAPFRLAHALAALAPARTDGCGGSIPAQSATEARGAETAGIHWYSOLLYHGTW 420
Db 361 RAFAPFRLAHALAALAPARTDGCGGSIPAQSATEARGAETAGIHWYSOLLYHGTW 420
Qy 421 LLDSETMHPGMVAKSS 437
Db 421 LLDSETMHPGMVAKSS 437

RESULT 8
US-09-021-660A-37
; Sequence 37, Application US/09/021660A
; PATENT NO. US20010041668A1
; GENERAL INFORMATION:
; APPLICANT: Baron, M.
; APPLICANT: Fairington, S.
; APPLICANT: Belauhoff, M.
; TITLE OF INVENTION: METHODS FOR MODULATING HEMATOPOIESIS AND VASCULAR
; TITLE OF INVENTION: GROWTH
; FILE REFERENCE: HU1P-PO1-050
; CURRENT APPLICATION NUMBER: US/09/021,660A
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 60/037,513
; PRIOR FILING DATE: 1997-02-10
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 37
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-021-660A-37

Query Match 99.9%; Score 2286; DB 10; Length 437;
Best Local Similarity 99.9%; Pred. No. 2.3e-197;
Matches 436; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLLARCFVLVILLASLLVCPGLACGPGRGFRGRKRPKKLTPLAYKQFIPNVAEKTGAS 60
Db 1 MLLLARCFVLVILLASLLVCPGLACGPGRGFRGRKRPKKLTPLAYKQFIPNVAEKTGAS 60
Qy 61 GRYEGKITRNSERKELETPNNPDIFKDEENTGADRMLTQRCKDLNALAISVMNQPG 120
Db 61 GRYEGKITRNSERKELETPNNPDIFKDEENTGADRMLTQRCKDLNALAISVMNQPG 120
Qy 121 VRLRVTEGWDCHHSEESLSHYGRAVDTTSDRDRSKYGMALARLAVEAGFDWVYESKA 180
Db 121 VRLRVTEGWDCHHSEESLSHYGRAVDTTSDRDRSKYGMALARLAVEAGFDWVYESKA 180
Qy 181 HICSVKAENSAAKSGCFCPOSATVILEQGGTKLUVKDRLPQCDRVLAAADDQGRLLSDFL 240
Db 181 HICSVKAENSAAKSGCFCPOSATVILEQGGTKLUVKDRLPQCDRVLAAADDQGRLLSDFL 240
Qy 241 TFLDRDEGAKKVYETLERERLLTAHHLFVAPHNDSCPPGSALFASVVRPGQ 300
Db 241 TFLDRDEGAKKVYETLERERLLTAHHLFVAPHNDSCPPGSALFASVVRPGQ 300

Db 241 TFLDRDEGAKKVYVITLEPERRLLTAAHILFVAPHNDSGPTPGPSALFASRVPGQR 300
 Qy 301 VVVAERGGDRRLPAAVHSVTLREEEAGAYAPLTAHTGTLINRVLASCYVIEEWSWAH 360
 Db 301 VVVAERGGDRRLPAAVHSVTLREEEAGAYAPLTAHTGTLINRVLASCYVIEEWSWAH 360
 ; Sequence No. 1, Application US/09969520A
 ; Patent No. US2002017163A1
 ; GENERAL INFORMATION:
 ; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
 ; APPLICANT: BEACHY, PHILIP A.
 ; TITLE OF INVENTION: METHOD OF USE OF SONIC HEDGEHOG PROTEIN AS A LIGAND FOR PATCHED FILE REFERENCE: JHU1670-1
 ; CURRENT APPLICATION NUMBER: US/09/969,520A
 ; CURRENT FILING DATE: 2002-06-04
 ; PRIORITY APPLICATION NUMBER: US 60/235,153
 ; PRIORITY FILING DATE: 2000-09-22
 ; NUMBER OF SEQ ID NOS: 17
 ; SEQ ID NO 3
 ; LENGTH: 437
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Altered sonic hedgehog protein
 ; US-09-969-520A-3
 Query Match 99.5%; Score 2280; DB 9; Length 437;
 Best Local Similarity 99.5%; Pred. No. 7; seq=197; Matches 434; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Matches 435; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 MILLARCFVLVIASSLIVCPGLACGGGRGGRARRKKLTPLAYQFIPNVAEKTIGAS 60
 Db 1 MILLARCFVLVIASSLIVCPGLACGGGRGGRARRKKLTPLAYQFIPNVAEKTIGAS 60
 Qy 61 GRVEGKTRNSERFKELTPNYNPDIIFKDEENGTADRLMTORCKDKNALAISVMQWPG 120
 Db 61 GRVEGKTRNSERFKELTPNYNPDIIFKDEENGTADRLMTORCKDKNALAISVMQWPG 120
 Qy 121 VRLRVTEGWDENGHHSEESLHYEGRAVDITSDRDRSKYGMALARLAVEAGEDDWVYESKA 180
 Db 121 VKLRVTEGWDENGHHSEESLHYEGRAVDITSDADRAKYGMALARLAVEAGEDDWVYESKA 180
 Qy 181 HHCsvkaensyaaksgccfpssatvileqoggtklykdlrpdrvladodgrllsdf 240
 Db 181 HHCsvkaensyaaksgccfpssatvileqoggtklykdlrpdrvladodgrllsdf 240
 Qy 241 TFLDRDEGAKKVYVITLEPERRLLTAAHILFVAPHNDSGPTPGPSALFASRVPGQR 300
 Db 241 TFLDRDEGAKKVYVITLEPERRLLTAAHILFVAPHNDSGPTPGPSALFASRVPGQR 300
 Qy 301 VVVAERGGDRRLPAAVHSVTLREEEAGAYAPLTAHTGTLINRVLASCYVIEEWSWAH 360
 Db 301 VVVAERGGDRRLPAAVHSVTLREEEAGAYAPLTAHTGTLINRVLASCYVIEEWSWAH 360
 ; Sequence No. 11, Application US/09969520A
 ; Patent No. US2002017163A1
 ; GENERAL INFORMATION:
 ; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
 ; APPLICANT: BEACHY, Philip A.
 ; TITLE OF INVENTION: METHOD OF USE OF SONIC HEDGEHOG PROTEIN AS A LIGAND FOR PATCHED FILE REFERENCE: JHU1670-1
 ; CURRENT APPLICATION NUMBER: US/09/969,520A
 ; CURRENT FILING DATE: 2002-06-04
 ; PRIORITY APPLICATION NUMBER: US 60/235,153
 ; NUMBER OF SEQ ID NOS: 17
 ; SEQ ID NO 10
 ; LENGTH: 437
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Altered sonic hedgehog protein
 ; US-09-969-520A-10
 Query Match 99.5%; Score 2277; DB 9; Length 437;
 Best Local Similarity 99.3%; Pred. No. 1; seq=196; Matches 434; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Matches 435; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 MILLARCFVLVIASSLIVCPGLACGGGRGGRARRKKLTPLAYQFIPNVAEKTIGAS 60
 Db 1 MILLARCFVLVIASSLIVCPGLACGGGRGGRARRKKLTPLAYQFIPNVAEKTIGAS 60
 Qy 61 GRVEGKTRNSERFKELTPNYNPDIIFKDEENGTADRLMTORCKDKNALAISVMQWPG 120
 Db 61 GRVEGKTRNSERFKELTPNYNPDIIFKDEENGTADRLMTORCKDKNALAISVMQWPG 120
 Qy 121 VRLRVTEGWDENGHHSEESLHYEGRAVDITSDRDRSKYGMALARLAVEAGEDDWVYESKA 180
 Db 121 VKLRVTEGWDENGHHSEESLHYEGRAVDITSDADRAKYGMALARLAVEAGEDDWVYESKA 180
 Qy 181 HHCsvkaensyaaksgccfpssatvileqoggtklykdlrpdrvladodgrllsdf 240
 Db 181 HHCsvkaensyaaksgccfpssatvileqoggtklykdlrpdrvladodgrllsdf 240
 Qy 241 TFLDRDEGAKKVYVITLEPERRLLTAAHILFVAPHNDSGPTPGPSALFASRVPGQR 300
 Db 241 TFLDRDEGAKKVYVITLEPERRLLTAAHILFVAPHNDSGPTPGPSALFASRVPGQR 300
 Qy 301 VVVAERGGDRRLPAAVHSVTLREEEAGAYAPLTAHTGTLINRVLASCYVIEEWSWAH 360
 Db 301 VVVAERGGDRRLPAAVHSVTLREEEAGAYAPLTAHTGTLINRVLASCYVIEEWSWAH 360
 ; Sequence No. 11, Application US/09969520A
 ; Patent No. US2002017163A1
 ; GENERAL INFORMATION:
 ; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
 ; APPLICANT: BEACHY, Philip A.
 ; TITLE OF INVENTION: METHOD OF USE OF SONIC HEDGEHOG PROTEIN AS A LIGAND FOR PATCHED FILE REFERENCE: JHU1670-1
 ; CURRENT APPLICATION NUMBER: US/09/969,520A
 ; CURRENT FILING DATE: 2002-06-04

PRIOR APPLICATION NUMBER: US 60/235,153
 PRIORITY FILING DATE: 2000-09-22
 NUMBER OF SEQ ID NOS: 17
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 11
 LENGTH: 437
 TYPE: PRT
 ORGANISM: Artificial sequence
 OTHER INFORMATION: Altered sonic hedgehog protein
 US-09-969-520A-11

Query Match 99.5%; Score 2277; DB 9; Length 437;
 Best Local Similarity 99.3%; Pred. No. 1.Se-196;
 Matches 434; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLLIARCVLVIASSLLVCPGLACGPGRGKRRHPPKLTPLAYKOPTPVAEKTIGAS 60
 Db 1 MLLIARCVLVIASSLLVCPGLACGPGRGKRRHPPKLTPLAYKOPTPVAEKTIGAS 60
 Qy 61 GRYEGKITRNSERFKELTPNYNPDLIFKDEENTGADRMLTQRCKDKLNALATSVMNQPG 120
 Db 61 GRYEGKITRNSERFKELTPNYNPDLIFKDEENTGADRMLTQRCKDKLNALATSVMNQPG 120
 Qy 121 VRLRVTEGMDGHSESSLHYGRAVDTTSRDRSYGMLARLAVAGFDWVYYESKA 180
 Db 121 VRLRVTEGMDGHSESSLHYGRAVDTTSRDRSYGMLARLAVAGFDWVYYESKA 180
 Qy 61 GRYEGKITRNSERFKELTPNYNPDLIFKDEENTGADRMLTQRCKDKLNALATSVMNQPG 120
 Db 61 GRYEGKITRNSERFKELTPNYNPDLIFKDEENTGADRMLTQRCKDKLNALATSVMNQPG 120
 Qy 121 VRLRVTEGMDGHSESSLHYGRAVDTTSRDRSYGMLARLAVAGFDWVYYESKA 180
 Db 121 VRLRVTEGMDGHSESSLHYGRAVDTTSRDRSYGMLARLAVAGFDWVYYESKA 180
 Qy 181 HIHCSVKAKNSVAKSGCFPSATVHLEQGGTKLVKDLRPGDRLVLAADDGGRLLSDEL 240
 Db 181 HIHCSVKAKNSVAKSGCFPSATVHLEQGGTKLVKDLRPGDRLVLAADDGGRLLSDEL 240
 Qy 241 TFLDRDEGAKKVYVITLEPRERLITTAHLFVAPHDNSGPTPGPSALFAVRPGQR 300
 Db 241 TFLDRDEGAKKVYVITLEPRERLITTAHLFVAPHDNSGPTPGPSALFAVRPGQR 300
 Qy 301 VVVAERGDRRLPAAVSHVLUREEAGAYAPLTANGTILINRVLASCYAVIEENSWAH 360
 Db 301 VVVAERGDRRLPAAVSHVLUREEAGAYAPLTANGTILINRVLASCYAVIEENSWAH 360
 Qy 361 RAFAFRLLAHALLALAPRTDGGSISIPAQSAATEARGAEPTAGIHWSQLLHIGTW 420
 Db 361 RAFAFRLLAHALLALAPRTDGGSISIPAQSAATEARGAEPTAGIHWSQLLHIGTW 420
 Qy 421 LIDSETMHPGMVKSS 437
 Db 421 LIDSETMHPGMVKSS 437

RESULT 12
 US-09-969-520A-2
 ; Sequence 2, Application US/09969520A
 ; Patent No. US200217163A1
 ; GENERAL INFORMATION:
 ; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
 ; TITLE OF INVENTION: METHOD OF USE OF SONIC HEDGEHOG PROTEIN AS A LIGAND FOR PATCHED FILE REFERENCE: JHU1670-1
 ; CURRENT APPLICATION NUMBER: US/09/969, 520A
 ; CURRENT FILING DATE: 2002-06-04
 ; PRIOR APPLICATION NUMBER: US 60/235,153
 ; PRIORITY FILING DATE: 2000-09-22
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 9
 ; LENGTH: 437
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; OTHER INFORMATION: Altered sonic hedgehog protein
 US-09-969-520A-9

Query Match 99.3%; Score 2277; DB 9; Length 437;
 Best Local Similarity 99.3%; Pred. No. 4.1e-196;
 Matches 434; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MLLIARCVLVIASSLLVCPGLACGPGRGKRRHPPKLTPLAYKOPTPVAEKTIGAS 60
 Db 1 MLLIARCVLVIASSLLVCPGLACGPGRGKRRHPPKLTPLAYKOPTPVAEKTIGAS 60
 Qy 61 GRYEGKITRNSERFKELTPNYNPDLIFKDEENTGADRMLTQRCKDKLNALATSVMNQPG 120
 Db 61 GRYEGKITRNSERFKELTPNYNPDLIFKDEENTGADRMLTQRCKDKLNALATSVMNQPG 120
 Qy 121 VRLRVTEGMDGHSESSLHYGRAVDTTSRDRSYGMLARLAVAGFDWVYYESKA 180

Db 121 VKLRVTEGDEGHSEESLHYSGRAVDTTSRDRSKYGMALARLAVAGEDFDWVYESKA 180
 Qy 181 HIHSVKAENSAVAKSGGGPPGSATVHLEQGGTKLVKDLRPGDVLADDQGRILYSDFL 240
 Db 181 HIHSVKAENSAVAKSGGGPPGSATVHLEQGGTKLVKDLRPGDVLADDQGRILYSDFL 240
 Qy 241 TFLDRDEGAKKVVFVIELEPRERLLTAHLIFVAPHDNSGTPGPSALFASRVPCQR 300
 Db 241 TFLDRDEGAKKVVFVIELEPRERLLTAHLIFVAPHDNSGTPGPSALFASRVPCQR 300
 Qy 301 VVVAERGDRRLPAAMVSUTREEEAGAYAPATHTAHLIFVAPHDNSGTPGPSALFASRVPCQR 360
 Db 301 VVVAERGDRRLPAAMVSUTREEEAGAYAPATHTAHLIFVAPHDNSGTPGPSALFASRVPCQR 360
 ;
 ; RESULT 14
 ; US 09-969-520A-4
 ; Sequence 4 Application US/09969520A
 ; Patent No. US20030177163A1
 ; GENERAL INFORMATION:
 ; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
 ; APPLICANT: BEACHY, PHILIP A.
 ; TITLE OF INVENTION: METHOD OF USE OF SONIC HEDGEHOG PROTEIN AS A LIGAND FOR PATCHED
 ; FILE REFERENCE: JHU1670-1
 ; CURRENT APPLICATION NUMBER: US/09/969, 520A
 ; CURRENT FILING DATE: 2002-06-04
 ; PRIORITY APPLICATION NUMBER: US 60/235, 153
 ; PRIOR FILING DATE: 2000-09-22
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 437
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Altered sonic hedgehog protein
 ; US 09-969-520A-4
 ;
 ; Query Match 99 %; Score 2270; DB 9; Length 437;
 ; Best Local Similarity 99.1%; Pred. No. 1.4e-195; Matches 433; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 ; Matches 434; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 ;
 Qy 1 MLLARCLIVLASSLLVCPGLACGPFGFGKRRHPKKLTPLAYKQIPNVAEKTGAS 60
 Db 1 MLLARCLIVLASSLLVCPGLACGPFGFGKRRHPKKLTPLAYKQIPNVAEKTGAS 60
 Qy 61 GRYGKIKRNSEPKELTNPYNPDTIKDEENTGADRMLTORCKDKLNLALASVMNQPG 120
 Db 61 GRYGKIKRNSEPKELPYNPDIFKDAENTGADRMLTORCKDKLNLALASVMNQPG 120
 Qy 121 VRLVTEGDEGHSEESLHYSGRAVDTTSRDRSKYGMALARLAVAGEDFDWVYESKA 180
 Db 121 VKLRVTEGDEGHSEESLHYSGRAVDTTSRDRSKYGMALARLAVAGEDFDWVYESKA 180
 Qy 181 HIHSVKAENSAVAKSGGGPPGSATVHLEQGGTKLVKDLRPGDVLADDQGRILYSDFL 240
 Db 181 HIHSVKAENSAVAKSGGGPPGSATVHLEQGGTKLVKDLRPGDVLADDQGRILYSDFL 240
 Qy 241 TFLDRDEGAKKVVFVIELEPRERLLTAHLIFVAPHDNSGTPGPSALFASRVPCQR 300
 Db 241 TFLDRDEGAKKVVFVIELEPRERLLTAHLIFVAPHDNSGTPGPSALFASRVPCQR 300
 Qy 301 VVVAERGDRRLPAAMVSUTREEEAGAYAPATHTAHLIFVAPHDNSGTPGPSALFASRVPCQR 360
 Db 301 VVVAERGDRRLPAAMVSUTREEEAGAYAPATHTAHLIFVAPHDNSGTPGPSALFASRVPCQR 360
 ;
 ; RESULT 15
 ; US-09-969-520A-8
 ; Sequence 8 Application US/09969520A
 ; Patent No. US20030177163A1
 ; GENERAL INFORMATION:
 ; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
 ; APPLICANT: BEACHY, PHILIP A.
 ; TITLE OF INVENTION: METHOD OF USE OF SONIC HEDGEHOG PROTEIN AS A LIGAND FOR PATCHED
 ; FILE REFERENCE: JHU1670-1
 ; CURRENT APPLICATION NUMBER: US/09/969, 520A
 ; CURRENT FILING DATE: 2002-06-04
 ; PRIORITY APPLICATION NUMBER: US 60/235, 153
 ; PRIOR FILING DATE: 2000-09-22
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 8
 ; LENGTH: 437
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Altered sonic hedgehog protein
 ; US-09-969-520A-8
 ;
 ; Query Match 99.0%; Score 2266; DB 9; Length 437;
 ; Best Local Similarity 99.1%; Pred. No. 1.4e-195; Matches 433; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 ; Matches 434; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 ;
 Qy 1 MLLARCLIVLASSLLVCPGLACGPFGFGKRRHPKKLTPLAYKQIPNVAEKTGAS 60
 Db 1 MLLARCLIVLASSLLVCPGLACGPFGFGKRRHPKKLTPLAYKQIPNVAEKTGAS 60
 Qy 61 GRYGKIKRNSEPKELTNPYNPDTIKDEENTGADRMLTORCKDKLNLALASVMNQPG 120
 Db 61 GRYGKIKRNSEPKELPYNPDIFKDAENTGADRMLTORCKDKLNLALASVMNQPG 120
 Qy 121 VRLVTEGDEGHSEESLHYSGRAVDTTSRDRSKYGMALARLAVAGEDFDWVYESKA 180
 Db 121 VKLRVTEGDEGHSEESLHYSGRAVDTTSRDRSKYGMALARLAVAGEDFDWVYESKA 180
 Qy 181 HIHSVKAENSAVAKSGGGPPGSATVHLEQGGTKLVKDLRPGDVLADDQGRILYSDFL 240
 Db 181 HIHSVKAENSAVAKSGGGPPGSATVHLEQGGTKLVKDLRPGDVLADDQGRILYSDFL 240
 Qy 241 TFLDRDEGAKKVVFVIELEPRERLLTAHLIFVAPHDNSGTPGPSALFASRVPCQR 300
 Db 241 TFLDRDEGAKKVVFVIELEPRERLLTAHLIFVAPHDNSGTPGPSALFASRVPCQR 300
 Qy 301 VVVAERGDRRLPAAMVSUTREEEAGAYAPATHTAHLIFVAPHDNSGTPGPSALFASRVPCQR 360
 Db 301 VVVAERGDRRLPAAMVSUTREEEAGAYAPATHTAHLIFVAPHDNSGTPGPSALFASRVPCQR 360
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 ; Search completed: February 20, 2003, 10:14:42
 ; Job time : 8.84443 secs

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Om protein - protein search, using sw model

Run on: February 20, 2003, 10:06:28 ; Search time 28.1092 Seconds

(without alignments)

3203.314 Million cell updates/sec

Title: US-09-827-110a-13

Perfect score: 2289

Sequence: 1 MILLARCFLVILASSLLVC.....CTWLIDSETMHPLGMKVS 437

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp Rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: spUnclassified:*
- 15: sp_virus:*
- 16: sp_bacteria:*
- 17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	1537.5	67.2	434	13	057404
2	1451.4	63.4	414	13	09W709
3	1326	57.9	406	13	057567
4	1132.5	49.5	415	5	090526
5	1063.5	46.5	442	13	073803
6	1040.5	45.5	447	5	09GRAB
7	915.5	40.0	410	5	061676
8	842.5	36.8	161	11	09R179
9	736.2	32.2	150	13	09YGV7
10	732.0	32.0	6	13	09XSI6
11	710.0	31.0	139	13	Q9W6C1
12	698.0	30.5	177	11	Q9WW29
13	628.5	27.4	5	13	096699
14	528.2	23.1	199	13	08QGM4
15	22.9			13	042128
16				13	Oryzias lat

QY	2	LILLARCFVLVILASSLLVCPCGLACGPGGRGGPKRRHPPKKLTPPLAYKQFIPNVAEKTGLGASG	61
Db	4	MILRRDPLGGFISTLVPLGLUGPGKGRRRPRQKLTPLAYKQFPNVSETLGASG	63
QY	62	RVEGKTRNSERKELTPTNYPDTIKDEENTGADRMLTORKDKLNALATSYNQWPGV	121
Db	64	RVEGKTRNSERKELTPTNYPDTIKDEENTGADRMLTORKDKLNALATSYNQWPGV	123
QY	1	MILWTRIVLAGVICLSLVSAGMCGPGGRGYGRRHPRKLTPPLAYKQFIPNVAEKTGLGASG	60
Db	1	MILWTRIVLAGVICLSLVSAGMCGPGGRGYGRRHPRKLTPPLAYKQFIPNVAEKTGLGASG	60
QY	2	LILLARCFVLVILASSLLVCPCGLACGPGGRGGPKRRHPPKKLTPPLAYKQFIPNVAEKTGLGASG	61
Db	122	RLRVTEGWDGHSERSESLHYEGRAVDITTSDRSKYGMARLAVEAGFDWVYESKAH	181
Db	124	KLRVTEGWDGHSSEESLHYEGRAVDITTSDRSKYGMARLAVEAGFDWVYESKAH	183
QY	182	IHCSYKAENSAAKSGCCFGPSATVHLEGGTKLVKUDLRPGRVLAADDQGRLLSDFT	241
Db	184	IHCSYKAENSAVYKSGCCFGPSATVHLEGGTKLVKUDLRPGRVLAADDQGRLLSDFT	243
QY	242	FDRDEGAKKVVFVIELEPERLILTAHHLFVAPHMNSGPNPG-----SALF	291
Db	244	FDRDEGAKKVVFVIELEPERLILTAHHLFVAPHMNSGPNPG-----SALF	291
QY	292	ASRVYRGSRQYYWAERGSDRRLPAVAVSHVTEEEAGAYAVALTAHGTLINRYLASWA	351
Db	304	ASVRPGHHRV-LTEDREG-RGLREATAVDVRYL-EEATGAYAVALTAHGTLINRYLASWA	360
QY	352	VTEEHSMRAFAFPRLAHALLAALAPARTDGCGGSPIAAQOSATEARGAEPAGIHWY	411
Db	361	VTEEHSMRAFAFPRLGVYFLSFSPODYSHS---PPAPSQAE-----GHWMS	408
QY	412	OQYHIGWTWLDSETMHPGMAYKSS	437
Db	409	ELYRIGCWWLQADTIHPLGMAKSS	434
RESULT 2			
QW709			
ID	QW709	PRELIMINARY;	PRY;
RP	09W709		414 AA.
AC	09W709;		
DT	01-NOV-1999	(TREMBREL. 12, Created)	
DT	01-MAR-2002	(TREMBREL. 20, Last annotation update)	
DE	Sonic hedgehog.		
GN			
OS	Paralichthys olivaceus (Flounder)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Euteleosteii; Neoteleosteii;		
OC	Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;		
OC	Pleuronectoidei; Paralichthyidae; Paralichthys.		
OR	NCBI_TAXID=8255;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RN	MEDLINE=9928226; PubMed=10223710;		
RA	Suzuki T., Ichiro O., Kurokawa T.		
RT	"Retinoic acid given at late embryonic stage depresses sonic hedgehog and Hoxd-4 expression in the pharyngeal area and induces skeletal malformation in flounder (<i>Paralichthys olivaceus</i>) embryos."		
RT	Growth Differ. 41:143-152(1999).		
RL	Dev. Growth Differ. 41:143-152(1999).		
DR	EMBL: AB029448; BAA82360.1; -.		
DR	HSSP: Q62266; IVHH.		
DR	MEROPS: C46_001; -.		
DR	InterPro: IPR0167; Hedgehog_hint.		
DR	InterPro: IPR05386; Hedgehog_hintC.		
DR	InterPro: IPR03587; Hedgehog_hintN.		
DR	InterPro: IPR000320; HH_signal.		
DR	InterPro: IPR02203; Intein.		
DR	InterPro: IPR001657; SonICHH.		
DR	Pfam: PF01085; HH_signal; I.		
DR	Pfam: PF01079; Hint; I.		
DR	PRINTS: PR00632; SONICHHOG.		
DR	PRODOM: PD003042; HH_Signal; I.		
DR	SMART: SM00305; HinC; I.		
DR	SMART: SM00306; HinN; I.		
SEQUENCE	414 AA;	45945 MW;	50607BR3DB7C0DA3 CRC64;
RESULT 3			
QW757			
ID	057567	PRELIMINARY;	PRY;
RP	057567		406 AA.
AC	057567;		
DT	01-JUN-1998	(TREMBREL. 06, Created)	
DT	01-JUN-2002	(TREMBREL. 21, Last annotation update)	
DE	Hedgehog segment polarity homolog.		
OS	Notophthalmus viridescens (Eastern newt) (<i>Triturus viridescens</i>)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;		
OC	Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;		
OC	Noptophthalmus.		
OX	NCBI_TaxID=8316;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Stark D.R., Gates P.B., Brockes J.P., Farretti P.;		
RT	"Hedgehog homologue from <i>Notophthalmus viridescens</i> ."		
RL	Dev. Dyn. 0:0-0(1998).		
CC	-1 SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE PHOSPHORYLTRANSFERASE FAMILY.		
DR	EMBL: AF07466; AAC03108.1; -.		
DR	HSSP: Q62266; IVHH.		
DR	InterPro: IPR0167; Hedgehog_hint.		
DR	InterPro: IPR03586; Hedgehog_hintC.		
DR	InterPro: IPR003587; Hedgehog_hintN.		
DR	InterPro: IPR000320; HH_signal.		
DR	InterPro: IPR02203; Intein.		
DR	InterPro: IPR001657; SonICHH.		
DR	Pfam: PF01085; HH_signal; I.		
DR	Pfam: PF01079; Hint; I.		
DR	PRINTS: PR00632; SONICHHOG.		
DR	PRODOM: PD003042; HH_Signal; I.		
DR	SMART: SM00305; HinC; I.		
DR	SMART: SM00306; HinN; I.		
DR	PROSITE: PS00013; PUR_PYR_TRANSFER; I.		

KW GLYCOSYLTRANSFERASE; Transferase.
SQ SEQUENCE 406 AA; 45072 MW; 5842CCAD5314D4D0 CRC64;

Query Match 57.9%; Score 1326; DB 13; Length 406;
Best Local Similarity 62.3%; Pred. No. 1.7e-98; No. of Mismatches 89; Indels 27; Gaps 8;
Matches 268; Conservative 41; Mismatches 89; Indels 32; Gaps 6;

Qy 4 LLARCFLYLASSILVCPG-LAGGGPGFGKRRHKKLTPLAKQFIPNVAEKTGLASGR 62
Db 3 LLLPLPLAVACALLIGGGPGALGCGCPGRVIGRPRPRLPLSKQFLPHPEKTLGASGR 62

Qy 63 YEKITRISEREFELTPYNPDIKFDEENTGADRMLMQRCOKDKLNALAISTMQNQWGV 122
Db 63 YEKICKIARNSEREFELTPYNPDIKFDEENTGADRMLMQRCOKDKLNALAISTMQNQWGVK 122

Qy 123 LRYTVEGWDGHISEESLHYEGRAVDTTSDRSKYGMALARAVEAGFDWVYYESKAHI 182
Db 123 LRTEGWDGHIDESLHYEGRAVDTTSDRDKYGMALARAEAGFDWVYYESKAHI 182

Qy 183 HCSVKAENSAAKSGGCCPGSATVHLEOGGTKLVKLDLPGDRYLAADDQGRLLYSDFL 242
Db 183 HCSVKESEHSAAKKGCGCPARALATLESGEKIDTIADELPGRHVLCDMDEGGRRTYSDFL 242

Qy 243 LDDEGAKKVYVIELEPRERLLTAAHLFVAPHNDSGPPGSAFSLAFSRVRPQGVY 302
Db 243 LDPUSTAVKFEVYVETOPRPRRALTAAHLFVA-DNEPTVPLDEFSTVEASHVQPGO-- 299

Qy 303 VVERGGDRRLPAVHSVTLREEEAGAYAPLTAHTGTLINRVLASCYAVIEHSAWA 362
Db 300 ILTE-GVLGQLPARVSVT-TQTDGAYAPLTSHTSHGTLVDDVVSCFAVQKHOLA 356

Qy 363 FAFRLAHLAAALAPARTDGGGGSIPAAQSATEARGAEPTAGTHWYQOLYHGTWLL 422
Db 357 FWPLRLYHSV-----GRPETQPEGMHWSLLYRLGVLL 391

Qy 423 DSIITMHPLGM 432
Db 392 MKBQFHPPGM 401

RESULT 4
091526 PRELIMINARY; PRT; 415 AA.
ID 091526 ID 01499 PRELIMINARY; PRT; 415 AA.
AC 091526 AC 01499; PRELIMINARY; PRT; 415 AA.
DT 01-MAY-2000 DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-DEC-2001 DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-JUN-2002 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Hedgehog protein.
GN HEDGEHOG.
OS Branchiostoma belcheri (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
NCBI_TAXID=1;

[1]
RP SEQUENCE FROM N.A.
RA Mao B., Zhang Y., Zhang H.;
RT "A preliminary study on Qingdao amphioxus hedgehog gene.";
RL Submitted (Sep-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: AU245812; CAB5812; 2.

HSSP: Q62265; 1VHH.
InterPro: IPR001767; Hedgehog_hint.
InterPro: IPR00356; Hedgehog_hintC.
InterPro: IPR00357; Hedgehog_hintN.
InterPro: IPR002203; Intein.
InterPro: IPR001657; SonichH.
Pfam: PF01085; HH_Signal; 2.
DR PRINTS; PR00532; SONICHHOG.
DR InterPro; IPR00357; Hedgehog_hintN.
DR InterPro; IPR00350; HH_Signal; 1.
DR SMART; SM00305; HHNC; 2.
DR SMART; SM00306; HHNTN; 1.
SQ SEQUENCE 415 AA; 46765 MW; 5B8D2BD215BD931 CRC64;

Query Match 49.5%; Score 1132.5; DB 5; Length 415;
Best Local Similarity 53.7%; Pred. No. 6.8e-83; No. of Mismatches 116; Indels 27; Gaps 8;
Matches 231; Conservative 56; Mismatches 116; Indels 27; Gaps 8;

Qy 4 LLARCFLYLASSILVCPG--PGIACGPORGFGKRRHKKLTPLAKQFIPNVAEKTGLASGR 60
Db 4 VLRMMWVIVAITALGTHWGPSEACGFCOTRIGRRRPRKLTPTVQOMPAVSENTFGS 63

Qy 61 GRYEGKIKTRNSEREFELTPYNPDIKFDEENTGADRMLMQRCOKDKLNALAISTMQNQWGV 120
Db 64 GLFNGRGRIDSERFTLQKNFNIDIRDEEKIGADRMTOCKDKLNALAISTMQNQWEG 123

Qy 121 VRLVTEGWDGHISEESLHYEGRAVDTTSDRSKYGMALARAVEAGFDWVYYESKA 180
Db 124 VKLRTVEGWDGHEDCFHTEBSLHYEGRAVDTTSDRDKYGMALARAVEAGFDWVYYESKA 183

Qy 181 HCSVKAENSAAKSGGCCPGSATVHLEOGGTKLVKLDLPGDRYLAADDQGRLLYSDFL 240
Db 184 HCSVKAENSAAKSGGCCPGSATVHLEOGGTKLVKLDLPGDRYLAADDQGRLLYSDFL 243

Qy 241 TFLDRDEGAKKVYVIELEPRERLLTAAHLFVAPHND-SGTPERSALASRVRPQ 299
Db 244 TFMQRDSRGCPWPWVYTIKEDRNITVATPSHLVFTVRSRDLSPR---VAKRMSDVRGE 300

Qy 300 RVVVAERGGDRRLPAVHSVTLREEEAGAYAPLTAHTGTLINRVLASCYAVIEHSA 359
Db 301 FLLTPESDGGER--KVEIVSVYMEER-KAYAPLTVHGTWVYDVNAMSYALIESALA 357

Qy 360 HRAFAPFRALAAALAPARTDGGGGSIPAAQSATEARGAEPTAGTHWYQOLYHGT 419
Db 358 HWTFAPEFLYVQTSL---WDG---PSHDQTLQ----EGVHWYPSFFYRYI 400

Qy 420 WLJLSETMPHP 429
Db 401 SLVEPTLHP 410

RESULT 5
01499 ID 01499 PRELIMINARY; PRT; 415 AA.
AC 01499; PRELIMINARY; PRT; 415 AA.
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Amphiph. protein.
OS Branchiostoma floridae (Florida lancelet) (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
OX NCBI_TAXID=7739;
RN [1]
RP SEQUENCE FROM N.A.
RA Shmield S.M.;
RT "Sequence and expression of an amphioxus hedgehog gene.";
RL Submitted (Jun-1997) to the EMBL/GenBank/DDBJ databases.
DR EMBL: Y13858; CAA74169.1; -.
DR HSSP: Q62265; 1VHH.
DR InterPro: IPR001767; Hedgehog_hint.
DR InterPro: IPR00356; Hedgehog_hintC.
DR InterPro: IPR00357; Hedgehog_hintN.
DR InterPro: IPR003587; Hedgehog_hintN.
DR InterPro: IPR003597; HH_Signal.
DR InterPro: IPR002203; Intein.
DR InterPro: IPR001657; SonichH.
DR Pfam: PF01079; HH_Signal; 1.
DR PRINTS; PR00532; SONICHHOG.
DR Prodom: PD00342; HH_Signal; 1.
DR SMART; SM00305; HHNC; 1.
DR SMART; SM00306; HHNTN; 1.
SQ SEQUENCE 415 AA; 46765 MW; 5B8D2BD215BD931 CRC64;

Query Match 49.1%; Score 1124.5; DB 5; Length 415;

Best Local Similarity 53.7%; Pred. No. 3e-82; Matches 231; Conservative 53; Mismatches 119; Indels 27; Gaps 8;					
Qy 4 LARCFIVILASLLSLVCG--PGLACPGPGKRRPKPLTPNPKDDEENTGADRUMTQCKDKLNAISVMQPG 60					
Db 4 VLRWAVTLYVLSALCATHWGSEACPGGRGRKRPLPPVQMPAVSNTFGAS 63					
Qy 61 GRYEGKTRNSERKEELTPNPNPDIKFDEENTGADRUMTQCKDKLNAISVMQPG 120					
Db 64 GLFNGRITRDSERFHFLKONETDILFKDEEKTGADEPMTORCKOKLNALAISVNQWEG 123					
Qy 121 VRLRVTEGWDGDFHHSSEESLHYEGRADITTSDRDSKYGMALARJAVEAGEDDWVYYESKA 180					
Db 124 VKLRVTEGWDGDFHHSSEESLHYEGRADITTSDRDSKYGMALARJAVEAGEDDWVYYESKA 183					
Qy 181 HIHCSYKAESDITATGGCFRAESWTRDNRIRAKDVRGDKVLSMDSGHGPVSEVL 240					
Db 184 HIHCSYKAESDITATGGCFRAESWTRDNRIRAKDVRGDKVLSMDSGHGPVSEVL 243					
Qy 241 TFLDRDEGAKKVVFVYIETLERRERLTLAAHLFVAPHN- SGPPGPGSALFASVRPGQ 299					
Db 244 TMFDRESRSPGVWVYTIHTDDRNITVATPSHLVFTESRDLSSPR---IAKFMSPDRGE 300					
Qy 300 RVVYVAERGGDRRLPAVHSVTREAGAYAPLAHTAHTLILNRLVASCYAVIEHWSA 359					
Db 301 FLLTPPSDGGCFR--RKVIVSYTMREK-GAYAPLIVHGTWVDVAMSQYALISQALA 357					
Qy 360 HRAFAFPRLAHALLAALAPARDGGGGGSITPAASATEARGAEPAGTHMYSQOLYHIGT 419					
Db 358 HWWFAFPRLYVQITSSL---WDG ---PSHDQLQ----EGVHWPSPFIFYRGYI 400					
Qy 420 WILDSETMHP 429					
Db 401 SLEVEPTLHHP 410					
RESULT 6					
073803 PRELIMINARY; PRT; 442 AA.					
AC 073803; 01-AUG-1998 (TREMBrel. 07, Created)					
DT 01-AUG-1998 (TREMBrel. 07, Last sequence update)					
DT 01-JUN-2002 (TREMBrel. 21, Last annotation update)					
DE Fugu hedgehog.					
GN FHH.					
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).					
OC Euteleostomi; Actinopterygii; Neopterygii; Telostei; Buteleostei; Neoteleostei; Tetradontidae; Takifugu.					
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; OX NCBI_Taxid=3103;					
RN [1] SEQUENCE FROM N.A.					
RP MEDLINE=99177347; PubMed=10077531;					
RX Gellner K., Bremer S.; "Analysis of 148 kb of genomic DNA around the wnt1 locus of Fugu rubripes"; Genome Res. 9:251-258(1999).					
RX EMBL: AF056116; AAC34384.1; -.					
DR HSSP: Q62226; IYHH.					
DR InterPro; IPR001767; Hedgehog_hint.					
DR InterPro; IPR003586; Hedgehog_hintC.					
DR InterPro; IPR003587; Hedgehog_hintN.					
DR InterPro; IPR00320; HH_Signal.					
DR InterPro; IPR002203; Intein.					
DR Pfam; PF01085; HH_signal; 1.					
DR Pfam; PF01079; HH_Signal; 1.					
DR Prodrom; PPD003042; HH_Signal; 1.					
DR SMART; SM00305; HincC; 1.					
DR SMART; SM00306; Hinc; 1.					
SO SEQUENCE 442 AA; 49286 MW; 1CB2B423B4748E8 CRC64;					
Query Match 46.5%; Score 1063.5; DB 13; Length 442;					
Best Local Similarity 51.2%; Pred. No. 2.7e-77; Matches 230; Conservative 60; Mismatches 128; Indels 31; Gaps 12;					
Qy 5 LARCFIVILAS-SLV--CPGL--ACGGPGCGKRRPKPLTPNPKDDEENTGADRUMTQCKDKLNAISVMQPG 118					
Db 61 ASGRAGKTRNSERNEELCNYPDIDVDEENTNADPMTORCKDCLNRLALAVMQN 120					
Qy 119 PGVLRLVTEGDEDGHHSSEESLHYEGRADITTSDRDSKYGMALARJAVEAGEDDWVYYESKA 178					
Db 121 PGVLRLVTEAEDGHIPPSSLYHGRADITTSDRDSKYGMALARJAVEAGEDDWVYHYES 180					
Qy 179 KAHICSVKAENSAVAKSGCCFGSATVHPLKGKLUVKLURGCRVLAADDQGRLLSY 238					
Db 181 KYHICSVKAENSAVAKSGCCFGSATVHPLKGKLUVKLURGCRVLAADDQGRLLSY 240					
Qy 239 FLTFLDREGAKKVVFVYIETLERRERLTLAAHLFVAPHN- SGPPGPGSALFASVRPGP- SALFASVRP 297					
Db 241 VLFLLRDPSEWRWELSLQT-EDGRLLAVPHYIFSDAH--CGDSSQVOAOFASRAQT 297					
Qy 298 GQVYVAERGGDRRLPAVHSVTREENGAYAPLAHTAHTLILNRLVASCYAVIEHWSA 357					
Db 298 GTCV-LVHTAGGE- VHPSRIVSIT-EESVGAYAPLTAEGTAGSNSVFDGLVASSYALVEDHQ 353					
Qy 358 WAHRAPAPRLAHAA--LLAALAPARTDG-----GGGSIAPAASATEARGAEP 403					
Db 354 LAHWARGPVRIILSSYSQLMAREPEERSDGKTPLOPHALYGRDRKVCARNISTVSREAGO 413					
Qy 404 --TAGIHWMSQOLYHIGTWILDSETMHP 429					
Db 414 RGRTSEVHWYAQOLLHRLGWIVLNPDLFHP 442					
RESULT 7					
073803 OGRAB PRELIMINARY; PRT; 447 AA.					
AC 073803; 01-MAR-2001 (TREMBrel. 16, Created)					
DT 01-MAR-2001 (TREMBrel. 16, Last sequence update)					
DT 01-JUN-2002 (TREMBrel. 21, Last annotation update)					
DE Hedgehog protein (Fragment).					
OS Gryllus bimaculatus (two-spotted cricket).					
OC Bokaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Grylinae; Gryllus.					
OC Gryllidae; Gryllus.					
OC NCBI_Taxid=6999;					
RP SEQUENCE FROM N.A.					
RX MEDLINE=2046115; Pubmed=11003837;					
RX Niwa N., Inoue Y., Nozawa A., Saito M., Misumi Y., Ohuchi H., Yoshikawa H., Noji S.; "Correlation of diversity of leg morphology in Gryllus bimaculatus (cricket) with divergence in dpp expression pattern during leg development.", Development 127: 4373-4381(2000).					
RT EMBL: AB044709; BAB19658.1; -.					
DR HSSP: Q62226; IYHH.					
DR InterPro; IPR01767; Hedgehog_hint.					
DR InterPro; IPR003586; Hedgehog_hintC.					
DR InterPro; IPR003587; Hedgehog_hintN.					
DR InterPro; IPR00320; HH_Signal.					
DR InterPro; IPR002203; Intein.					
DR Pfam; PF01085; HH_Signal; 1.					
DR Pfam; PF01079; HH_Signal; 1.					
DR Prodrom; PPD003042; HH_Signal; 1.					
DR SMART; SM00305; HincC; 1.					
DR SMART; SM00306; Hinc; 1.					
SO SEQUENCE 447 AA; 48008 MW; 29AFB061C3EE6F0 CRC64;					

Query Match	45.5%	Score 1040.5; DB 5; Length 447;	Db 14 ITTACCLINLTQACHPGRS-GKTSRPRNRTPLQYKQWPNTSDFGASGPPEGRIDR 72
Best Local Similarity	54.1%	Pred. No. 1.9e-75; Indels 25; Gaps 9;	Db 71 SERKELTPNYNPDLIFIDEENTGADRMTORCKDKLNALATSYMNOQPGVRURVTEGWD 130
Matches	225;	Conservative 45; Mismatches 121;	Db 73 DERISKLSNNNDIVFDEEGTGADRMTORCKDKLNALATSYMNOQPGVRURVTEGWD 132
DR	4	LLARCFLVLASSILVCPCGLACCPGRCRGKRRRKRLPLAYQFIPNVAEKTIGASRY 63	Db 73 DERISKLSNNNDIVFDEEGTGADRMTORCKDKLNALATSYMNOQPGVRURVTEGWD 132
Qy	17	LLARWLLL--LMQGAARRACSGPGRGAGRRRSLPLVFOHNPVNSEHTLGAGPA 73	Db 73 DERISKLSNNNDIVFDEEGTGADRMTORCKDKLNALATSYMNOQPGVRURVTEGWD 132
Db	64	EKGKTRNSERFKELTPNYNPDLIFIDEENTGADRMTORCKDKLNALATSYMNOQPGVRURVTEGWD 123	Db 133 ED-OPNVEPLHAGCRAVDTTSRDKNNYKGLARLAVEGFDWVYETRGHH 193
Qy	74	ERRVARDDERFRDIDVPNPKADIVFDEEGTGADRMTORCKDKLNALATSYMNOQPGVRUL 133	Db 191 SVAAKSGGGPPGSATVHLQGKTLKLDRPGDR-VLAADDQGRLLYSDFLTF 242
Qy	124	RVTEGWDDEGHHSSESILHYEGRADITTSRDRSKYGMALARLAVEAGEDDWVYESKAITH 183	Db 192 AAKNSGGGPPGSATVHLQGKTLKLDRPGDR-VLAADDQGRLLYSDFLTF 242
Db	134	RVTEGWDDEBGHHAADSLHYEGRADITTSRDRSKYGMALARLAVEAGEDDWVYESKAITH 183	Db 133 ED-OPNVEPLHAGCRAVDTTSRDKNNYKGLARLAVEGFDWVYETRGHH 193
Qy	184	CSVIKAEVSAAKSGCFCPSATVHLQGKTLKLDRPGDR-VLAADDQGRLLYSDFLTF 242	Db 191 SVAAKSGGGPPGSATVHLQGKTLKLDRPGDR-VLAADDQGRLLYSDFLTF 242
Db	194	CSVKESSESSOAAKSGCFAESTVQ-TPGGLCALAELRVRGAGAGPGHGRFLSPVLF 252	Db 252 TLFWVIEET-EDKTVIOLTOPLHIVSEREN- FDQSRAVFASEVRTNQFVTTAQ NHD 307
Qy	243	LDRDEGAKKVYFTETLEPRERLITAHLFLVAPHNDSGPTPGPSALFAFSRVRPGQRY 302	Db 308 RGVRPMKVVSVTRLGH-AVAPVTRQGSLVQGVSSYAVRDEWAHASPAIRWY 366
Db	253	LDRPAP-APTRLVRVTASGR-TIALTPSHLPPARAGGG---EPEARADAVRPGDALL 306	Db 371 ALLALAPARTDGGGGSTPAAGSATEARGAEPAGIHWYSOLYHICWTWLSETMP 429
Qy	303	WVERRGGDRRLPAVHSVTLREAGAYAPLTAHGTLINRVLASCYAVIEHSAWAHAFPLAH 362	Db 367 YISHMLGITDTDG-----QEQR-----VHWTOGLYKLUKYM-SDRIP 406
Db	307	VADAGGAVR-PDPRVHYDAEANRGGVVAPLTAHGTLINRVLASCYAVIEHSAWAHAFPLAH 364	Db 367 YISHMLGITDTDG-----QEQR-----VHWTOGLYKLUKYM-SDRIP 406
Qy	363	FAPPRLAHALLAALAPARTDGGGGSTPAAGSATEARGAEPAGIHWYSOLYHICWTWLSETMP 418	Db 367 YISHMLGITDTDG-----QEQR-----VHWTOGLYKLUKYM-SDRIP 406
Db	365	FAPPVRWAWHLTA-----WGHAAPOVYAHPPPAPARA--POVHWYAKALYSLG 408	Db 367 YISHMLGITDTDG-----QEQR-----VHWTOGLYKLUKYM-SDRIP 406
RESULT 8			
ID	061676	PRELIMINARY; PRT; 410 AA.	Db 09R179 PRELIMINARY; PRT; 161 AA.
AC	061676;		Db 09R179; PRELIMINARY; PRT; 161 AA.
DT	01-AUG-1998	(TREMBLrel. 07, Created)	Db 09R179; PRELIMINARY; PRT; 161 AA.
DT	01-AUG-1998	(TREMBLrel. 07, Last sequence update)	Db 09R179; PRELIMINARY; PRT; 161 AA.
DE	Hedgehog.		Db 09R179; PRELIMINARY; PRT; 161 AA.
OS	Lytechinus variegatus (Sea urchin).		Db 09R179; PRELIMINARY; PRT; 161 AA.
OC	Eukaryota; Metazoa; Echinodermata; Echinida; Echinoidea; Euechinoidea; Echinacea; Temnopleuroidea; Toxopneustidae; Lytechinida; Lytechinidae.		Db 09R179; PRELIMINARY; PRT; 161 AA.
OX			Db 09R179; PRELIMINARY; PRT; 161 AA.
RN	[1]	SEQUENCE FROM N.A.	Db 09R179; PRELIMINARY; PRT; 161 AA.
RP			Db 09R179; PRELIMINARY; PRT; 161 AA.
RC			Db 09R179; PRELIMINARY; PRT; 161 AA.
RA			Db 09R179; PRELIMINARY; PRT; 161 AA.
RT			Db 09R179; PRELIMINARY; PRT; 161 AA.
RL			Db 09R179; PRELIMINARY; PRT; 161 AA.
RP			Db 09R179; PRELIMINARY; PRT; 161 AA.
SEQUENCE FROM N.A.			Db 09R179; PRELIMINARY; PRT; 161 AA.
RA			Db 09R179; PRELIMINARY; PRT; 161 AA.
RT			Db 09R179; PRELIMINARY; PRT; 161 AA.
RL			Db 09R179; PRELIMINARY; PRT; 161 AA.
RP			Db 09R179; PRELIMINARY; PRT; 161 AA.
SEQUENCE FROM N.A.			Db 09R179; PRELIMINARY; PRT; 161 AA.
RA			Db 09R179; PRELIMINARY; PRT; 161 AA.
RT			Db 09R179; PRELIMINARY; PRT; 161 AA.
RL			Db 09R179; PRELIMINARY; PRT; 161 AA.
RP			Db 09R179; PRELIMINARY; PRT; 161 AA.
SEQUENCE FROM N.A.			Db 09R179; PRELIMINARY; PRT; 161 AA.
RA			Db 09R179; PRELIMINARY; PRT; 161 AA.
RT			Db 09R179; PRELIMINARY; PRT; 161 AA.
RL			Db 09R179; PRELIMINARY; PRT; 161 AA.
RP			Db 09R179; PRELIMINARY; PRT; 161 AA.
SEQUENCE FROM N.A.			Db 09R179; PRELIMINARY; PRT; 161 AA.
RA			Db 09R179; PRELIMINARY; PRT; 161 AA.
RT			Db 09R179; PRELIMINARY; PRT; 161 AA.
RL			Db 09R179; PRELIMINARY; PRT; 161 AA.
RP			Db 09R179; PRELIMINARY; PRT; 161 AA.
SEQUENCE FROM N.A.			Db 09R179; PRELIMINARY; PRT; 161 AA.
RA			Db 09R179; PRELIMINARY; PRT; 161 AA.
RT			Db 09R179; PRELIMINARY; PRT; 161 AA.
RL			Db 09R179; PRELIMINARY; PRT; 161 AA.
RP			Db 09R179; PRELIMINARY; PRT; 161 AA.
SEQUENCE FROM N.A.			Db 09R179; PRELIMINARY; PRT; 161 AA.
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RP			Db 09R179; PRELIMINARY; PRT; 161 AA.
SEQUENCE FROM N.A.			Db 09R179; PRELIMINARY; PRT; 161 AA.
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RT			Db 09R179; PRELIMINARY; PRT; 161 AA.
RL			Db 09R179; PRELIMINARY; PRT; 161 AA.
RP			Db 09R179; PRELIMINARY; PRT; 161 AA.
SEQUENCE FROM N.A.			Db 09R179; PRELIMINARY; PRT; 161 AA.
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RT			Db 09R179; PRELIMINARY; PRT; 161 AA.
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RP			Db 09R179; PRELIMINARY; PRT; 161 AA.
SEQUENCE FROM N.A.			Db 09R179; PRELIMINARY; PRT; 161 AA.
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SEQUENCE FROM N.A.			Db 09R179; PRELIMINARY; PRT; 161 AA.
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SEQUENCE FROM N.A.			Db 09R179; PRELIMINARY; PRT; 161 AA.
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SEQUENCE FROM N.A.			Db 09R179; PRELIMINARY; PRT; 161 AA.
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RT			Db 09R179; PRELIMINARY; PRT; 161 AA.
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SEQUENCE FROM N.A.			Db 09R179; PRELIMINARY; PRT; 161 AA.
RA			Db 09R179; PRELIMINARY; PRT; 161 AA.
RT			Db 09R179; PRELIMINARY; PRT; 161 AA.
RL			Db 09R179; PRELIMINARY; PRT; 161 AA.
RP			

Db 121 AGEDWVYVESKAHICCSV 138
 RESULT 13
 Q9WV29 PRELIMINARY; PRT; 177 AA.
 AC 09WV29; DR
 DT 01-NOV-1999 (TREMBIrel. 12, Created)
 DT 01-MAY-1999 (TREMBIrel. 12, Last sequence update)
 DT 01-MAR-2002 (TREMBIrel. 20, Last annotation update)
 DE Indian hedgehog protein (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TAXID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=KIDNEY;
 RA Garges P.L., Meyer R.A. Jr., Brown C.A., Price D.K.;
 RT "Indian hedgehog in rat." Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF162914; AAC45372.1; -.
 DR HSSP; 052226; 1VHH
 DR MEROPS; C46.003; -.
 DR InterPro; IPR01767; Hedgehog_hint.
 DR InterPro; IPR00387; Hedgehog_hintN.
 DR InterPro; IPR001657; SonichH.
 DR Pfam; PF01085; HH_signal; 1.
 DR Pfam; PF01079; Hint; 1.
 DR PRINTS; PR00532; SONICHIOG.
 DR PRODOM; PDO03042; HH_signal; 1.
 DR SMART; SM0306; HINTN; 1.
 FT NON-TER 177 AA; 19739 MW; CA5871626A565F65 CRC64;
 SQ SEQUENCE 177 AA: ...
 Query Match 30.5%; Score 698; DB 11; Length 177;
 Best Local Similarity 73.4%; Pred. No. 1.9e-48;
 Matches 130; Conservative 17; Mismatches 30; Indels 0; Gaps 0;
 Qy 98 LMPIORCKDKMLNALAISVANQWPGVSKYRLRVTEGWDGHISEESLHYEGRAVDITSDRRS 157
 Db 1 LMPIORCKDKMLNALAISVANQWPGVSKYRLRVTEGWDGHISEESLHYEGRAVDITSDRRN 60
 Qy 158 KYGMILARLAVEAGDWWVYVESKAHICCSVRAENSAVAKSGGCFCPGSATVHLGGTKLVK 217
 Db 61 KYGLARLAVEAGDWWVYVESKAHICCSVSEISAANKTGGCPAGQVHLERGVALS 120
 Qy 218 DLRRGDRVLAADOGRLYLSDFTFLDRDEGAKVYFYVIETLPRERLLTAHHLF 274
 Db 121 AVKPGDVRVLAMGEGNPTEFSDVLFLDREPNRRAFOVIETOPRRLALTPAHLF 177
 RESULT 14
 Q96699 PRELIMINARY; PRT; 185 AA.
 AC 096699; DR
 DT 01-MAY-1999 (TREMBIrel. 10, Created)
 DT 01-JUN-2001 (TREMBIrel. 17, Last annotation update)
 DE Hedgehog protein (Fragment).
 GN HH.
 OC Junonia coenia (Peacock butterfly) (Precis coenia).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Papilionoidea; Nymphalidae; Nymphalinae; Junonia.
 OX NCBI_TAXID=39708;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Keys D.N., Lewis D.L., Selegue J.E., Pearson B.J., Goodrich L.V.,
 RA Johnson R.L., Gates J., Scott M.P., Carroll S.B.;
 RT *Recruitment of a hedgehog regulatory circuit in butterfly eyespot

RT evolution. n;
 RL Science 0:0-01999.
 DR AF117712; AAC08931.1; -.
 DR HSSP; 052226; 1VHH
 DR InterPro; IPR000340; HH_Signal.
 DR InterPro; IPR01657; SonichH.
 DR Pfam; PR01085; HH_Signal; 1.
 DR PRINTS; PR00632; SONICHIOG.
 DR PRODOM; PDO03042; HH_Signal; 1.
 FT NON-TER 185 AA; 20745 MW; E9B9F4CE2FAAE662 CRC64;
 SQ SEQUENCE 185 AA: ...
 Query Match 27.4%; Score 628; DB 5; Length 185;
 Best Local Similarity 69.4%; Pred. No. 8.9e-43;
 Matches 118; Conservative 20; Mismatches 30; Indels 2; Gaps 2;
 Qy 59 ASGRVEGKTRNSRBFKEITPNYNDIFKDEENTGADRMLTORCKRNLAISVANQW 118
 Db 3 ASGPPEGRITRDDEKFDRDLPNTNPDDIFKDEENTGADRMLTORCKRNLAISVANQW 62
 Qy 119 PGVLRVPGWDEGGHHSSESLYEGRAVDITSDRRSKYGLARLAVEGFDWVYES 178
 Db 63 PGVLRVPGWDEBNSHDSLNLVINGRAVDITSDRRSKYGLARLAVEGFDWVYES 122
 Qy 179 KAHICCSVKAENSAVAKSGCCFGPSATVHLGGTKLVKDLRGDRVLA 228
 Db 123 RSYIHCSVKTTESVGT-GAGCFPSGAHVHTENGSPXD-TASLKKGNKVLA 170

RESULT 15
 Q80GNA PRELIMINARY; PRT; 99 AA.
 ID Q80GNA; DR
 AC 080GNA; DR
 DT 01-JUN-2002 (TREMBIrel. 21, Last annotation update)
 DT 01-JUN-2002 (TREMBIrel. 21, Last sequence update)
 DE Sonic hedgehog (Fragment).
 OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichtyes;
 OC Elasmobranchii; Galeomorphi; Galeoidea; Carcarhiniiformes;
 OC Scyliorhinidae; Scyliorhinus.
 OX NCBI_TAXID=7830;
 RN [1]
 RP SEQUENCE FROM N.A.
 MEDLINE-2193058; Pubmed-11932743;
 RA Tanaka M., Munsterberg A., Anderson W.G., Prescott A.R., Hazen N.,
 RA Tickle C.;
 RT "Fin development in a cartilaginous fish and the origin of vertebrate
 RT 1imb. n;
 RL Nature 416:527-531(2002).
 DR EMBL; AF393835; AAC08228.1; -.
 DR EMBL; AF393835; AAC08228.1; -.
 FT NON-TER 99 AA; 99
 FT SEQUENCE 99 AA: ...
 SQ SEQUENCE 99 AA: ...
 Query Match 23.1%; Score 528; DB 13; Length 99;
 Best Local Similarity 97.0%; Pred. No. 4e-35;
 Matches 96; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 Qy 79 PNYNDIFERDEEKGADLMTORCKDKMLNALAISVANQWPGVSKYRLRVTEGWDGHISEE 138
 Db 1 PNINPDIFKDEEKGADLMTORCKDKMLNALAISVANQWPGVSKYRLRVTEGWDGHISEE 60
 Qy 139 SLHYEGRAVDITSDRRSKYGLARLAVEGFDWVYES 177
 Db 61 SLHYEGRAVDITSDRRSKYGLARLAVEGFDWVYES 99

Search completed: February 20, 2003, 10:11:51
 Job time : 29.1092 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on:

February 20, 2003, 10:05:32 ; Search time 34.4615 seconds

(without alignments)
1836.661 Million cell updates/sec

Title: US-09-827-110a-15

Perfect score: 2469

Sequence: 1 MLLARCLLVLVSSILVCS GMAVKSSXSRGAGGGAREGA 475

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002:*

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Minimum DB seq length: 0
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Maximum Match 100%
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Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002:*

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002:*

Minimum DB seq length: 0
Maximum DB seq length: 200000000

ALIGNMENTS

RESULT 1

ID AAR77341

ID AAR77341 standard; Protein: 475 AA.

AC AAR77341;

XX

DT 14-MAR-1996 (first entry)

XX DE Human sonic hedgehog protein.

XX KW Human; sonic hedgehog protein; probe; primer; diagnostic;

KW nervous system disorder; gene therapy; antibody.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Peptide 24..29 "conserved sequence (AAR77349)"

FT Misc-difference 463 "/note= "unspecified amino acid"

FT /note= "

PN W09518856-A1.

XX

XX 13-JUL-1995.

PD

PF 30-DEC-1994; 94WO-US14992.

XX

PR 14-DEC-1994; 94US-0356060.

PR 30-DEC-1993; 93US-0176427.

XX

PA (HARD) HARVARD COLLEGE RES TECHNOLOGY.

PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.

XX

Human sonic hedgehog

11 2467 99.9 475 22 AAB84674 Amino acid sequenc
 12 2457 99.9 475 22 AAEQ4687 Human sonic hedgehog
 13 2467 99.9 475 22 AAEU5377 Human sonic hedgehog
 14 2467 99.9 475 22 AAB31222 Human sonic hedgehog
 15 2457 99.9 475 22 AAB60265 Human sonic hedgehog
 16 2467 99.9 475 23 AAU99483 Human mutated sonic hedgehog
 17 2467 99.9 475 23 AB379137 Human sonic hedgehog
 18 2457 99.9 475 23 AAO20923 Human Shh protein
 19 2467 99.9 475 23 AAEI4297 Human sonic hedgehog
 20 2407 97.5 462 22 AAB85085 Human sonic hedgehog
 21 2407 97.5 463 22 AAB85738 Human sonic hedgehog
 22 2403 97.3 462 19 AAW8736 Human mutated sonic hedgehog
 23 2401 97.2 462 19 AAW48735 Mouse sonic hedgehog
 24 2065 83.8 437 19 AAW61498 Mouse sonic hedgehog
 25 2068 83.8 437 22 AAE9292 Human sonic hedgehog
 26 2065 83.8 437 20 AAW97768 Mouse Shh hedgehog
 27 2068 83.8 437 21 AAY97559 Mouse sonic hedgehog
 28 2065 83.8 437 23 AAO1264 437-mer wild-type mouse sonic hedgehog
 29 2065 83.6 437 16 AAR77339 Mouse sonic hedgehog
 30 2065 83.6 437 20 AAY05513 Mouse sonic hedgehog
 31 2065 83.6 437 21 AAY0679 Mouse sonic hedgehog
 32 2065 83.6 437 20 AAW97471 Mouse sonic hedgehog
 33 2065 83.6 437 21 AAY94471 Mouse sonic hedgehog
 34 2065 83.6 437 21 AAY95975 Mouse sonic hedgehog
 35 2065 83.6 437 21 AAY95284 Partial mouse Shh.
 36 2065 83.6 437 21 AAY96246 Mouse sonic hedgehog
 37 2065 83.6 437 22 AAG65746 Mouse sonic hedgehog
 38 2065 83.6 437 22 AAB85736 Mouse sonic hedgehog
 39 2065 83.6 437 22 AAB850263 Mouse sonic hedgehog
 40 2065 83.6 437 22 AAB84672 Amino acid sequence
 41 2065 83.6 437 22 AAEQ4685 Mouse sonic hedgehog
 42 2065 83.6 437 22 AAB85075 Mouse sonic hedgehog
 43 2065 83.6 437 22 AAB851220 Amino acid sequence
 44 2065 83.6 437 22 AAB850263 Mouse sonic hedgehog
 45 2065 83.6 437 23 AAU99481 Mouse sonic hedgehog

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

PI	Ingham PW, McMahon AP, Tabin CJ;	KW	folliculitis; pseudofolliculitis; keratoacanthoma; callosities;
XX		KW	Darier's disease; scar; autoimmune disease; pemphigus;
WPI;	1995-255060/33.	KW	epidemolysis; lupus lesion; desquamative lesion; carcinoma;
DR	N-PSDB; AAY091639.	KW	therapy; hedgehog therapeutic; ptc therapeutic; patched.
XX		XX	Hedgehog-like protein(s) and nucleic acid(s) encoding them - useful
PT	to treat degenerative nervous system disorder(s) and in gene	PT	therapy.
PT	Claim 17: Page 143-45; 210pp; English.	FH	therapy.
XX		Key	
PS	The sequence represents a human sonic hedgehog protein, homologous	Location/Qualifiers	
XX	to a <i>Drosophila</i> hedgehog protein (AA77337), and is encoded by a cDNA	/note=	"encoded by NNN"
CC	isolated from a human fetal lung cDNA library. Probes and primers	PN	W09920298-A1.
CC	derived from the sonic hedgehog gene may be used as diagnostic	XX	29-APR-1999.
CC	agents for neuromuscular, autonomic or central nervous system	PD	
CC	disorders, and the gene may also be used in gene therapy.	XX	20-OCT-1998;
CC	Antibodies generated from the protein may be used as therapeutic or	PF	98WO-US22227.
CC	research reagents.	XX	11-SEP-1998;
XX	Sequence 475 AA;	PR	98US-015199.
SO		XX	20-OCT-1997;
Query Match	99.9%; Score 2467; DB 16; Length 475;	PA	97US-095552.
Best Local Similarity	100.0%; Pred. No. 5.9e-218;	XX	(ONTO-) ONTOGENY INC.
Matches	475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	PI	
Qy	1 MLLARCLLUVLSSILVCGGLACGPGRGKRRPKKLTPLAYKQFIPNVAEKTIGASG	XX	
Db	1 MLLARCLLUVLSSILVCGGLACGPGRGKRRPKKLTPLAYKQFIPNVAEKTIGASG 60	DR	
Qy	61 RYEKTSRNRSERKELTNPNNPDIIFKDEENTGADRMLTORCKDKLNALISVMNQPGV	XX	
Db	61 RYEKTSRNRSERKELTNPNNPDIIFKDEENTGADRMLTORCKDKLNALISVMNQPGV 120	DR	
Qy	121 KLRVTVGWDDEGHHSLESLHYEGRAVDITASDRDRSKYGMALIAVEAGDWWYYESKAH	XX	
Db	121 KLRVTVGWDDEGHHSLESLHYEGRAVDITASDRDRSKYGMALIAVEAGDWWYYESKAH 180	DR	
Qy	181 IHCNSVKAENSTAASKSGCPFGSQTAVHLEQGKTKVLKDLSGPDRVLAADDGRLYSDFT	XX	
Db	181 IHCNSVKAENSTAASKSGCPFGSQTAVHLEQGKTKVLKDLSGPDRVLAADDGRLYSDFT 240	DR	
Qy	241 FLDRDGAKKVFYVIEPREPPLITAHLFWPHNDSATGEPEASSSGPPGGALG 300	XX	
Db	241 FLDRDGAKKVFYVIEPREPPLITAHLFWPHNDSATGEPEASSSGPPGGALG 300	DR	
Qy	301 PRALFASRVPGQRVYVAERDGDRLLPAVHVSYTSLSERAGAYAPLTQGTILINRVL	XX	
Db	301 PRALFASRVPGQRVYVAERDGDRLLPAVHVSYTSLSERAGAYAPLTQGTILINRVL 360	DR	
Qy	361 ASCYAVIEEHSAHRAFAFPFLAHALLAALAPARDRGSGGGDRGGGGGRVALTARGA	XX	
Db	361 ASCYAVIEEHSAHRAFAFPFLAHALLAALAPARDRGSGGGDRGGGGGRVALTARGA 420	DR	
Qy	421 ADPGAGATAGIHWMSQLQIQLTGWLSEALHPGMAVSSXSRGAGGAREGA 475	XX	
Db	421 ADPGAGATAGIHWMSQLQIQLTGWLSEALHPGMAVSSXSRGAGGAREGA 475	DR	
RESULT 2		XX	
AY05559		XX	
ID	AY05859 standard; Protein: 475 AA.	SO	
XX		Sequence 475 AA;	
AC			
XX			
DT	02-AUG-1999 (first entry)	Query Match	99.9%; Score 2467; DB 20; Length 475;
XX		Best Local Similarity	100.0%; Pred. No. 5.9e-218;
DE	Human Sonic hedgehog Shh protein.	Matches	475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Sonic hedgehog; Shh; human; epithelial tissue; epithelium;	Qy	1 MLLARCLLUVLSSILVCGGLACGPGRGKRRPKKLTPLAYKQFIPNVAEKTIGASG	60
cutaneous tissue; skin; hair; wound healing; vulvar; folliculitis; and	Db	1 MLLARCLLUVLSSILVCGGLACGPGRGKRRPKKLTPLAYKQFIPNVAEKTIGASG 60	
burn; skin grafting; pressure sore; ulcer; ulcerative colitis; disorders, e.g. aphthous ulcers, pemphigus vulgaris, pemphigus foliaceus, pemphigus vegetans, pemphigus erythematosus, idiopathies, lupus lesions, desquamative lesions or carcinomas. The methods can also be used to counteract the effects of ageing on skin.	Qy	61 RYEKTSRNRSERKELTNPNNPDIIFKDEENTGADRMLTORCKDKLNALISVMNQPGV	120
alopecia; psoriasis; keratosis; acne; comedogenic lesion;	Db	61 RYEKTSRNRSERKELTNPNNPDIIFKDEENTGADRMLTORCKDKLNALISVMNQPGV 120	

PN XX	W09904775-A2.	QY 361	ASCVAYEEHSHWAHAFAPFRILAHALLAALAPARTDRGGSGGGDRGGGGRVALTAPGA
PD 04-FEB-1999.		Db 361	ASCVAYEEHSHWAHAFAPFRILAHALLAALAPARTDRGGSGGGDRGGGGRVALTAPGA
XX			420
PR 24-JUL-1998;	98WO-US15419.	QY 421	ADAPGAGATAGTHWYQOLLYQIGTWLDSALHPIGMAVKSXRSGGGAREGA
XX		Db 421	475
PA (ONTO-) ONTOGENY INC.			ADAPGAGATAGTHWYSQQLQIGTWLDSALHPIGMAVSSXSRGAGGGAREGA
PI XX	Mahanthappa NK, Miao N, Pang K, Wang M;		
DR XX	WPI; 1999-142578/12.		
N-PSDB; AXM07275.			
PS XX			
PT PT	Increasing the survival of neuronal, dopaminergic and GABA-ergic cells - by using a ptc therapeutic such as a protein kinase inhibitor, or an agent derived from hedgehog polypeptides, useful in the treatment of parkinson's disease		
PT PT			
CC CC	This polypeptide is human Shh sonic hedgehog protein. The invention is based on the finding that hedgehog proteins are useful as protective agents in the treatment and prophylaxis of neurodegenerative disorders resulting from the loss of dopaminergic and/or GABA-ergic neurons, or the general loss of tissue from the substantia nigra. Exemplary disorders include parkinson's disease, huntington's disease (both claimed), amyotrophic lateral sclerosis and cerebral ischaemia. The invention relates to hedgehog therapeutics (i.e. hedgehog polypeptides and gene therapy constructs e.g. constructs encoding recombinant hedgehog polypeptides and trans activation constructs for altering hedgehog gene regulatory sequences) and ptc therapeutics (i.e. agents which mimic the effect of naturally occurring hedgehog proteins on patched signalling) that are effective in both human and animal subjects. Human Ih and Dhn polypeptides (see WO97/63764) are preferred. The products can also be used for the maintenance of differentiated neurons in cultures, and to enhance the implantation of such neuronal cells in an animal. They can be used to prevent or treat neurodegenerative conditions arising from the use of certain drugs, and in the prevention and/or treatment of hypoxia, e.g. as a neuroprotective agent.		
CC CC			
SO Sequence	475 AA;		
Query Match	99.9%	Score 2467; DB 20;	Length 475;
Best Local Similarity	100.0%	Pred. No. 5.9e-218;	Length 475;
Matches	475;	Conservative	0;
Oy	1	MILLARCLLVLYSSLVCSGLACGGRGCGKRRHKKLPLAKQKIFPVAEKGTLGASG	60
Db	1	MILLARCLLVLYSSLVCSGLACGGRGCRKRHRPKKLPLAKQFIPVAEKGTLGASG	60
Oy	61	RVEGKISRNNSRFKELPNPKDIFRKDEETGADRMLQRCKDKNALISMVQWPGV	120
Db	61	RVEGKISRNNSRFKELPNPKDIFRKDEETGADRMLQRCKDKNALISMVQWPGV	120
Oy	121	KLRVVTGCGEDGHHSRSLSLYEGRAVDITTSDRDRSKYGMALARAVEAGFDWVYBESKAH	180
Db	121	KLRVVTGCGEDGHHSRSLSLYEGRAVDITTSDRDRSKYGMALARAVEAGFDWVYBESKAH	180
Oy	181	IHCsvkaensvaaksgcgcfpsatvileqogtkvlkdspdrvlaaddogrrlysdflt	240
Db	181	IHCsvkaensvaaksgcgcfpsatvileqogtkvlkdspdrvlaaddogrrlysdflt	240
Oy	241	FLLDRGAKKYVIEPREFLITAAHLFVARHNDSTGEPEASSSSGPSSGALG	300
Db	241	FLLDRGAKKYVIEPREFLITAAHLFVARHNDSTGEPEASSSSGPSSGALG	300
Oy	301	PRALFAASRVPGQRVVAERDGDRRLPAAVHVSVILSEEEAGAYAPLTAQTLINRVL	360
Db	301	PRALFAASRVPGQRVVAERDGDRRLPAAVHVSVILSEEEAGAYAPLTAQTLINRVL	360
SO Sequence	475 AA;		
Query Match	99.9%	Score 2467; DB 20;	Length 475;
Best Local Similarity	100.0%	Pred. No. 5.9e-218;	Length 475;
Matches	475;	Conservative	0;
Oy	1	MILLARCLLVLYSSLVCSGLACGGRGCGKRRHKKLPLAKQKIFPVAEKGTLGASG	60
Db	1	MILLARCLLVLYSSLVCSGLACGGRGCRKRHRPKKLPLAKQFIPVAEKGTLGASG	60
Oy	61	RVEGKISRNNSRFKELPNPKDIFRKDEETGADRMLQRCKDKNALISMVQWPGV	120
Db	61	RVEGKISRNNSRFKELPNPKDIFRKDEETGADRMLQRCKDKNALISMVQWPGV	120
Oy	121	KLRVVTGCGEDGHHSRSLSLYEGRAVDITTSDRDRSKYGMALARAVEAGFDWVYBESKAH	180
Db	121	KLRVVTGCGEDGHHSRSLSLYEGRAVDITTSDRDRSKYGMALARAVEAGFDWVYBESKAH	180
Oy	181	IHCsvkaensvaaksgcgcfpsatvileqogtkvlkdspdrvlaaddogrrlysdflt	240
Db	181	IHCsvkaensvaaksgcgcfpsatvileqogtkvlkdspdrvlaaddogrrlysdflt	240
Oy	241	FLLDRGAKKYVIEPREFLITAAHLFVARHNDSTGEPEASSSSGPSSGALG	300
Db	241	FLLDRGAKKYVIEPREFLITAAHLFVARHNDSTGEPEASSSSGPSSGALG	300
Oy	301	PRALFAASRVPGQRVVAERDGDRRLPAAVHVSVILSEEEAGAYAPLTAQTLINRVL	360
Db	301	PRALFAASRVPGQRVVAERDGDRRLPAAVHVSVILSEEEAGAYAPLTAQTLINRVL	360
SO Sequence	475 AA;		
Query Match	99.9%	Score 2467; DB 20;	Length 475;
Best Local Similarity	100.0%	Pred. No. 5.9e-218;	Length 475;
Matches	475;	Conservative	0;
Oy	1	MILLARCLLVLYSSLVCSGLACGGRGCGKRRHKKLPLAKQKIFPVAEKGTLGASG	60
Db	1	MILLARCLLVLYSSLVCSGLACGGRGCRKRHRPKKLPLAKQFIPVAEKGTLGASG	60
Oy	61	RVEGKISRNNSRFKELPNPKDIFRKDEETGADRMLQRCKDKNALISMVQWPGV	120
Db	61	RVEGKISRNNSRFKELPNPKDIFRKDEETGADRMLQRCKDKNALISMVQWPGV	120
Oy	121	KLRVVTGCGEDGHHSRSLSLYEGRAVDITTSDRDRSKYGMALARAVEAGFDWVYBESKAH	180
Db	121	KLRVVTGCGEDGHHSRSLSLYEGRAVDITTSDRDRSKYGMALARAVEAGFDWVYBESKAH	180
Oy	181	IHCsvkaensvaaksgcgcfpsatvileqogtkvlkdspdrvlaaddogrrlysdflt	240
Db	181	IHCsvkaensvaaksgcgcfpsatvileqogtkvlkdspdrvlaaddogrrlysdflt	240
Oy	241	FLLDRGAKKYVIEPREFLITAAHLFVARHNDSTGEPEASSSSGPSSGALG	300
Db	241	FLLDRGAKKYVIEPREFLITAAHLFVARHNDSTGEPEASSSSGPSSGALG	300
Oy	301	PRALFAASRVPGQRVVAERDGDRRLPAAVHVSVILSEEEAGAYAPLTAQTLINRVL	360
Db	301	PRALFAASRVPGQRVVAERDGDRRLPAAVHVSVILSEEEAGAYAPLTAQTLINRVL	360
SO Sequence	475 AA;		
Query Match	99.9%	Score 2467; DB 20;	Length 475;
Best Local Similarity	100.0%	Pred. No. 5.9e-218;	Length 475;
Matches	475;	Conservative	0;
Oy	1	MILLARCLLVLYSSLVCSGLACGGRGCGKRRHKKLPLAKQKIFPVAEKGTLGASG	60
Db	1	MILLARCLLVLYSSLVCSGLACGGRGCRKRHRPKKLPLAKQFIPVAEKGTLGASG	60
Oy	61	RVEGKISRNNSRFKELPNPKDIFRKDEETGADRMLQRCKDKNALISMVQWPGV	120
Db	61	RVEGKISRNNSRFKELPNPKDIFRKDEETGADRMLQRCKDKNALISMVQWPGV	120
Oy	121	KLRVVTGCGEDGHHSRSLSLYEGRAVDITTSDRDRSKYGMALARAVEAGFDWVYBESKAH	180
Db	121	KLRVVTGCGEDGHHSRSLSLYEGRAVDITTSDRDRSKYGMALARAVEAGFDWVYBESKAH	180
Oy	181	IHCsvkaensvaaksgcgcfpsatvileqogtkvlkdspdrvlaaddogrrlysdflt	240
Db	181	IHCsvkaensvaaksgcgcfpsatvileqogtkvlkdspdrvlaaddogrrlysdflt	240
Oy	241	FLLDRGAKKYVIEPREFLITAAHLFVARHNDSTGEPEASSSSGPSSGALG	300
Db	241	FLLDRGAKKYVIEPREFLITAAHLFVARHNDSTGEPEASSSSGPSSGALG	300
Oy	301	PRALFAASRVPGQRVVAERDGDRRLPAAVHVSVILSEEEAGAYAPLTAQTLINRVL	360
Db	301	PRALFAASRVPGQRVVAERDGDRRLPAAVHVSVILSEEEAGAYAPLTAQTLINRVL	360
SO Sequence	475 AA;		
Query Match	99.9%	Score 2467; DB 20;	Length 475;
Best Local Similarity	100.0%	Pred. No. 5.9e-218;	Length 475;
Matches	475;	Conservative	0;
Oy	1	MILLARCLLVLYSSLVCSGLACGGRGCGKRRHKKLPLAKQKIFPVAEKGTLGASG	60
Db	1	MILLARCLLVLYSSLVCSGLACGGRGCRKRHRPKKLPLAKQFIPVAEKGTLGASG	60
Oy	61	RVEGKISRNNSRFKELPNPKDIFRKDEETGADRMLQRCKDKNALISMVQWPGV	120
Db	61	RVEGKISRNNSRFKELPNPKDIFRKDEETGADRMLQRCKDKNALISMVQWPGV	120
Oy	121	KLRVVTGCGEDGHHSRSLSLYEGRAVDITTSDRDRSKYGMALARAVEAGFDWVYBESKAH	180
Db	121	KLRVVTGCGEDGHHSRSLSLYEGRAVDITTSDRDRSKYGMALARAVEAGFDWVYBESKAH	180
Oy	181	IHCsvkaensvaaksgcgcfpsatvileqogtkvlkdspdrvlaaddogrrlysdflt	240
Db	181	IHCsvkaensvaaksgcgcfpsatvileqogtkvlkdspdrvlaaddogrrlysdflt	240
Oy	241	FLLDRGAKKYVIEPREFLITAAHLFVARHNDSTGEPEASSSSGPSSGALG	300
Db	241	FLLDRGAKKYVIEPREFLITAAHLFVARHNDSTGEPEASSSSGPSSGALG	300
Oy	301	PRALFAASRVPGQRVVAERDGDRRLPAAVHVSVILSEEEAGAYAPLTAQTLINRVL	360
Db	301	PRALFAASRVPGQRVVAERDGDRRLPAAVHVSVILSEEEAGAYAPLTAQTLINRVL	360
SO Sequence	475 AA;		
Query Match	99.9%	Score 2467; DB 20;	Length 475;
Best Local Similarity	100.0%	Pred. No. 5.9e-218;	Length 475;
Matches	475;	Conservative	0;
Oy	1	MILLARCLLVLYSSLVCSGLACGGRGCGKRRHKKLPLAKQKIFPVAEKGTLGASG	60
Db	1	MILLARCLLVLYSSLVCSGLACGGRGCRKRHRPKKLPLAKQFIPVAEKGTLGASG	60
Oy	61	RVEGKISRNNSRFKELPNPKDIFRKDEETGADRMLQRCKDKNALISMVQWPGV	120
Db	61	RVEGKISRNNSRFKELPNPKDIFRKDEETGADRMLQRCKDKNALISMVQWPGV	120
Oy	121	KLRVVTGCGEDGHHSRSLSLYEGRAVDITTSDRDRSKYGMALARAVEAGFDWVYBESKAH	180
Db	121	KLRVVTGCGEDGHHSRSLSLYEGRAVDITTSDRDRSKYGMALARAVEAGFDWVYBESKAH	180
Oy	181	IHCsvkaensvaaksgcgcfpsatvileqogtkvlkdspdrvlaaddogrrlysdflt	240
Db	181	IHCsvkaensvaaksgcgcfpsatvileqogtkvlkdspdrvlaaddogrrlysdflt	240
Oy	241	FLLDRGAKKYVIEPREFLITAAHLFVARHNDSTGEPEASSSSGPSSGALG	300
Db	241	FLLDRGAKKYVIEPREFLITAAHLFVARHNDSTGEPEASSSSGPSSGALG	300
Oy	301	PRALFAASRVPGQRVVAERDGDRRLPAAVHVSVILSEEEAGAYAPLTAQTLINRVL	360
Db	301	PRALFAASRVPGQRVVAERDGDRRLPAAVHVSVILSEEEAGAYAPLTAQTLINRVL	360
SO Sequence	475 AA;		
Query Match	99.9%	Score 2467; DB 20;	Length 475;
Best Local Similarity	100.0%	Pred. No. 5.9e-218;	Length 475;
Matches	475;	Conservative	0;
Oy	1	MILLARCLLVLYSSLVCSGLACGGRGCGKRRHKKLPLAKQKIFPVAEKGTLGASG	60
Db	1	MILLARCLLVLYSSLVCSGLACGGRGCRKRHRPKKLPLAKQFIPVAEKGTLGASG	60
Oy	61	RVEGKISRNNSRFKELPNPKDIFRKDEETGADRMLQRCKDKNALISMVQWPGV	120
Db	61	RVEGKISRNNSRFKELPNPKDIFRKDEETGADRMLQRCKDKNALISMVQWPGV	120
Oy	121	KLRVVTGCGEDGHHSRSLSLYEGRAVDITTSDRDRSKYGMALARAVEAGFDWVYBESKAH	180
Db	121	KLRVVTGCGEDGHHSRSLSLYEGRAVDITTSDRDRSKYGMALARAVEAGFDWVYBESKAH	180
Oy	181	IHCsvkaensvaaksgcgcfpsatvileqogtkvlkdspdrvlaaddogrrlysdflt	240
Db	181	IHCsvkaensvaaksgcgcfpsatvileqogtkvlkdspdrvlaaddogrrlysdflt	240
Oy	241	FLLDRGAKKYVIEPREFLITAAHLFVARHNDSTGEPEASSSSGPSSGALG	300
Db	241	FLLDRGAKKYVIEPREFLITAAHLFVARHNDSTGEPEASSSSGPSSGALG	300
Oy	301	PRALFAASRVPGQRVVAERDGDRRLPAAVHVSVILSEEEAGAYAPLTAQTLINRVL	360
Db	301	PRALFAASRVPGQRVVAERDGDRRLPAAVHVSVILSEEEAGAYAPLTAQTLINRVL	360
SO Sequence	475 AA;		
Query Match	99.9%	Score 2467; DB 20;	Length 475;
Best Local Similarity	100.0%	Pred. No. 5.9e-218;	Length 475;
Matches	475;	Conservative	0;
Oy	1	MILLARCLLVLYSSLVCSGLACGGRGCGKRRHKKLPLAKQKIFPVAEKGTLGASG	60
Db	1	MILLARCLLVLYSSLVCSGLACGGRGCRKRHRPKKLPLAKQFIPVAEKGTLGASG	60
Oy	61	RVEGKISRNNSRFKELPNPKDIFRKDEETGADRMLQRCKDKNALISMVQWPGV	120
Db	61	RVEGKISRNNSRFKELPNPKDIFRKDEETGADRMLQRCKDKNALISMVQWPGV	120
Oy	121	KLRVVTGCGEDGHHSRSLSLYEGRAVDITTSDRDRSKYGMALARAVEAGFDWVYBESKAH	180
Db	121	KLRVVTGCGEDGHHSRSLSLYEGRAVDITTSDRDRSKYGMALARAVEAGFDWVYBESKAH	180
Oy	181	IHCsvkaensvaaksgcgcfpsatvileqogtkvlkdspdrvlaaddogrrlysdflt	240
Db	181	IHCsvkaensvaaksgcgcfpsatvileqogtkvlkdspdrvlaaddogrrlysdflt	240
Oy	241	FLLDRGAKKYVIEPREFLITAAHLFVARHNDSTGEPEASSSSGPSSGALG	300
Db	241	FLLDRGAKKYVIEPREFLITAAHLFVARHNDSTGEPEASSSSGPSSGALG	300
Oy	301	PRALFAASRVPGQRVVAERDGDRRLPAAVHVSVILSEEEAGAYAPLTAQTLINRVL	360
Db	301	PRALFAASRVPGQRVVAERDGDRRLPAAVHVSVILSEEEAGAYAPLTAQTLINRVL	360
SO Sequence	475 AA;		
Query Match	99.9%	Score 2467; DB 20;	Length 475;
Best Local Similarity	100.0%	Pred. No. 5.9e-218;	Length 475;
Matches	475;	Conservative	0;
Oy	1	MILLARCLLVLYSSLVCSGLACGGRGCGKRRHKKLPLAKQKIFPVAEKGTLGASG	60
Db	1	MILLARCLLVLYSSLVCSGLACGGRGCRKRHRPKKLPLAKQFIPVAEKGTLGASG	60
Oy	61	RVEGKISRNNSRFKELPNPKDIFRKDEETGADRMLQRCKDKNALISMVQWPGV	120
Db	61	RVEGKISRNNSRFKELPNPKDIFRKDEETGADRMLQRCKDKNALISMVQWPGV	120
Oy	121	KLRVVTGCGEDGHHSRSLSLYEGRAVDITTSDRDRSKYGMALARAVEAGFDWVYBESKAH	180
Db	121	KLRVVTGCGEDGHHSRSLSLYEGRAVDITTSDRDRSKYGMALARAVEAGFDWVYBESKAH	180
Oy	181	IHCsvkaensvaaksgcgcfpsatvileqogtkvlkdspdrvlaaddogrrlysdflt	240
Db	181	IHCsvkaensvaaksgcgcfpsatvileqogtkvlkdspdrvlaaddogrrlysdflt	240
Oy	241	FLLDRGAKKYVIEPREFLITAAHLFVARHNDSTGEPEASSSSGPSSGALG	300
Db	241	FLLDRGAKKYVIEPREFLITAAHLFVARHNDSTGEPEASSSSGPSSGALG	300
Oy	301	PRALFAASRVPGQRVVAERDGDRRLPAAVHVSVILSEEEAGAYAPLTAQTLINRVL	360
Db	301	PRALFAASRVPGQRVVAERDGDRRLPAAVHVSVILSEEEAGAYAPLTAQTLINRVL	360
SO Sequence	475 AA;		
Query Match	99.9%	Score 2467; DB 20;	Length 475;
Best Local Similarity	100.0%	Pred. No. 5.9e-218;	Length 475;
Matches	475;	Conservative	0;
Oy	1	MILLARCLLVLYSSLVCSGLACGGRGCGKRRHKKLPLAKQKIFPVAEKGTLGASG	60
Db	1	MILLARCLLVLYSSLVCSGLACGGRGCRKRHRPKKLPLAKQFIPVAEKGTLGASG	60
Oy	61	RVEGKISRNNSRFKELPNPKDIFRKDEETGADRMLQRCKDKNALISMVQWPGV	120
Db	61	RVEGKISRNNSRFKELPNPKDIFRKDEETGADRMLQRCKDKNALISMVQWPGV	120
Oy	121	KLRVVTGCGEDGHHSRSLSLYEGRAVDITTSDRDRSKYGMALARAVEAGFDWVYBESKAH	180
Db	121	KLRVVTGCGEDGHHSRSLSLYEGRAVDITTSDRDRSKYGMALARAVEAGFDWVYBESKAH	180
Oy	181	IHCsvkaensvaaksgcgcfpsatvileqogtkvlkdspdrvlaaddogrrlysdflt	240
Db	181	IHCsvkaensvaaksgcgcfpsatvileqogtkvlkdspdrvlaaddogrrlysdflt	240
Oy	241	FLLDRGAKKYVIEPREFLITAAHLFVARHNDSTGEPEASSSSGPSSGALG	300
Db	241	FLLDRGAKKYVIEPREFLITAAHLFVARHNDSTGEPEASSSSGPSSGALG	300
Oy	301	PRALFAASRVPGQRVVAERDGDRRLPAAVHVSVILSEEEAGAYAPLTAQTLINRVL	360
Db	301	PRALFAASRVPGQRVVAERDGDRRLPAAVHVSVILSEEEAGAYAPLTAQTLINRVL	360
SO Sequence	475 AA;		
Query Match	99.9%	Score 2467; DB 20;	Length 475;
Best Local Similarity	100.0%	Pred. No. 5.9e-218;	Length 475;
Matches	475;	Conservative	0;
Oy	1	MILLARCLLVLYSSLVCSGLACGGRGCGKRRHKKLPLAKQKIFPVAEKGTLGASG	60
Db	1	MILLARCLLVLYSSLVCSGLACGGRGCRKRHRPKKLPLAKQFIPVAEKGTLGASG	60
Oy	61	RVEGKISRNNSRFKELPNPKDIFRKDEETGADRMLQRCKDKNALISMVQWPGV	120
Db	61	RVEGKISRNNSRFKELPNPKDIFRKDEETGADRMLQRCKDKNALISMVQWPGV	120
Oy	121	KLRVVTGCGEDGHHSRSLSLYEGRAVDITTSDRDRSKYGMALARAVEAGFDWVYBESKAH	180
Db	121	KLRVVTGCGEDGHHSRSLSLYEGRAVDITTSDRDRSKYGMALARAVEAGFDWVYBESKAH	180
Oy	181	IHCsvkaensvaaksgcgcfpsatvileqogtkvlkdspdrvlaaddogrrlysdflt	240
Db	181	IHCsvkaensvaaksgcgcfpsatvileqogtkvlkdspdrvlaaddogrrlysdflt	240
Oy	241	FLLDRGAKKYVIEPREFLITAAHLFVARHNDSTGEPEASSSSGPSSGALG	300
Db	241	FLLDRGAKKYVIEPREFLITAAHLFVARHNDSTGEPEASSSSGPSSGALG	300
Oy	301	PRALFAASRVPGQRVVAERDGDRRLPAAVHVSVILSEEEAGAYAPLTAQTLINRVL	360
Db	301	PRALFAASRVPGQRVVAERDGDRRLPAAVHVSVILSEEEAGAYAPLTAQTLINRVL	360
SO Sequence	475 AA;		
Query Match	99.9%	Score 2467; DB 20;	Length 475;
Best Local Similarity	100.0%	Pred. No. 5.9e-218;	Length 475;
Matches	475;	Conservative	0;
Oy	1	MILLARCLLVLYSSLVCSGLACGGRGCGKRRHKKLPLAKQKIFPVAEKGTLGASG	60
Db	1	MILLARCLLVLYSSLVCSGLACGGRGCRKRHRPKKLPLAK	

Db	361 ASCYAVIEEHSWAHRAPFRLLAHALLAALAPARTDRGGDSGGDRGGGRVALTAPGA 420
QY	421 ADAPGAGATAGIHWYSOLLYQIGTWLIDSEALHPLGMAVKSSXSRGAGGAREGA 475
Db	421 ADAPGAGATAGIHWYSOLLYQIGTWLIDSEALHPLGMAVKSSXSRGAGGAREGA 475
RESULT 7	
XX	
ID	AAV95286 standard; Protein; 475 AA.
XX	AAV95286;
AC	
XX	
DT	12-SEP-2000 (first entry)
XX	
DE	Human Sonic hedgehog Shh protein.
XX	
KW	Sonic hedgehog; Shh; human; excitotoxicity; Parkinson's disease; Huntington's disease; neuronal degeneration; neuroprotective; depaminergic; GABergic; substantia nigra; therapy.
XX	
OS	Homo sapiens.
FH	Key Location/Qualifiers
FT	Misc-difference 463
FT	/note= "encoded by NNN"
XX	WO20035948-A1.
XX	22-JUN-2000.
XX	03-DEC-1999; 99WO-US28721.
XX	03-DEC-1998; 98WO-US25676.
PR	27-JAN-1999; 99US-0338243.
PR	03-JUN-1999; 99US-0325602.
PA	(BIOJ) BIOCEN INC.
PA	(ONTO-) ONTOGENY INC.
PT	Galdes A, Mahanthappa N;
XX	WPI: 2000-431570/37.
DR	N-PSDB; AIA95281.
XX	
PT	treating disorders involving exotoxicity, e.g. trauma, hypoglycemia, senile dementia and Korsakoff's disease, by using lipophilic modified hedgehog polypeptide -
PT	disclosure; Page 157-159; 174PP; English.
CC	The present sequence of that of human Sonic hedgehog (Shh) protein. The invention relates to a method for promoting the survival and/or functional performance of neuronal cells, especially substantia nigra, dopaminergic and GABAergic neurons that are susceptible to exotoxicity, by contacting the cells, <i>in vitro</i> or <i>in vivo</i> , with a lipophilic (e.g., cholesterol) modified hedgehog polypeptide. The method is used to treat or prevent Parkinson's disease, Huntington's disease, domoic acid poisoning, spinal cord trauma, hypoglycemia, mechanical trauma to the nervous system, multi-infarct dementia, mood disorders, depression, chemical toxicity, neuronal damage associated with uncontrolled seizures such as epileptic seizures, neuronal injury associated with HIV and AIDS, neurodegeneration associated with Down's syndrome, neuropathic pain syndrome, olivopontocerebral atrophy, amyotrophic lateral sclerosis, mitochondrial abnormalities, Alzheimer's disease, hepatic encephalopathy, Tourette's syndrome and drug addiction (all claimed). The lipophilic modified hedgehog polypeptide is also useful for promoting survival and/or functional performance of neuronal cells susceptible to exotoxicity.
XX	
RESULT 8	
XX	
ID	AAV96248 standard; Protein; 475 AA.
XX	AAV96248;
AC	
XX	
DT	11-SEP-2000 (first entry)
XX	
DE	Partial human Shh.
XX	
KW	Human; sonic hedgehog; Shh; neuromuscular disorder; neuropathy; Guillain-Barre syndrome; peripheral neuropathy; diabetes; alcoholism; chronic inflammatory demyelinating polyneuropathy; CIDP; gene therapy; infection; inflammation; hereditary neuropathy; Charcot-Marie-Tooth disease; vasculitis; lung cancer; tumour; multiple myeloma; nutritional imbalance; kidney disease; hypothyroid neuropathy; trauma; Refsum's disease; abetalipoproteinemia; Tanger disease; Krabbe's disease; Metachromatic leukodystrophy; Fabry's disease; CMT; GBS; Dejerine-Sottas syndrome; acute neuropathy; Amyotrophic lateral sclerosis; ALS; Miller-Fisher syndrome; amyloidosis; hereditary sensory neuropathy type II; HSN II; B-cell lymphoma; Waldenstrom's Macroglobulinaemia; Chronic lymphocytic leukaemia; neuroprotective; cytoprotective; patched-mediated signal transduction.
XX	
OS	Homo sapiens.
FH	Key Location/Qualifiers
FT	Misc-difference 463
FT	/label= unknown
XX	/note= "Encoded by NNN"
PN	WO20035948-A2.
XX	

Sequence	475 AA;	score 2467; DB 21; Length 475; Best Local Similarity 100.0%; Pred. No. 5.9e-218; Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	1 MLLARCLLVLVSSLLIVCGLACGPGRGFGKRRHPKKLTPLAYQFTIPVAEKTIGASC 60	
Db	1 MLLARCLLVLVSSLLIVCGLACGPGRGFGKRRHPKKLTPLAYQFTIPVAEKTIGASC 60	
QY	61 RVEGKISRNSERKELPPNNPDIPIKEENIGADRLMQRCKDKLNALAIYSMQPGV 120	
Db	61 RVEGKISRNSERKELPPNNPDIPIKEENIGADRLMQRCKDKLNALAIYSMQPGV 120	
QY	121 KLRVTEGMDEDGHSEESIHYEGRAVDTTSDRDRSKYGMARLAVAEAGFDWVYESKAH 180	
Db	121 KLRVTEGMDEDGHSEESIHYEGRAVDTTSDRDRSKYGMARLAVAEAGFDWVYESKAH 180	
QY	241 FLDRDGAKKVYVIERPREPRLILTAHLLVAPHNDSDATGEPEAASSGGPSGGALG 300	
Db	241 FLDRDGAKKVYVIERPREPRLILTAHLLVAPHNDSDATGEPEAASSGGPSGGALG 300	
QY	301 PRALFASRVPRPGORYVVAERDDRRLPAVAVHSVTLSBAAAGAVAPTAQGTILINRYL 360	
Db	301 PRALFASRVPRPGORYVVAERDDRRLPAVAVHSVTLSBAAAGAVAPTAQGTILINRYL 360	
QY	361 ASCYAVTEEHSHWAHRAFPRLAHALLALAPARTDRCGSQGDGRGGGRVALTAPCA 420	
Db	361 ASCYAVTEEHSHWAHRAFPRLAHALLALAPARTDRCGSQGDGRGGGRVALTAPCA 420	
OY	421 ADAPGAGATAGTHWSQLYQIGTMLDSEALHPLGMWAKSSXSRGACCGAREGA 475	
Db	421 ADAPGAGATAGTHWSQLYQIGTMLDSEALHPLGMWAKSSXSRGACCGAREGA 475	
RESULT 10		
AAG65748	ID AAG65748 standard; Protein; 475 AA.	
XX	XX	
AC	AC	
XX	XX	
DT	07-JAN-2002 (first entry)	
DE	Human sonic hedgehog (Shh) polypeptide.	
XX	XX	
DE	Human sonic hedgehog (Shh) polypeptide.	
KW	adipocyte; hedgehog polypeptide; desert hedgehog; Indian hedgehog; Dhh; Ihh; sonic hedgehog; Shh; therapeutic; cytostatic; tumor.	
KW	KW	
OS	Homo sapiens.	
XX	XX	
FH	Key Location/Qualifiers	
FT	M1sc-difference 463	
FT	/note= "encoded by NNN"	
XX	WO20164238-A2.	
PN		
XX	07-SEP-2001.	
XX	28-FEB-2001; 2001WO-US06450.	
XX	29-FEB-2000; 2000US-186058P.	
PR	(CURRI-) CURIS INC.	
PA	Zehentner B, Leiser-Reiff U, Burtscher H;	
XX		
DR	WPI; 2001-607352/69.	
N-PSDB: AAf666776.		

Method for regulating formation and/or maintenance of adipocyte tissue
PT by contacting pre-adipocyte or adipocyte cells with a hedgehog
PT polypeptide or ptc therapeutic -
XX

PS Disclosure; Page 102-104; 132pp; English.

The invention provides a method for regulating formation and/or maintenance of adipocyte tissue that comprises contacting pre adipocyte or adipocyte cells with a hedgehog polypeptide or ptc therapeutic. The method is used for regulating the growth state of an adipocyte stem/progenitor cell, and treating or preventing disorders of, or surgical or cosmetic repair of, adipocyte tissues, e.g. for treating or preventing hyperplastic or neoplastic conditions affecting adipocyte tissue, such as soft tissue tumors, especially adipose cell tumors, e.g. lipomas, fibrolipomas, lipoblastomas, lipomatosis, hibernomas, hemangiomas and/or liposarcomas. Hedgehog polypeptides can be used in combination with other therapeutic agents. The present sequence represents a human sonic hedgehog (Shh) polypeptide.

SQ Sequence 475 AA;

KW hyperproliferative disease; eczematous dermatitis; urticaria;
KW vasculitis; scleroderma.
XX

OS Homo sapiens.

Key Misc-difference 463
Location/Qualifiers /note= "unspecified residue encoded by NNN"
FT 361 ASCYAVIEHSHWAHRAFAPRFLAHALLAALAPARTDGGDSGGDRGGGVALTAPG 420
XX 421 ADAPGAGATAGIHWYSQQLXQIGTWLSDSEALHPLGMVAKSSSRGAGGAREGA 475
PN 421 ADAPGAGATAGIHWYSQQLXQIGTWLSDSEALHPLGMVAKSSSRGAGGAREGA 475
XX

PD 07-JUN-2001.

XX 30-NOV-2000; 2000WO-US32590.

PF XX

PR 30-NOV-1999; 99US-0168112.

XX

PA (CURI-) CURIS INC.

XX

PI Crompton T;

XX

WPI: 2001-441484/7.

DR N-PDB; AAH20451.

XX

PT Modulating immune function comprises administration of a hedgehog or ptc agent, for treating e.g. diabetes, eczematous dermatitis, urticaria or vasculitis -

PT XX

PS Claim 4; Page 84-86; 105pp; English.

XX

CC The present sequence represents a hedgehog (Shh) polypeptide. Hedgehog gene products and signal transduction pathways involving hedgehog are involved in the maturation of T lymphocytes. The specification describes a method for modulating immune function, by administration of a hedgehog or patched (ptc) polypeptide agonists or antagonists. The method is used to treat disorders affecting the regulation of lymphocytes, particularly maturation and/or activation of T lymphocytes. It is used, to treat bacterial or viral infection, diabetes, nutritional deficiencies, graft rejection or other hyperacute response such as kidney, heart, lung, bone marrow, spleen, skin or cornea transplant or autoimmune disorders such as multiple sclerosis, psoriasis or atopic dermatitis. The method is used to treat inflammatory, proliferative and hyperproliferative diseases, as well as cutaneous manifestations of immunological disorders such as eczematous dermatitis, urticaria, vasculitis and scleroderma.

SQ Sequence 475 AA;

Query Match Best Local Similarity 99.9%; Score 2477; DB 22; Length 475; Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLARCLLIVVSSLVCGSLACGPGRGFKRHPKKLTPLAYKQIFIPNVAEKTGASG 60
DB 1 MLLARCLLIVVSSLVCGSLACGPGRGFKRHPKKLTPLAYKQIFIPNVAEKTGASG 60
QY 61 RYEGKISRNSERKELTPNYPDIKFKEENIGADRLMTQRCDKLNALISTMNQWGV 120
DB 61 RYEGKISRNSERKELTPNYPDIKFKEENIGADRLMTQRCDKLNALISTMNQWGV 120
QY 121 KLRTEGEGDEGHSEESLHYEGRADITTSDRSKIGMLAVERAGFDWYYESAH 180
DB 121 KLRTEGEGDEGHSEESLHYEGRADITTSDRSKIGMLAVERAGFDWYYESAH 180
QY 181 IHESVKAENSAVAKSGGCPPGSAVHLRQGTKLVKDLSPGDRVLAADDQGRILYSDLT 240
DB 181 IHESVKAENSAVAKSGGCPPGSAVHLRQGTKLVKDLSPGDRVLAADDQGRILYSDLT 240
QY 241 FLRQDGAKKVYVIETREPRERLTAAHLVWAPHDSATEPEAASSGGSPGGALG 300
DB 241 FLRQDGAKKVYVIETREPRERLTAAHLVWAPHDSATEPEAASSGGSPGGALG 300
QY 301 PRALEASRVPGQVVVVAERDQRRLPAPAVIVSLSSEEAGAYAIPLAGTQGTLINRL 360

Db 301 PRALFASRVPGQVVVVAERDQRRLPAPAVIVSLSSEEAGAYAIPLAGTQGTLINRL 360
Qy 361 ASCYAVIEHSHWAHRAFAPRFLAHALLAALAPARTDGGDSGGDRGGGVALTAPG 420
Db 361 ASCYAVIEHSHWAHRAFAPRFLAHALLAALAPARTDGGDSGGDRGGGVALTAPG 420
Qy 421 ADAPGAGATAGIHWYSQQLXQIGTWLSDSEALHPLGMVAKSSSRGAGGAREGA 475
Db 421 ADAPGAGATAGIHWYSQQLXQIGTWLSDSEALHPLGMVAKSSSRGAGGAREGA 475
RESULT 12
AEE04687
ID AAE04687 standard; Protein; 475 AA.

XX

AC AAE04687:
XX

DT 04-SEP-2001 (first entry)

XX

DE Human sonic hedgehog (Shh) protein.

XX

KW Human; hedgehog protein; nootropic; neuroprotective; anticonvulsant; cytostatic; therapy; Alzheimer's disease; injury; Huntington's chorea; amyotrophic lateral sclerosis; multiple sclerosis; nervous system aging; neurodegenerative disease; immunological disease; malignant glioma; medulloblastoma; neuroectodermal tumour; cancer; extracellular signalling protein.

KW

OS Homo sapiens.

XX

FH Key Region 24..197

FT Location/Qualifiers /note= "N-terminal fragment"

FT Misc-difference 463
FT /label= Unknown
FT /note= "Encoded by NNN"

XX

PN WO200134654-A1.

XX

PD 17-MAY-2001.

XX

PF 02-NOV-2000; 2000WO-US30405.

XX

PR 05-NOV-1999; 99US-0164025.

XX

PA (BIOJ) BIOPHARM INC.

XX

PI Strauch K;

XX

WPI: 2001-329075/34.

DR N-PDB; AAD09034.

XX

PT Novel isolated hedgehog fusion polypeptide useful for treating neurological conditions such as Alzheimer's disease, Parkinson's disease, Huntington's chorea, amyotrophic lateral sclerosis, and multiple sclerosis -

XX

PS Disclosure; Page 117-118; 178pp; English.

XX

CC The present invention relates to hedgehog fusion proteins. Hedgehog proteins are a family of extracellular signalling proteins that regulate various aspects of embryonic development both in vertebrates and in invertebrates. Hedgehog fusion protein is useful for the prophylaxis or treatment of any condition or disease state for which a hedgehog or patched protein constituent is efficacious and in the diagnosis of constituents or conditions of disease states in biological system or specimens and for diagnostic purposes in non-physiological systems.

CC Hedgehog fusion protein is useful for treating neurological conditions due to injury, aging of nervous system, including Alzheimer's disease, chronic neurodegenerative diseases of the nervous system, including Parkinson's disease, Huntington's chorea, amyotrophic lateral sclerosis and chronic immunological diseases of nervous system including multiple

CC	sclerosis and malignant gliomas, medulloblastomas, neuroectodermal tumours and to specifically target medical therapies against cancers and tumours which express the receptor for the protein. The present sequence is human sonic hedgehog (Shh) protein.
XX	sequence 475 AA;
SO	Query Match 99.9%; Score 2467; DB 22; Length 475; Best Local Similarity 100.0%; Pred. No. 5.9e-218; Mismatches 0; Indels 0; Gaps 0;
OY	1 MLLARCLLVLVSSILVCSGLACGPGRGKRRRKPPLTPLAYQFIPNVAEKTIGASG 60 1 MLLARCLLVLVSSILVCSGLACGPGRGKRRRKPPLTPLAYQFIPNVAEKTIGASG 60
Db	RYEKISRNSRERKELTPTNPDIFKDEENTGADRMLTORCKDKLNALISVNQWPGV 120
OY	1 KLRVTEGWDGHSEESLVEGRADITSDRDRSKYGMARAVEAGFDWVYESKAH 180 1 KLRVTEGWDGHSEESLVEGRADITSDRDRSKYGMARAVEAGFDWVYESKAH 180
Db	IHCsvkaensvaaksgccfgsatvhleogktklykdlsqdrvladdogrlylsdflt 240
OY	IHCsvkaensvaaksgccfgsatvhleogktklykdlsqdrvladdogrlylsdflt 240 IHCsvkaensvaaksgccfgsatvhleogktklykdlsqdrvladdogrlylsdflt 240
Db	FLDRDGAKKVFVYIETREPRERLLTAAHLFVAPHDNSATGEPPEAASSGGPSSGALG 300
OY	FLDRDGAKKVFVYIETREPRERLLTAAHLFVAPHDNSATGEPPEAASSGGPSSGALG 300 FLDRDGAKKVFVYIETREPRERLLTAAHLFVAPHDNSATGEPPEAASSGGPSSGALG 300
Db	PRALFAVRPGQRTWVAERDGRRLPAVHSVTLSEERAGAYAPLTAQGTILINRVL 360
OY	PRALFAVRPGQRTWVAERDGRRLPAVHSVTLSEERAGAYAPLTAQGTILINRVL 360 PRALFAVRPGQRTWVAERDGRRLPAVHSVTLSEERAGAYAPLTAQGTILINRVL 360
Db	ASCYAVIEEHSAHRAPPLAHALLAALAPARDGGGGGGDRGGGGGRVLTAPGA 420
OY	ASCYAVIEEHSAHRAPPLAHALLAALAPARDGGGGGGDRGGGGGRVLTAPGA 420 ASCYAVIEEHSAHRAPPLAHALLAALAPARDGGGGGGDRGGGGGRVLTAPGA 420
Db	ADPGAGATAGIHWSQLQIGTWLDSERALPIGMAMVSSXSRGAGGAREGA 475
OY	ADPGAGATAGIHWSQLQIGTWLDSERALPIGMAMVSSXSRGAGGAREGA 475 ADPGAGATAGIHWSQLQIGTWLDSERALPIGMAMVSSXSRGAGGAREGA 475
Db	ADPGAGATAGIHWSQLQIGTWLDSERALPIGMAMVSSXSRGAGGAREGA 475
RESULT 13	
AAE05377	
ID	AAE05377 standard; protein; 475 AA.
XX	
AC	AAE05377;
XX	
DT	12-SEP-2001 (first entry)
DE	Human Sonic hedgehog protein.
XX	
KW	Human; Sonic hedgehog; Shh; morphogenic signal; neuron; chromosome 7q; embryonic patterning; cell culture; cell differentiation; ischaemia; cell proliferative disorder; intracerebral grafting; Huntington's chorea; neurological disorder; Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis; ALS; multiple sclerosis.
OS	Homo sapiens.
XX	
PH	Key Location/Qualifiers
FT	Misc-difference 463 Label= Unknown /note= "Encoded by NNN"
XX	US6261786-B1.
XX	17-JUL-2001.
PD	
XX	02-JUL-1996; 96US-0674509.
XX	
PR	30-DEC-1993; 93US-017627.
PR	14-DEC-1994; 94US-035600.
PR	04-MAY-1995; 95US-043503.
PR	05-JUN-1995; 95US-046090.
PR	05-JUN-1995; 95US-0462386.
XX	(IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD. (HARD) HARVARD COLLEGE.
PA	Marijo V, Tabin CJ, Ingham PW, McMahon AP;
XX	DR WPI; 2001-440859/47.
XX	N-PSDB; AAD10151.
PT	Screening compounds that potentiate or inhibit binding of hedgehog polypeptide to naturally occurring patched receptor, comprises contracting Polypeptide with receptor and test compound, and detecting change in binding
XX	PS claim 2; column 163-166; 127pp: English.
XX	The present invention relates to assay for screening compounds that potentiate or inhibit binding of hedgehog polypeptide to naturally occurring patched receptor. The hedgehog proteins comprise morphogenetic signals produced by embryonic patterning centres, and are involved in the formation and maintenance of ordered spatial arrangements of differentiated tissues in vertebrates, both adult and embryonic. The proteins can be used to generate and/or maintain an array of different vertebrate tissues both in vitro and in vivo. The invention also relates to a method for modulating growth, differentiation or survival of a mammalian cell (e.g. neuron, testicular cell) responsive to hedgehog induction. Hedgehog agonists and antagonists can be used in cell culture techniques to enhance survival and maintenance of neurons and various vertebrate organogenic pathways. The hedgehog gene is useful in determining whether a patient is at the risk of disorder characterised by unwanted cell proliferation or aberrant control of differentiation. The hedgehog proteins or mimetics can be used to induce foetal neurons especially neuronal stem cells in intracerebral grafting. The protein or its mimetic can be used in the treatment of neurological conditions e.g. injury to nervous system, ischaemia resulting from stroke, Alzheimer's disease, Parkinson's disease, Huntington's chorea, amyotrophic lateral sclerosis (ALS) and multiple sclerosis. The present sequence is human Sonic hedgehog (Shh) protein. The shh gene is located on human chromosome 7q.
XX	SQ Sequence 475 AA;
SO	Query Match 99.9%; Score 2467; DB 22; Length 475; Best Local Similarity 100.0%; Pred. No. 5.9e-218; Mismatches 0; Indels 0; Gaps 0;
OY	1 MLLARCLLVLVSSILVCSGLACGPGRGKRRRKPPLTPLAYQFIPNVAEKTIGASG 60 1 MLLARCLLVLVSSILVCSGLACGPGRGKRRRKPPLTPLAYQFIPNVAEKTIGASG 60
Db	RYEKISRNSRERKELTPTNPDIFKDEENTGADRMLTORCKDKLNALISVNQWPGV 120
OY	1 KLRVTEGWDGHSEESLVEGRADITSDRDRSKYGMARAVEAGFDWVYESKAH 180 1 KLRVTEGWDGHSEESLVEGRADITSDRDRSKYGMARAVEAGFDWVYESKAH 180
Db	IHCsvkaensvaaksgccfgsatvhleogktklykdlsqdrvladdogrlylsdflt 240
OY	IHCsvkaensvaaksgccfgsatvhleogktklykdlsqdrvladdogrlylsdflt 240 IHCsvkaensvaaksgccfgsatvhleogktklykdlsqdrvladdogrlylsdflt 240
Db	FLDRDGAKKVFVYIETREPRERLLTAAHLFVAPHDNSATGEPPEAASSGGPSSGALG 300
OY	FLDRDGAKKVFVYIETREPRERLLTAAHLFVAPHDNSATGEPPEAASSGGPSSGALG 300 FLDRDGAKKVFVYIETREPRERLLTAAHLFVAPHDNSATGEPPEAASSGGPSSGALG 300
Db	PRALFAVRPGQRTWVAERDGRRLPAVHSVTLSEERAGAYAPLTAQGTILINRVL 360
OY	PRALFAVRPGQRTWVAERDGRRLPAVHSVTLSEERAGAYAPLTAQGTILINRVL 360

Db 301 PRALFASRVRPGORVYVAERODDRRLPAAVHSVTLEEAAGAYAPLTAQTLINRVL 360
Qy 361 ASCYAVIEEHSHWARAFPFRLAHALLAALAPARTDRGGDSGGDRGGGRVVALPAGA 420
Db 361 ASCYAVIEEHSHWARAFPFRLAHALLAALAPARTDRGGDSGGDRGGGRVVALPAGA 420
Qy 421 ADAPGAGATAGIHWYSOLLYQIGTWLIDSEALHPLGMKVKSSXSRGAGGAREGA 475
Db 421 ADAPGAGATAGIHWYSOLLYQIGTWLIDSEALHPLGMKVKSSXSRGAGGAREGA 475

RESULT 14

AAB31222
ID AAB31222 standard; Protein; 475 AA.
XX
AC AAB31222;
XX
DT 20-APR-2001 (first entry)

DE Amino acid sequence of human sonic hedgehog protein (Shh).
XX
KW Hedgehog related protein; sonic hedgehog protein; Shh; ischemia; stroke; desert hedgehog protein; Dh; Indian hedgehog protein; Ihh; neuron; neurological condition; nervous system injury; tumour-induced injury; aging; Alzheimer's disease; chronic neurodegenerative disease; Parkinson's disease; Huntington's chorea; amyotrophic lateral sclerosis; spinocerebellar degeneration; chronic immunological disease; multiple sclerosis.

XX
OS Homo sapiens.

XX
Key Location/Qualifiers
FH
FT Msc-difference 463 /note- "unspecified amino acid encoded by NNN"
XX
US6165747-A.

XX
PD 26-DEC-2000.
XX
PF 05-JUN-1995; 95US-0460900.
XX
PR 30-DEC-1993; 93US-0176427.
PR 14-DEC-1994; 94US-0356060.
PR 04-MAY-1995; 95US-0335093.
XX
PA (HARD) HARVARD COLLEGE.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.

PT Ingham PW, McMahon AP, Tabin CJ, Marti-gorostiza E, Buncrot DA;
XX
DR WPI; 2001-079847/09.
DR N-PSDB; AAC87079.

XX
PT Polynucleotides encoding hedgehog proteins; useful for treating diseases of nervous system such as Alzheimer's disease, Parkinson's disease, Huntington's chorea, amyotrophic lateral sclerosis, multiple sclerosis .
PT Claim 10: Columns 147-150; 119pp; English.

XX
The present sequence represents a hedgehog related-protein. The specification describes a sonic hedgehog protein (Shh), a desert hedgehog protein (Dhh), and an Indian hedgehog protein (Ihh). The hedgehog polynucleotides are useful in diagnostic, in antisense therapy and in therapeutic assays for detecting and treating disorders involving, e.g., aberrant expression of vertebrate hedgehog homologue. Hedgehog polypeptides are useful therapeutically to enhance survival of neurons and other neuron cells and in treating neurological conditions deriving from acute, subacute, or chronic injury to the nervous system, including traumatic injury, chemical injury, vasal injury and deficits (such as the ischemia resulting from stroke), together with infectious/inflammatory and induced-induced injury, aging of the nervous system including Alzheimer's disease, chronic

CC neurodegenerative diseases of the nervous system, including Parkinson's disease, Huntington's chorea, amyotrophic lateral sclerosis, spinocerebellar degenerations, and chronic immunological diseases of the nervous system or affecting the nervous system, including multiple sclerosis.

XX
SO Sequence 475 AA;

Query Match	Best Local Similarity	Score	Length	Matches	Conservative	Mismatches	Indels	Gaps
Qy	1 MLLARCLLVLVSSLLVSLVSGLACGPGERGEGRRPKLTPLAYKOPIPNVAEKTGAG 60	99.9%	2467	DB 22;	99.9%	0	0	0
Db	1 MLLARCLLVLVSSLLVSGLACGPGERGEGRRPKLTPLAYKOPIPNVAEKTGAG 60	100.0%	2467	DB 22;	100.0%	0	0	0
Qy	61 RVEGKISRNSEERKEELTPNYNDIFKIDENTGADRMTQRKDKNLNLATSYMNOQPGV 120	99.9%	2467	DB 22;	99.9%	0	0	0
Db	61 RVEGKISRNSEERKEELTPNYNDIFKIDENTGADRMTQRKDKNLNLATSYMNOQPGV 120	100.0%	2467	DB 22;	100.0%	0	0	0
Qy	121 KLRVTEGMDEDGHSESSLHYSGRAVDITTSDRDRSKYGMALARLAVERAGFDWVYESKAH 180	99.9%	2467	DB 22;	99.9%	0	0	0
Db	121 KLRVTEGMDEDGHSESSLHYSGRAVDITTSDRDRSKYGMALARLAVERAGFDWVYESKAH 180	100.0%	2467	DB 22;	100.0%	0	0	0
Qy	181 IICSYVKAENSAAKSGCGFCPGSATVHLEGGTKLVQLSPGDYRLADDQRLYSDFL 240	99.9%	2467	DB 22;	99.9%	0	0	0
Db	181 IICSYVKAENSAAKSGCGFCPGSATVHLEGGTKLVQLSPGDYRLADDQRLYSDFL 240	100.0%	2467	DB 22;	100.0%	0	0	0
Qy	241 FLDRDGAKKVVFVIERPREPRLLTAAHLFVAPHNSDAGPEPEASSGSPGSGALG 300	99.9%	2467	DB 22;	99.9%	0	0	0
Db	241 FLDRDGAKKVVFVIERPREPRLLTAAHLFVAPHNSDAGPEPEASSGSPGSGALG 300	100.0%	2467	DB 22;	100.0%	0	0	0
Qy	301 PRALFASRVRPGORVYVAERODDRRLPAAVHSVTLEEAAGAYAPLTAQTLINRVL 360	99.9%	2467	DB 22;	99.9%	0	0	0
Db	301 PRALFASRVRPGORVYVAERODDRRLPAAVHSVTLEEAAGAYAPLTAQTLINRVL 360	100.0%	2467	DB 22;	100.0%	0	0	0
Qy	361 ASCYAVIEEHSHWARAFPFRLAHALLAALAPARTDRGGDSGGDRGGGRVVALPAGA 420	99.9%	2467	DB 22;	99.9%	0	0	0
Db	361 ASCYAVIEEHSHWARAFPFRLAHALLAALAPARTDRGGDSGGDRGGGRVVALPAGA 420	100.0%	2467	DB 22;	100.0%	0	0	0
Qy	421 ADAPGAGATAGIHWYSOLLYQIGTWLIDSEALHPLGMKVKSSXSRGAGGAREGA 475	99.9%	2467	DB 22;	99.9%	0	0	0
Db	421 ADAPGAGATAGIHWYSOLLYQIGTWLIDSEALHPLGMKVKSSXSRGAGGAREGA 475	100.0%	2467	DB 22;	100.0%	0	0	0

PA (BIOJ) BIOPRO INC.
 XX
 PI Pepinsky RB, Taylor F, Garber E;
 XX WPI; 2001-049922/06.
 DR N-PSDB; AAT27018.
 XX
 PT Modified hedgehog protein, useful in the treatment of Parkinson's disease and Huntington's chorea, comprises a polymer containing a polyalkylene glycol group linked to any residue other than the N-terminal and lysine residues -
 PT
 XX
 PS Disclosure: Page 138-140; 157pp; English.

CC The invention relates to novel polymer conjugates of hedgehog proteins which have increased bioavailability. The hedgehog proteins are conjugated to a non-naturally-occurring polymer comprising a polyalkylene glycol group, with the proviso that the polymer is not conjugated to the N-terminus, or to lysine residues of the hedgehog protein. The hedgehog protein used in the conjugate may be a wild type or mutant Sonic hedgehog (Shh), Indian hedgehog (Ihh) or Desert hedgehog (Dhh) protein, or may be a hedgehog fusion protein. The invention also relates to methods of defining and mapping functionally important regions of a protein by modifying accessible amino acid side chains, and determining the effect the position and/or type of modification have on the activity of the protein. The hedgehog polymer conjugates may be used in the management of various medical conditions including various neurological disorders, inflammatory and autoimmune diseases, and cancers. In particular, they may be used to prevent, preventing or ameliorate neurodegenerative disorders (e.g., Parkinson's disease, Huntington's disease, Alzheimer's disease; age-associated neurological disease; neurological injury and trauma; immunological diseases of the nervous system (e.g., multiple sclerosis); stroke; and malignant gliomas, medulloblastomas and neuroectodermal tumours. The modifications made to the hedgehog protein may result in increased half-life, altered tissue distribution (such as an improved ability to stay in the vasculature for longer periods of time), increased stability in solution, protection from proteolytic degradation, or reduced immunogenicity. In particular, the ability to remain in the vasculature for prolonged periods may allow a hedgehog protein of the invention to cross the blood brain barrier, and an increased thermal stability would be an advantage when formulating the hedgehog protein in powder form. The present sequence represents a member of the hedgehog family of proteins.
 CC
 XX
 SQ Sequence 475 AA;

Query Match 99.9%; Score 2467; DB 22; Length 475;
 Best Local Similarity 100.0%; Pred. No. 5.9e-218; Length 475;
 Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	Db	Qy	Db
1	1	361	361
MILLARCLLVLVYSSLLVCGSLACGCPGRGRGRKRRPKKKLPLAKQFIRWAETKLGASG	MILLARCLLVLVSSLLVCGSLACGCPGRGRGKRHRPKKKLPLAKQFIRWAETKLGASG	ASCYAVIEHSWAHRAFAPPRLAHALLAATAPARTDRGGISGGDRGGGGRVALTAPGA	ASCYAVIEHSWAHRAFAPPRLAHALLAATAPARTDRGGISGGDRGGGGRVALTAPGA
60	60	421	421
61 RYEKISRNSERKFELTPNPNPDKFDENTGADRMLTQCKOKNLALISVWQPGV	61 RYEKISRNSERKFELTPNPNPDKFDENTGADRMLTQCKOKNLALISVWQPGV	ADAPGAGATGTHWSQLIQIGTWMILDSRALTHPIGMAVSSXSGAGGCAREGA	ADAPGAGATAGIHWYSOLLYQIGTWMILDSRALTHPIGMAVSSXSGAGGCAREGA
120	120	475	475
121 KLRVTEGWDDEGHSEESLVEGRADITTSDRDRSKYGMALARLAVEAGFDWVYESKAH	121 KLRVTEGWDDEGHSEESLVEGRADITTSDRDRSKYGMALARLAVEAGFDWVYESKAH		
180	180		
181 IHCSYKAENSAAKSGCGFCGSGATVHLEGGTKVYKDLSPGDRRLAADDQGRGLYSDFT	181 IHCSYKAENSAAKSGCGFCGSGATVHLEGGTKVYKDLSPGDRRLAADDQGRGLYSDFT		
240	240		
241 FLDRDGAKKVYVTFREERERILTAHLFLPHNSATGPEASSGSGPPSGGA	241 FLDRDGAKKVYVTFREERERILTAHLFLPHNSATGPEASSGSGPPSGGA	300	300
300	300		
301 PRALEASRVPRGQTYVVAERDGRRLPAHVSEVTLSBAAAGYAPLIAQGTILINRVL	301 PRALEASRVPRGQTYVVAERDGRRLPAHVSEVTLSBAAAGYAPLIAQGTILINRVL	360	360
360	360		
301 PRALEASRVPRGQTYVVAERDGRRLPAHVSEVTLSBAAAGYAPLIAQGTILINRVL	301 PRALEASRVPRGQTYVVAERDGRRLPAHVSEVTLSBAAAGYAPLIAQGTILINRVL	360	360

Qy 361 ASCYAVIEHSWAHRAFAPPRLAHALLAATAPARTDRGGISGGDRGGGGRVALTAPGA 420
 Db 361 ASCYAVIEHSWAHRAFAPPRLAHALLAATAPARTDRGGISGGDRGGGGRVALTAPGA 420
 Qy 421 ADAPGAGATGTHWSQLIQIGTWMILDSRALTHPIGMAVSSXSGAGGCAREGA 475
 Db 421 ADAPGAGATAGIHWYSOLLYQIGTWMILDSRALTHPIGMAVSSXSGAGGCAREGA 475

Search completed: February 20, 2003, 10:10:20
 Job time: 36.4615 secs

Db 1 MLLARCLLYLVSSILVCGSLCPGPGKGRPKKLUPLAYQFIPVAEKTIGASG 60

Db 61 RVEGKTSRNSERFKELTPNPNPDIKFDEENTGADRMLTRCKDKLNALAI SVINQWPGV 120

Db 61 RVEGKTSRNSERFKELTPNPNPDIKFDEENTGADRMLTRCKDKLNALAI SVINQWPGV 120

Oy 121 KLRVTEGWDGDGHHSBESLHVEGRADITSDRDRSKYGMALARAVEAGFDWVYYESKAH 180

Db 121 KLRVTEGWDGDGHHSBESLHVEGRADITSDRDRSKYGMALARAVEAGFDWVYYESKAH 180

Oy 181 IHCSYKAENSAKSGCCFFPSATVHLEQGKTLVKLDLSQGDRVLAADDGRLXSDFT 240

Db 181 IHCSYKAENSAKSGCCFFPSATVHLEQGKTLVKLDLSQGDRVLAADDGRLXSDFT 240

Oy 241 FLDRDGAKKVYVETREPRERLITAHLFVAPHNDSDATGEPEASSGGPPSGGALG 300

Db 241 FLDRDGAKKVYVETREPRERLITAHLFVAPHNDSDATGEPEASSGGPPSGGALG 300

Oy 301 PRALAFSRVPGQRYVVAERDGRDLPLPAVHSVTLSERAGAYAPLTQGTILINRV 360

Db 301 PRALAFSRVPGQRYVVAERDGRDLPLPAVHSVTLSERAGAYAPLTQGTILINRV 360

Oy 361 ASCYAVIEEHSAHRAFAPPRLAHALLAALAPARDRGDSGGDRGGGGGRVALTAPGA 420

Db 361 ASCYAVIEEHSAHRAFAPPRLAHALLAALAPARDRGDSGGDRGGGGGRVALTAPGA 420

Oy 421 ADAPGAGATAGIHWYSQOLYQIGTWILDSEALHPLGMAYKSSXSRGAGGAREGA 475

Db 421 ADAPGAGATAGIHWYSQOLYQIGTWILDSEALHPLGMAYKSSXSRGAGGAREGA 475

RESULT 2
US-08-900C-13
; Sequence 13, Application US/08460900C

; GENERAL INFORMATION:
; APPLICANT: Ingham, Phillip W.
; APPLICANT: McMahon, Andrew P.
; APPLICANT: Tabin, Clifford J.
; APPLICANT: Buncrot, David A.
; APPLICANT: Marti-Gorostiza, Elisa

TITLE OF INVENTION: Vertebrate Embryonic Pattern Inducing
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,900C

FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/435,093
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.

REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HAV-006.05

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 832-1000
TELEFAX: (617) 832-7000

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 475 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

Query Match 99.9%; Score 2467; DB 4; Length 475;
Best Local Similarity 100 %; Pred. No. 8.2e-239;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MLLARCLLYLVSSILVCGSLCPGPGKGRPKKLUPLAYQFIPVAEKTIGASG 60

Db 61 RVEGKTSRNSERFKELTPNPNPDIKFDEENTGADRMLTRCKDKLNALAI SVINQWPGV 120

Oy 121 KLRVTEGWDGDGHHSBESLHVEGRADITSDRDRSKYGMALARAVEAGFDWVYYESKAH 180

Db 121 KLRVTEGWDGDGHHSBESLHVEGRADITSDRDRSKYGMALARAVEAGFDWVYYESKAH 180

Oy 181 IHCSYKAENSAKSGCCFFPSATVHLEQGKTLVKLDLSQGDRVLAADDGRLXSDFT 240

Db 181 IHCSYKAENSAKSGCCFFPSATVHLEQGKTLVKLDLSQGDRVLAADDGRLXSDFT 240

Oy 241 FLDRDGAKKVYVETREPRERLITAHLFVAPHNDSDATGEPEASSGGPPSGGALG 300

Db 241 FLDRDGAKKVYVETREPRERLITAHLFVAPHNDSDATGEPEASSGGPPSGGALG 300

Oy 301 PRALAFSRVPGQRYVVAERDGRDLPLPAVHSVTLSERAGAYAPLTQGTILINRV 360

Db 301 PRALAFSRVPGQRYVVAERDGRDLPLPAVHSVTLSERAGAYAPLTQGTILINRV 360

Oy 361 ASCYAVIEEHSAHRAFAPPRLAHALLAALAPARDRGDSGGDRGGGGGRVALTAPGA 420

Db 361 ASCYAVIEEHSAHRAFAPPRLAHALLAALAPARDRGDSGGDRGGGGGRVALTAPGA 420

Oy 421 ADAPGAGATAGIHWYSQOLYQIGTWILDSEALHPLGMAYKSSXSRGAGGAREGA 475

Db 421 ADAPGAGATAGIHWYSQOLYQIGTWILDSEALHPLGMAYKSSXSRGAGGAREGA 475

RESULT 3
US-08-674-509B-13
; Sequence 13, Application US/08674509B

; GENERAL INFORMATION:
; APPLICANT: Ingham, Phillip W.
; APPLICANT: McMahon, Andrew P.
; APPLICANT: Tabin, Clifford J.
; APPLICANT: Marigo, Valeria

TITLE OF INVENTION: SCREENING ASSAYS FOR HEDGESEG AGONISTS
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/435,093
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.

REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HAV-006.05

APPLICATION NUMBER: US/08/674, 509B
 FILING DATE: 02-JUL-1996
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/460, 900
 FILING DATE: 05-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Vincent, Matthew P.
 REGISTRATION NUMBER: 36,709
 REFERENCE/DOCKET NUMBER: HMV-006.05
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-832-1000
 TELEFAX: 617-832-7000
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 475 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-674-509B-13

Query Match 99 %; Score 2467; DB 4; Length 475;
 Best Local Similarity 100.0%; Pred. No. 8.2e-239; Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLARCLLVLVSSLVCSGLACGPGRGKRRHPPKKLTPLAYKQFIPNVAEKTIGASG 60
 Db 1 MLLARCLLVLVSSLVCSGLACGPGRGKRRHPPKKLTPLAYKQFIPNVAEKTIGASG 60
 QY 61 RYEKISRNSERFEKELTPNYPNDIFKDENTGADRMLTQRCOKLNALISTYNQPGV 120
 61 RYEKISRNSERFEKELTPNYPNDIFKDENTGADRMLTQRCOKLNALISTYNQPGV 120
 QY 121 KLRVTEGWDGHISEESHYEGRAVDITTSDRRSKYGMRLAVAEAGFDWVYYESAH 180
 Db 121 KLRVTEGWDGHISEESHYEGRAVDITTSDRRSKYGMRLAVAEAGFDWVYYESAH 180
 QY 181 IHCSVKAENSAVAKSGCCPGSATVHLEQGTIKVLKDLSPGDRVLAAADDQGRILYSDELT 240
 Db 181 IHCSVKAENSAVAKSGCCPGSATVHLEQGTIKVLKDLSPGDRVLAAADDQGRILYSDELT 240
 QY 241 FLDRDGAKKVYVETTRPREPRLTAAHLFVAPHNDSDATGEPEASSGGSPGSGALG 300
 241 FLDRDGAKKVYVETTRPREPRLTAAHLFVAPHNDSDATGEPEASSGGSPGSGALG 300
 QY 301 PRAFLASRVRPGORYVWAERDGDRLPAVHSVTLSEBAAAGAYAPLTAQGTILINRVL 360
 301 PRAFLASRVRPGORYVWAERDGDRLPAVHSVTLSEBAAAGAYAPLTAQGTILINRVL 360
 Db 361 ASCYAVIEEHSAWAHRAPFLRALAHALLAALAPARTDRGGDSGGDRGGGRVALTARGA 420
 361 ASCYAVIEEHSAWAHRAPFLRALAHALLAALAPARTDRGGDSGGDRGGGRVALTARGA 420
 QY 421 ADPGAGATAGIHWSOLLYQIGWLDSREALHPLGMAVKSSXSRGAGGAREGA 475
 Db 421 ADPGAGATAGIHWSOLLYQIGWLDSREALHPLGMAVKSSXSRGAGGAREGA 475
 RESULT 4
 US-08-954-698-13
 Sequence 13, Application US/08954698
 Patient No. 6271363
 GENERAL INFORMATION:
 APPLICANT: Ingham, Phillip W.
 APPLICANT: McMahon, Andrew P.
 APPLICANT: Tabin, Clifford J.
 TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
 NUMBER OF SEQUENCES: 48
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FOLLY, HOAG & ELIOT LLP
 STREET: One Post Office Square
 CITY: Boston

STATE: MA
 COUNTRY: USA
 ZIP: 02109-2170
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/954, 698
 FILING DATE: 20-OCT-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/462, 386
 FILING DATE: 05-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/435, 093
 FILING DATE: 04-MAY-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/356, 060
 FILING DATE: 14-DEC-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/176, 427
 FILING DATE: 30-DEC-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Vincent, Matthew P.
 REGISTRATION NUMBER: 36,709
 REFERENCE/DOCKET NUMBER: HMV-006.10
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-832-1000
 TELEFAX: 617-832-7000
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 475 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-954-698-13

Query Match 99 %; Score 2467; DB 4; Length 475;

Best Local Similarity 100.0%; Pred. No. 8.2e-239; Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLARCLLVLVSSLVCSGLACGPGRGKRRHPPKKLTPLAYKQFIPNVAEKTIGASG 60
 Db 1 MLLARCLLVLVSSLVCSGLACGPGRGKRRHPPKKLTPLAYKQFIPNVAEKTIGASG 60
 QY 61 RYEKISRNSERFEKELTPNYPNDIFKDENTGADRMLTQRCOKLNALISTYNQPGV 120
 61 RYEKISRNSERFEKELTPNYPNDIFKDENTGADRMLTQRCOKLNALISTYNQPGV 120
 QY 121 KLRVTEGWDGHISEESHYEGRAVDITTSDRRSKYGMRLAVAEAGFDWVYYESAH 180
 Db 121 KLRVTEGWDGHISEESHYEGRAVDITTSDRRSKYGMRLAVAEAGFDWVYYESAH 180
 QY 181 IHCSVKAENSAVAKSGCCPGSATVHLEQGTIKVLKDLSPGDRVLAAADDQGRILYSDELT 240
 Db 181 IHCSVKAENSAVAKSGCCPGSATVHLEQGTIKVLKDLSPGDRVLAAADDQGRILYSDELT 240
 QY 241 FLDRDGAKKVYVETTRPREPRLTAAHLFVAPHNDSDATGEPEASSGGSPGSGALG 300
 241 FLDRDGAKKVYVETTRPREPRLTAAHLFVAPHNDSDATGEPEASSGGSPGSGALG 300
 QY 301 PRAFLASRVRPGORYVWAERDGDRLPAVHSVTLSEBAAAGAYAPLTAQGTILINRVL 360
 301 PRAFLASRVRPGORYVWAERDGDRLPAVHSVTLSEBAAAGAYAPLTAQGTILINRVL 360
 Db 361 ASCYAVIEEHSAWAHRAPFLRALAHALLAALAPARTDRGGDSGGDRGGGRVALTARGA 420
 361 ASCYAVIEEHSAWAHRAPFLRALAHALLAALAPARTDRGGDSGGDRGGGRVALTARGA 420
 QY 421 ADPGAGATAGIHWSOLLYQIGWLDSREALHPLGMAVKSSXSRGAGGAREGA 475
 Db 421 ADPGAGATAGIHWSOLLYQIGWLDSREALHPLGMAVKSSXSRGAGGAREGA 475
 RESULT 4
 US-08-954-698-13
 Sequence 13, Application US/08954698
 Patient No. 6271363
 GENERAL INFORMATION:
 APPLICANT: Ingham, Phillip W.
 APPLICANT: McMahon, Andrew P.
 APPLICANT: Tabin, Clifford J.
 TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
 NUMBER OF SEQUENCES: 48
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FOLLY, HOAG & ELIOT LLP
 STREET: One Post Office Square
 CITY: Boston

RESULT 5
 US-08-957-874-13
 ; Sequence 13, Application US/08957874
 ; Patent No. 6384192

GENERAL INFORMATION:

APPLICANT: Ingham, Phillip W.
 APPLICANT: McMahon, Andrew P.
 APPLICANT: Tabin, Clifford J.

TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
 NUMBER OF SEQUENCES: 47
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FOLEY, HOAG & ELIOT LLP
 STREET: One Post Office Square
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII (text)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/957,874
 FILING DATE: 20-OCT-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/462,386
 FILING DATE: 5-JUNE-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/435,093
 FILING DATE: 4-MAY-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/356,060
 FILING DATE: 14-DEC-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/176,427
 FILING DATE: 30-DEC-1993

ATTORNEY/AGENT INFORMATION:

NAME: Vincent, Matthew P.
 REFERENCE/DOCKET NUMBER: 36,709
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 832-1000
 TELEFAX: (617) 832-7000

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:
 LENGTH: 475 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-957-874-13

Query Match 99.9%; Score 2467; DB 4; Length 475;
 Best Local Similarity 100.0%; Pred. No. 8.2e-239; Indels 0; Gaps 0;
 Matches 475; Conservative 0; Mismatches 0; Delins 0;

Qy 1 MLLARCLLVLVYSSLVCGSLACGPGRGKRRKPKKLPLAKQKFIPNVAEKTIGASG 60
 Db 1 MLLARCLLVLVYSSLVCGSLACGPGRGKRRKPKKLPLAKQKFIPNVAEKTIGASG 60

Qy 61 RYEKTSRNSRERKELTTPNNPNDIFKDEENTGADRMLTORKCKOKNALAISVMNQPGV 120
 Db 61 RYEKTSRNSRERKELTTPNNPNDIFKDEENTGADRMLTORKCKOKNALAISVMNQPGV 120

Qy 121 KLRVTEGWDGDGHRSRESLYVEGRADITPSDRDRSKYMLARLAVEAGFDWVYESKAH 180
 Db 121 KLRVTEGWDGDGHRSBESLHYVEGRADITPSDRDRSKYMLARLAVEAGFDWVYESKAH 180

Qy 181 IHCSVKAENSAAKSGCCFCQSATVHLEGGTKLVKLDLSGDRVLAADDGRLKSDFLT 240
 ; OTHER INFORMATION: Xaa may be any amino acid

US-09-325-256-22

Query Match 99.9%; Score 2467; DB 4; Length 475;
 Best Local Similarity 100.0%; Pred. No. 8.2e-239; Indels 0; Gaps 0;
 Matches 475; Conservative 0; Mismatches 0; Delins 0;

Qy 1 MLLARCLLVLVYSSLVCGSLACGPGRGKRRKPKKLPLAKQKFIPNVAEKTIGASG 60
 Db 1 MLLARCLLVLVYSSLVCGSLACGPGRGKRRKPKKLPLAKQKFIPNVAEKTIGASG 60

Qy 61 RYEKTSRNSRERKELTTPNNPNDIFKDEENTGADRMLTORKCKOKNALAISVMNQPGV 120
 Db 61 RYEKTSRNSRERKELTTPNNPNDIFKDEENTGADRMLTORKCKOKNALAISVMNQPGV 120

Qy 121 KLRVTEGWDGDGHRSRESLYVEGRADITPSDRDRSKYMLARLAVEAGFDWVYESKAH 180
 Db 61 RYEKTSRNSRERKELTTPNNPNDIFKDEENTGADRMLTORKCKOKNALAISVMNQPGV 120

Qy 121 KLRVTEGWDGDGHRSBESLHYVEGRADITPSDRDRSKYMLARLAVEAGFDWVYESKAH 180
 Db 121 KLRVTEGWDGDGHRSBESLHYVEGRADITPSDRDRSKYMLARLAVEAGFDWVYESKAH 180

QY 181 IHCSVKAENSAAKSGCSPGSGATVHLEGGTRLVKOLSPGRVLAADDQGILYSDFT 240
Db 181 IHCSVKAENSAAKSGCSPGSGATVHLEGGTRLVKOLSPGRVLAADDQGILYSDFT 240
Qy 241 FLRDDGAKKVVFVIEPREPRLTAHLLEVAPHSADSGATEPEASSGSPPSGALG 300
Db 241 FLRDDGAKKVVFVIEPREPRLTAHLLEVAPHSADSGATEPEASSGSPPSGALG 300
Qy 301 PRALFASRVPGORVYVAERDODRRLIPAAVHSVTSEEAGAYAQLTAQGTILINRL 360
Db 301 PRALFASRVPGORVYVAERDODRRLIPAAVHSVTSEEAGAYAQLTAQGTILINRL 360
Qy 361 ASCYAVIERSHWRAFAFRLLAHALLALAPARTDGGDSGGDRGGGGRVALTAPGA 420
Db 361 ASCYAVIERSHWRAFAFRLLAHALLALAPARTDGGDSGGDRGGGGRVALTAPGA 420
Qy 421 ADPGAGATAGIHWYSQLYQIGTWLIDSEALHPLGMANKSSSRGAGGARBGA 475
Db 421 ADPGAGATAGIHWYSQLYQIGTWLIDSEALHPLGMANKSSSRGAGGARBGA 475
RESULT 7
US-08-748-591-4
; Sequence 4, Application US/08748591
; Patient No. 5759811
; GENERAL INFORMATION:
; APPLICANT: Epstein, Ervin
; APPLICANT: Hu, Zillian
; APPLICANT: Bonifis, Jeanette
; TITLE OF INVENTION: Mutant Human Hedgehog Gene
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish and Richardson
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,591
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sherwood, Pamela J
; REGISTRATION NUMBER: 36,677
; REFERENCE/DOCKET NUMBER: 06510/067001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 322-5070
; TELEFAX: (415) 854-0875
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 462 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-748-591-4
Query Match 97.5%; Score 2407; DB 1; Length 462;
Best Local Similarity 100.0%; Pred. No. 8.2e-233;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLLARCLLIVLVSLLVCGAGCPGRGFGRKKRPKLPFLPLAYKQFPNVAEKTGLGAG 60
Db 1 MLLARCLLIVLVSLLVCGAGCPGRGFGRKKRPKLPFLPLAYKQFPNVAEKTGLGAG 60
Qy 61 RVECKISRISRFELTPNYPNPDKDENTGADRMLMTCRDKDNLALISTNNQWGV 120
Db 61 RVECKISRISRFELTPNYPNPDKDENTGADRMLMTCRDKDNLALISTNNQWGV 120
Db 61 RVEGKISRNSRFKELPTPNYPNPDIIFKDEENTGADRMLMTCRDKDNLALISTNNQWPGV 120
Qy 121 KLRVTEGMDDEGHISEEBSLLHYEGRAVDITTSDDRSKYGMLARLAVEAGDWWYSEKAH 180
Db 121 KLRVTEGMDDEGHISEEBSLLHYEGRAVDITTSDDRSKYGMLARLAVEAGDWWYSEKAH 180
Qy 181 IHCSVKAENSAAKSGCSPGSGATVHLEGGTRLVKOLSPGRVLAADDQGILYSDFT 240
Db 181 IHCSVKAENSAAKSGCSPGSGATVHLEGGTRLVKOLSPGRVLAADDQGILYSDFT 240
Qy 241 FLRDDGAKKVVFVIEPREPRLTAHLLEVAPHSADSGATEPEASSGSPPSGALG 300
Db 241 FLRDDGAKKVVFVIEPREPRLTAHLLEVAPHSADSGATEPEASSGSPPSGALG 300
Qy 301 PRALFASRVPGORVYVAERDODRRLIPAAVHSVTSEEAGAYAQLTAQGTILINRL 360
Db 301 PRALFASRVPGORVYVAERDODRRLIPAAVHSVTSEEAGAYAQLTAQGTILINRL 360
Qy 361 ASCYAVIERSHWRAFAFRLLAHALLALAPARTDGGDSGGDRGGGGRVALTAPGA 420
Db 361 ASCYAVIERSHWRAFAFRLLAHALLALAPARTDGGDSGGDRGGGGRVALTAPGA 420
Qy 421 ADPGAGATAGIHWYSQLYQIGTWLIDSEALHPLGMANKSSSRGAGGARBGA 475
Db 421 ADPGAGATAGIHWYSQLYQIGTWLIDSEALHPLGMANKSSSRGAGGARBGA 475
Qy 361 ASCYAVIERSHWRAFAFRLLAHALLALAPARTDGGDSGGDRGGGGRVALTAPGA 420
Db 361 ASCYAVIERSHWRAFAFRLLAHALLALAPARTDGGDSGGDRGGGGRVALTAPGA 420
Qy 421 ADPGAGATAGIHWYSQLYQIGTWLIDSEALHPLGMANKSS 462
Db 421 ADPGAGATAGIHWYSQLYQIGTWLIDSEALHPLGMANKSS 462
RESULT 8
US-08-748-591-9
; Sequence 9, Application US/08748591
; Patient No. 5759811
; GENERAL INFORMATION:
; APPLICANT: Epstein, Ervin
; APPLICANT: Hu, Zillian
; APPLICANT: Bonifis, Jeanette
; TITLE OF INVENTION: Mutant Human Hedgehog Gene
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish and Richardson
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,591
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sherwood, Pamela J
; REGISTRATION NUMBER: 36,677
; REFERENCE/DOCKET NUMBER: 06510/067001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 322-5070
; TELEFAX: (415) 854-0875
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 462 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-748-591-9
Query Match 97.5%; Score 2407; DB 1; Length 462;
Best Local Similarity 100.0%; Pred. No. 8.2e-233;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 9
US-08-946-329A-20
; Sequence 20, Application US/08946329A
; Patent No. 605091
GENERAL INFORMATION:
APPLICANT: Beacky, Philip A.
TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES
NUMBER OF SEQUENCES: 109
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.00
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/946, 329A
FILING DATE: 07-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/061, 323
FILING DATE: 07-OCT-1996
APPLICATION NUMBER: 08/729, 743
FILING DATE: 10-JUL-1996
APPLICATION NUMBER: 08/567, 357
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/349, 498
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/140001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099

1 MLLARCCULLVLVSSLVSLVSGLACGPGFGRGFRHRKKPLPLAYKOFIPNPAEKTIGAS 6
1 MLLARCCULLVLVSSLVSLVSGLACGPGFGRGFRHRKKPLPLAYKOFIPNPAEKTIGAS 6
QY 61 RYSGKISNSRERKELTPYNPDITFDENTGADRMLTORCKDKNLNALISVMQWPGV 1
DB 61 RYEGKISNSRERKELTPYNPDITFDENTGADRMLTORCKDKNLNALISVMQWPGV 1
QY 121 KLVTEGHDGHSSESHLYECRAVDTTSDRDSKGMLARLAVEAGDWVYESKAH 1
DB 121 KLVTEGHDGHSSESHLYECRAVDTTSDRDSKGMLARLAVEAGDWVYESKAH 1
QY 181 IHSSVKAENSAAKGGCFPGSATVHLEQQGKLVLDSPEQDRLVADDDGRLYSDFLT 2
DB 181 IHSSVKAENSAAKGGCFPGSATVHLEQQGKLVLDSPEQDRLVADDDGRLYSDFLT 2
QY 241 FLDRDDEAKKVYVIEPREPRERLILTAHHLFVAPHNDA-TGEPEASSSGPPGGA 3
DB 241 FLDRDDEAKKVYVIEPREPRERLILTAHHLFVAPHNDA-TGEPEASSSGPPGGA 3
QY 301 PRALFASRVRPGQRVYVAERDGRILLPAAVHSVILSEAGAYAPLTAQTIILNRV 3
DB 301 PRALFASRVRPGQRVYVAERDGRILLPAAVHSVILSEAGAYAPLTAQTIILNRV 3
QY 361 ASGYAVEEHWSWAHRAFAPRILAHALLA LAPARTORGSGGGDGGGGRVALTAPGA 4
DB 361 ASGYAVEEHWSWAHRAFAPRILAHALLA LAPARTORGSGGGDGGGGRVALTAPGA 4
QY 421 ADPAGAGATAGTHWYSOLYQIQTWLIDSEALHPIGMAVKS 462
DB 421 ADPAGAGATAGTHWYSOLYQIQTWLIDSEALHPIGMAVKS 462

US-08-946-329A-20

INFORMATION FOR SEO ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 437 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

Query Match	Score	DB	Length	Best Local Similarity	Pred.	No.	Mismatches	Indels	Gaps
QY 1 MILLARCLLIVVSSLLWVGCGAGCPRGGFGRKRHKPLTPAYKOPTPNVAEKTGASG	83.8%	3	437	87.4%		7	199		
QY 2 LILLARCLFLVIASSLILWCPLACGPGRGFGRKRPKLTPLAYKOPTPNVAEKTIGASG						8	24		
QY 61 RVEGKLSRNSEKFELTPNNYNDIIFDEENGADRIMTQRCKDLNIALATEVMNQFGV						6	240		
QY 121 KLRVTGKWDEDGHSEFSLHVEGRAVDITTSORDRSKYGMALARLAVEAGFDVYYSKKH						122	180		
Db 122 KLRVTGKWDEDGHSEFSLHVEGRAVDITTSORDRSKYGMALARLAVEAGFDVYYSKKH						181			
QY 181 IHCSVKRANSVAKSGCCPGSATVHLQEGGKFLVKDLSGDRVLAADQSGTLYSDFLT						182	240		
Db 182 IHCSVKRANSVAKSGCCPGSATVHLQEGGKFLVKDLSGDRVLAADQSGTLYSDFLT						183	180		
QY 241 FLDRDGAKKVYVIEPRERPRRLTAHLIFVAPHDNSATGEPEASGSQPPSGALG						242	300		
Db 242 FLDRDGAKKVYVIEPRERPRRLTAHLIFVAPHDNSATGEPEASGSQPPSGALG						243	286		
QY 301 PRALPSRVRQGQRTVVAERGDRRLPAAVHSVTLSEEAGAYAPLTAQGTLTILNRVL						302	360		
Db 302 PRALPSRVRQGQRTVVAERGDRRLPAAVHSVTLSEEAGAYAPLTAQGTLTILNRVL						303	346		
QY 361 ASCYAVIEHSWAHRAFAPFRLAHALLAPARTDGGDGGDRGGGVALTARGA						347	420		
Db 347 ASCYAVIEHSWAHRAFAPFRLAHALLAPARTDGGDGGDRGGGVALTARGA						348	395		
QY 421 ADAPGAGATAGTHWYQOLLYQIGTWLIDSEALHPLGMVAKSS						422	462		
Db 422 ADAPGAGATAGTHWYQOLLYQIGTWLIDSEALHPLGMVAKSS						423	437		
Db . . . 396 TEARGAEPTAGIHWISQOLLYQIGTWLIDSEALHPLGMVAKSS 437									

RESULT 10

US-08-567-357A-20

; Sequence 20, Application US/08567357A

PATENT NO. 612728

GENERAL INFORMATION:

APPLICANT: Beachy, Philip A.

APPLICANT: Moon, Randall T.

APPLICANT: Porter, Jeffrey A.

TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: FASTSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/567,357A

FILING DATE: 04-DEC-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 108/349,498

FILING DATE: 09-DEC-1994

ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/057, 860A
 FILING DATE: 09-Apr-1998
 CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
 NAME: Srobova, Craig G
 REGISTRATION NUMBER: 39, 044
 REFERENCE/DOCKET NUMBER: P1364

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/925-1489
 TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 437 amino acids
 TYPE: amino Acid
 TOPOLOGY: Linear

US-09-057-860A-6

Query Match 83.8%; Score 2068; DB 4;
 Best Local Similarity 87.4%; Pred. No. 7.5e-199;
 Matches 404; Conservative 8; Mismatches 24; Indels 26; Gaps 3;

QY 1 MILLARCLLVLVSSHLVCGSLACGCPGRGKGRRKRPKKLTPLAYKQFIPNVAEKTIGASG 60
 Db 2 LLLARCFLVLIASSLIVCPLACGCPGRGKGRRKRPKKLTPLAYKQFIPNVAEKTIGASG 61

QY 61 RYEKTSRNSRKFELTPNPNPDIIFKDEENTGADRMLTORCKDKNLALISVMNQPGV 120
 Db 62 RYEKTKTRNSRKFELTPNPNPDIIFKDEENTGADRMLTORCKDKNLALISVMNQPGV 121

Qy 121 KLRVTEGWDDEGHHSBESLIVEGRAVITTSDRDRSKYGMALARLAVEAGEDFWVYESKAH 180
 Db 122 KLRVTEGWDDEGHHSBESLIVEGRAVITTSDRDRSKYGMALARLAVEAGEDFWVYESKAH 181

Qy 181 IHCSVKAENSAKSGCCFPGSATVHLEQGTTKLYKDSLPGDRVLAADDOGRLLSDFLT 240
 Db 182 IHCSVKAENSAKSGCCFPGSATVHLEQGTTKLYKDSLPGDRVLAADDOGRLLSDFLT 241

Qy 241 FLRDGGAKKVYVETREPRERLILTAHLFVAPHNDSATGEPEAASSGGPPSGALG 300
 Db 242 FLDRDGGAKKVYVETLEPRERLILTAHLFVAPHN-----SGPTPG 286

Qy 301 PRALFASRVPGQRYVWAERDGDRLLPAHVSTLSEBAAAGAYAPLQTQGTILINRVL 360
 Db 287 PSALFASRVPGQRYVWAERDGDRLLPAHVSTLSEBAAAGAYAPLQTQGTILINRVL 345

Qy 361 ASCYAVIEEHSAWAHRFAFPRLAHALLAALAPARLDRGGDGGDRGGGRVALTAGA 420
 Db 347 ASCYAVIEEHSAWAHRFAFPRLAHALLAALAPARL-----GGGGSIP-AQSA 395

Qy 421 ADAPGAGATAGIHWSQLQIGWILDSEBALPIGLMAVKS 462
 Db 396 TEARGAEPTAGIHWSQLQIGWILDSETMPIGLMAVKS 437

RESULT 13
 US-08-349-498-20
 ; Sequence 20, Application US/08349498
 ; Patent No. 6261332
 ; GENERAL INFORMATION:
 ; APPLICANT: Beachy, Philip A.
 ; APPLICANT: Moon, Randall T.

Query Match 83.8%; Score 2068; DB 4;
 Best Local Similarity 87.4%; Pred. No. 7.5e-199;
 Matches 404; Conservative 8; Mismatches 24; Indels 26; Gaps 3;

QY 1 MILLARCLLVLVSSHLVCGSLACGCPGRGKGRRKRPKKLTPLAYKQFIPNVAEKTIGASG 60
 Db 2 LLLARCFLVLIASSLIVCPLACGCPGRGKGRRKRPKKLTPLAYKQFIPNVAEKTIGASG 61

QY 61 RYEKTSRNSRKFELTPNPNPDIIFKDEENTGADRMLTORCKDKNLALISVMNQPGV 120
 Db 62 RYEKTKTRNSRKFELTPNPNPDIIFKDEENTGADRMLTORCKDKNLALISVMNQPGV 121

Qy 121 KLRVTEGWDDEGHHSBESLIVEGRAVITTSDRDRSKYGMALARLAVEAGEDFWVYESKAH 180
 Db 122 KLRVTEGWDDEGHHSBESLIVEGRAVITTSDRDRSKYGMALARLAVEAGEDFWVYESKAH 181

Qy 181 IHCSVKAENSAKSGCCFPGSATVHLEQGTTKLYKDSLPGDRVLAADDOGRLLSDFLT 240
 Db 182 IHCSVKAENSAKSGCCFPGSATVHLEQGTTKLYKDSLPGDRVLAADDOGRLLSDFLT 241

Qy 241 FLRDGGAKKVYVETREPRERLILTAHLFVAPHNDSATGEPEAASSGGPPSGALG 300
 Db 242 FLDRDGGAKKVYVETLEPRERLILTAHLFVAPHN-----SGPTPG 286

Qy 301 PRALFASRVPGQRYVWAERDGDRLLPAHVSTLSEBAAAGAYAPLQTQGTILINRVL 360
 Db 287 PSALFASRVPGQRYVWAERDGDRLLPAHVSTLSEBAAAGAYAPLQTQGTILINRVL 345

Qy 361 ASCYAVIEEHSAWAHRFAFPRLAHALLAALAPARLDRGGDGGDRGGGRVALTAGA 420
 Db 347 ASCYAVIEEHSAWAHRFAFPRLAHALLAALAPARL-----GGGGSIP-AQSA 395

Qy 421 ADAPGAGATAGIHWSQLQIGWILDSEBALPIGLMAVKS 462
 Db 396 TEARGAEPTAGIHWSQLQIGWILDSETMPIGLMAVKS 437

RESULT 14
 PCT-US95-15463-20
 ; Sequence 20, Application PC/TUS9515463

GENERAL INFORMATION:

APPLICANT: The Johns Hopkins University School of Medicine

TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla

STATE: CA

COUNTRY: U.S.A.

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/15463

FILING DATE: 01-DEC-1995

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Haile, Lisa A.

REGISTRATION NUMBER: 38,347

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619/678-5070

TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 437 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US95-15463-20

Query Match 83.8%; Score 2068; DB 5; Length 437;
 Best Local Similarity 87.4%; Pred. No. 7.5e-199; Indels 24; Gaps 3;
 Matches 404; Conservative 8; Mismatches 24;

Qy 1 MLLARCLLIVLVLSSLLVSGLAGCPGRGKRRHKPKKLTPLAYQFIPNVAEKTIGASG 60
 Db 2 LLILARCLFLVLLASSLLVSGLAGCPGRGKRRHKPKKLTPLAYQFIPNVAEKTIGASG 61

Qy 61 RYEGKTRNSRERKELTTPNYNPDIKFDENTGADRMLTQRCKOKNLALISVNQWPGV 120
 Db 62 RYEGKTRNSRERKELTTPNYNPDIKFDENTGADRMLTQRCKOKNLALISVNQWPGV 121

Qy 121 KLRVTEGWDGDGHSEESLHYGRAVDTTSDRDRSKYGMALARAVEAGFDWVYESKAH 180
 Db 122 KLRVTEGWDGDGHSEESLHYGRAVDTTSDRDRSKYGMALARAVEAGFDWVYESKAH 181

Qy 181 IHCSYKAENSAVAKSGGCPPGSATVHLEQGTKLVDLDRPGDRYLADDOGRRLYSDFLT 240
 Db 182 IHCSYKAENSAVAKSGGCPPGSATVHLEQGTKLVDLDRPGDRYLADDOGRRLYSDFLT 241

Qy 241 FLDRDGAKKVYVETREPRLILTAHLFVAPHNDSATGEPEAASSGGCPGSGALG 300
 Db 242 FLDRDGAKKVYVETREPRLILTAHLFVAPHND-----SGPTPG 286

Qy 301 PRALEASRVPRGQRTVWAERDGRRLPAWSVTLSEAGAYAPLTAQGTILINRYL 360
 Db 302 PRALEASRVPRGQRTVWAERDGRRLPAWSVTLSEAGAYAPLTAQGTILINRYL 360

Db 287 PSALFASRVRPGQRTVWAERGDRRLPAWSVTLREBEAGAYAPLTAQGTILINRYL 346

Qy 361 ASCYAVIEEHSAWAHRAPFLRALLAALAPARDTRGGDSGGDRGGGRVALTAGA 420

Db 347 ASCYAVIEEHSAWAHRAPFLRALLAALAPARD-----GGGGSIP-AAOSA 395

Qy 421 ADPAGAGATGAGIHWQSOLQXQITWLDSBALHPLGMAYKSS 462

Db 396 TEARGAEPTAGIHWQSOLQXQITWLDSBTMHPGLGMAYKSS 437

PCT-US95-15923-20

Sequence 20, Application PC/TUS9515923

GENERAL INFORMATION:

APPLICANT: The Johns Hopkins University School of Medicine, et al.

TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla

STATE: CA

COUNTRY: U.S.A.

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/15923

FILING DATE: 04-DEC-1995

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Haile, Lisa A.

REGISTRATION NUMBER: 38,347

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619/678-5070

TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 437 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US95-15923-20

Query Match 83.8%; Score 2068; DB 5; Length 437;
 Best Local Similarity 87.4%; Pred. No. 7.5e-199; Indels 24; Gaps 3;
 Matches 404; Conservative 8; Mismatches 24;

Qy 1 MLLARCLLIVLVLSSLLVSGLAGCPGRGKRRHKPKKLTPLAYQFIPNVAEKTIGASG 60
 Db 2 LLILARCLFLVLLASSLLVSGLAGCPGRGKRRHKPKKLTPLAYQFIPNVAEKTIGASG 61

Qy 61 RYEGKTRNSRERKELTTPNYNPDIKFDENTGADRMLTQRCKOKNLALISVNQWPGV 120
 Db 62 RYEGKTRNSRERKELTTPNYNPDIKFDENTGADRMLTQRCKOKNLALISVNQWPGV 121

Qy 121 KLRVTEGWDGDGHSEESLHYGRAVDTTSDRDRSKYGMALARAVEAGFDWVYESKAH 180
 Db 122 KLRVTEGWDGDGHSEESLHYGRAVDTTSDRDRSKYGMALARAVEAGFDWVYESKAH 181

Qy 181 IHCSYKAENSAVAKSGGCPPGSATVHLEQGTKLVDLDRPGDRYLADDOGRRLYSDFLT 240
 Db 182 IHCSYKAENSAVAKSGGCPPGSATVHLEQGTKLVDLDRPGDRYLADDOGRRLYSDFLT 241

Qy 241 FLDRDGAKKVYVETREPRLILTAHLFVAPHNDSATGEPEAASSGGCPGSGALG 300
 Db 242 FLDRDGAKKVYVETREPRLILTAHLFVAPHND-----SGPTPG 286

Qy 301 PRALEASRVPRGQRTVWAERDGRRLPAWSVTLSEAGAYAPLTAQGTILINRYL 360
 Db 302 PRALEASRVPRGQRTVWAERGDRRLPAWSVTLREBEAGAYAPLTAQGTILINRYL 360

Db 287 PSALFASRVRPGQRTVWAERGDRRLPAWSVTLREBEAGAYAPLTAQGTILINRYL 346

Qy 361 ASCYAVIEEHSAWAHRAPFLRALLAALAPARDTRGGDSGGDRGGGRVALTAGA 420

Db 347 ASCYAVIEEHSAWAHRAPFLRALLAALAPARD-----GGGGSIP-AAOSA 395

Qy 421 ADPAGAGATGAGIHWQSOLQXQITWLDSBALHPLGMAYKSS 462

Db 396 TEARGAEPTAGIHWQSOLQXQITWLDSBTMHPGLGMAYKSS 437

Thu Feb 20 10:43:53 2003

Search completed: February 20, 2003, 10:14:13
Job time : 14.4346 secs

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GanCore version 5.1.3

OM protein - protein search, using sw model

Run on: February 20, 2003, 10:08:18 ; Search time 15.632 Seconds

(without alignments)

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

searched: 283224 seqs., 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

database : PIR 73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2062	83.5	A49425	Sonic hedgehog protein precursor - mouse
2	2060	83.4	B53193	C.Species: Mus musculus (house mouse)
3	1807	73.2	A49424	C.Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 10-Dec-1999
4	1506	61.0	A51193	C.Accession: A49425
5	1498	60.7	S56765	R.Echelard, Y.; Epstein, D.J.; St-Jacques, B.; Shen, L.; Mohler, J.; McMahon, J.A.; Cell 75, 1417-1430, 1993
6	1459	59.1	A49425	A;Title: Sonic hedgehog, a member of a family of putative signaling molecules, is im
7	1183	47.9	B49425	A;Reference number: A49425; MUID:94094334; PMID:7916661
8	1027.5	41.6	C49425	A;Accession: A49425;
9	890	36.0	A46400	A>Status: preliminary; nucleic acid sequence not shown
10	449	18.2	G02735	A;Molecule type: mRNA
11	159.5	6.5	615	A;Residues: 1-437 <ECH>
12	149	6.0	T29550	A;Cross-references: GB:X76290
13	138.5	5.6	1207	A;Note: authors translation is shown for the codon TCC at position 436
14	135.5	5.5	1226	C;Genetics:
15	134.5	5.4	T24045	C;Gene: Shh
16	129	5.2	484	C;Superfamily: sonic hedgehog protein
17	128	5.2	T27665	Query Match Best Local Similarity 83.5%; Score 2062; DB 2; Length 437; Matches 402; Conservative 10; Mismatches 24; Indels 26; Gaps 3;
18	126.5	5.1	T23552	Db 1 MLLIARCLLIVLVSSLVSLVSGLAGGPGKGRHKPKKTPPLAYQFIPNVAEKTLAGSG 60
19	123.5	5.0	1250	Db 2 LLLIARCLLIVLVSSLVSLVSGLAGGPGKGRHKPKKTPPLAYQFIPNVAEKTLAGSG 61
20	121	4.9	868	Db 61 RYEGKISRNSERKELTPTNPNDIFKOBENTGADRUMTORCKDKNLAISYNQWGV 120
21	119	4.8	T2281	Db 62 RYEGRKIRNSERKELTPTNPNDIFKOBENTGADRUMTORCKDKNLAISYNQWGV 121
22	118.5	4.8	T35213	Db 121 KLRVTEGMEDGHSEESUHYGRAVIDITTSDRSKYGMARLAVAGFDWVYESKAH 180
23	116	4.7	1329	Db 122 RLRYTGEDEGHHSSEESUHYGRAVDITTSDRSKYGMARLAVAGFDWVYESKAH 181
24	115.5	4.7	E70917	Db 181 IHCSVKAENSAVAKSGCGTPGSATVHLEOGGTKLVKUDSPGDRVLADDQGRILYSDFL 240
25	115	4.7	940	Db 182 IHCSVKAENSAVAKSGCGTPGSATVHLEOGGTKLVKUDSPGDRVLADDQGRILYSDFL 241
26	114	4.6	E87750	Db 241 FLDRDGAKKVYVETTRPERRILTAHHLYVAPHNDSATGEPPEASSGGSPGSPGALG 300
27	111	4.5	H87311	Db 242 FLDRDGAKKVYVETTRPERRILTAHHLYVAPHNDSATGEPPEASSGGSPGSPGALG 306
28	111	4.5	G70917	Db 301 PRALEASRVPRGPQVYVVAERDGRRLPAAVSUTLSREAGAYAVALTAQGTLINRVL 360
29	110	4.5	A39055	Db 347 PSALFASRVPRGPQVYVVAERDGRRLPAAVSUTLSREAGAYAVALTAQGTLINRVL 346
			Db 361 ASCVAVIEEHSAWAFAFPFLAHALLAALAPARTDDRGDSGGDRGGGRVALTAPGA 420	
			Db 347 ASCVAVIEEHSAWAFAFPFLAHALLAALAPARTDDGGGSIP-AQOSA 395	

QY	181	IHC SVKAENSAVAKSGCCFPGSATVHLQGGTCKLKDLSQGRVLAADDQGRLLSDPFLT	240
Db	181	IHC SVKAENSAVAKSGCCFPGSATVHLQGGTCKLKDLSQGRVLAADDQGRLLSDPFLT	240
QY	241	FID RDGAKKVVFVIEPREPRLLTAAHLFVPL--DNS TEDLHMT-----	286
Db	241	FID RDGAKKVVFVIEPREPRLLTAAHLFVPL--DNS TEDLHMT-----	286
QY	301	PRA LFASVRPGORYVVAERD QDRR LPAAVHSVTLS EAA GAYA PLTAQ TLIN RV	300
Db	287	- -AYA VSSVRAQMVY---DDSG QLKSVT QV RYI E QRS FAP TAHG TIV D	340
QY	361	ASC YAVIEBHSWAHRAPRFLAHALLA ALAPART DRG DSG GDR GGG GRY VAL TARG A	420
Db	341	ASC YAVIEBHSWAHRAPRFLAHALLA ALAPART DRG DSG GDR GGG GRY VAL TARG A	420
QY	421	AD A PGAG ATAG IHWY S QLX QIG TWIL DSEAL HLG M AV KSS	462
Db	376	--SSR SNATLQ QEGVHWI SRLX OMGIWLLDSNMLHPJGMSVNS	418
RESULT 5			
S6765	morphogen	xhh precursor - African clawed frog	
C;Species:	Xenopus laevis	(African clawed frog)	
C;Date:	10-Oct-1995	#sequence_revision 03-Nov-1995	#text_change 21-Jul-2000
C;Accession:	S56765		
R;Stolow, M.A.; Shi, Y.B.			
A;Title:	Xenopus sonic hedgehog as a potential morphogen during embryogenesis and thyroid		
A;Reference number:	S56765; MUID:95357169; PMID:7630736		
A;Status:	preliminary; nucleic acid sequence not shown		
A;Molecule type:	mRNA		
A;Residues:	1-444 <STOP>		
A;Cross-references:	EMBL:L392113; NID:9790937; PIDN: AAC42227.1; PID:9790938		
C;Superfamily:	sonic hedgehog protein		
Query Match	60.7%	Score 1498; DB 2; Length 444;	
Best Local Similarity	64.3%	Pred. No. 8; Se-105;	
Matches	305;	Conservative 38; Mismatches 87; Indels 46; Gaps 7;	
QY	1	MULL ARCLLVLVYSSLVCSGLACGPGCFCGKRRPKLTPLAYQFIPNVAEKTGAS	60
Db	1	MULL ARCLLVLVYSSLVCSGLACGPGCFCGKRRPKLTPLAYQFIPNVAEKTGAS	60
QY	61	RYE CKISRN SERKELTNPYNPDTIFKDEENTGADRMLTQRCRKDLKNAISWMNQPGV	120
Db	61	RYE CKISRN SERKELTNPYNPDTIFKDEENTGADRMLTQRCRKDLKNAISWMNQPGV	120
QY	121	KLR VTEG EGDGHHS EESLHYGRAV DITTSDR SKY GLAR LVA EAG FDW Y ESKA H	180
Db	121	KLR VTEG EGDGHHS EESLHYGRAV DITTSDR SKY GLAR LVA EAG FDW Y ESKA H	180
QY	181	IHC SVKAENSAVAKSGCCFPGSATVHLQGGTCKLKDLSQGRVLAADDQGRLLSDPFLT	240
Db	181	IHC SVKAENSAVAKSGCCFPGSATVHLQGGTCKLKDLSQGRVLAADDQGRLLSDPFLT	240
QY	241	FID RDGAKKVVFVIEPREPRLLTAAHLFVPL--DNS TEDLHMT-----	286
Db	241	FID RDGAKKVVFVIEPREPRLLTAAHLFVPL--DNS TEDLHMT-----	286
QY	301	PRA LFASVRPGORYVVAERD QDRR LPAAVHSVTLS EAA GAYA PLTAQ TLIN RV	300
Db	287	- -AYA VSSVRAQMVY---DDSG QLKSVT QV RYI E QRS FAP TAHG TIV D	340
QY	361	ASC YAVIEBHSWAHRAPRFLAHALLA ALAPART DRG DSG GDR GGG GRY VAL TARG A	420
Db	341	ASC YAVIEBHSWAHRAPRFLAHALLA ALAPART DRG DSG GDR GGG GRY VAL TARG A	420
QY	421	AD A PGAG ATAG IHWY S QLX QIG TWIL DSEAL HLG M AV KSS	459
Db	395	C-----HQMGTWLLDSNMLHPJGMSV	415
RESULT 6			
A49426	sonic hedgehog gene shh protein - zebra fish		
N;Alternate names:	local cell-cell interaction signaling protein		
C;Species:	Brachydanio rerio (zebra fish)		
C;Date:	06-Oct-1994	#sequence_revision 18-Nov-1994	#text_change 10-Dec-1999
C;Accession:	A49426		
R;Krauss, S.; Conardet, J.P.; Ingham, P.W.			
Cell 75, 1431-1444, 1993			
A;Title:	A functionally conserved homolog of the <i>Drosophila</i> segment polarity gene hh		
A;Reference number:	A49426; MUID:94094335; PMID:8269519		
A;Accession:	A49426		
A;Status:	preliminary; not compared with conceptual translation		
A;Molecule type:	nucleic acid		
A;Experimental source:	embryo		
A;Note:	sequence extracted from NCBI backbone (NCBIP:142459)		
C;Superfamily:	sonic hedgehog protein		
Query Match	59.1%	Score 1459; DB 2; Length 415;	
Best Local Similarity	64.3%	Pred. No. 6; Se-102;	
Matches	235;	Conservative 47; Mismatches 73; Indels 44; Gaps 6;	
QY	1	MULL ARCLLVLVYSSLVCSGLACGPGCFCGKRRPKLTPLAYQFIPNVAEKTGAS	60
Db	1	MULL ARCLLVLVYSSLVCSGLACGPGCFCGKRRPKLTPLAYQFIPNVAEKTGAS	60
QY	61	RYE CKISRN SERKELTNPYNPDTIFKDEENTGADRMLTQRCRKDLKNAISWMNQPGV	120
Db	61	RYE CKISRN SERKELTNPYNPDTIFKDEENTGADRMLTQRCRKDLKNAISWMNQPGV	120
QY	121	KLR VTEG EGDGHHS EESLHYGRAV DITTSDR SKY GLAR LVA EAG FDW Y ESKA H	180
Db	121	KLR VTEG EGDGHHS EESLHYGRAV DITTSDR SKY GLAR LVA EAG FDW Y ESKA H	180
QY	181	IHC SVKAENSAVAKSGCCFPGSATVHLQGGTCKLKDLSQGRVLAADDQGRLLSDPFLT	240
Db	181	IHC SVKAENSAVAKSGCCFPGSATVHLQGGTCKLKDLSQGRVLAADDQGRLLSDPFLT	240
QY	241	FID RDGAKKVVFVIEPREPRLLTAAHLFVPL--DNS TEDLHMT-----	286
Db	241	FID RDGAKKVVFVIEPREPRLLTAAHLFVPL--DNS TEDLHMT-----	286
QY	301	PRA LFASVRPGORYVVAERD QDRR LPAAVHSVTLS EAA GAYA PLTAQ TLIN RV	300
Db	287	- -AYA VSSVRAQMVY---DDSG QLKSVT QV RYI E QRS FAP TAHG TIV D	340
QY	361	ASC YAVIEBHSWAHRAPRFLAHALLA ALAPART DRG DSG GDR GGG GRY VAL TARG A	420
Db	341	ASC YAVIEBHSWAHRAPRFLAHALLA ALAPART DRG DSG GDR GGG GRY VAL TARG A	420
QY	421	AD A PGAG ATAG IHWY S QLX QIG TWIL DSEAL HLG M AV KSS	459
Db	395	C-----HQMGTWLLDSNMLHPJGMSV	415
RESULT 7			
B49425	Desert hedgehog protein precursor - mouse		
C;Species:	Mus musculus (house mouse)		
C;Date:	06-Jan-1995	#sequence_revision 06-Jan-1995	#text_change 10-Dec-1999
C;Accession:	B49425		
R;Echard, Y.; Epstein, D.J.; St-Jacques, B.; Shen, L.; Mohler, J.; McMahon, J.A.; Cell 75, 1417-1430, 1993			
A;Title:	Sonic hedgehog, a member of a family of putative signaling molecules, is imp		
A;Reference number:	A49425; MUID:94094334; PMID:7916661		
A;Accession:	B49425		
A;Status:	preliminary		
A;Molecule type:	DNA		
A;Residues:	1-396 <ECH>		

A;Cross-references: GB:X76292; NID:9443941; PID:CAA53924.1; PID:9443942
 C;Genetics:
 A;Gene: Dhh
 C;superfamily: sonic hedgehog protein

Query Match 47.9%; Score 1183; DB 2; Length 396;
 Best Local Similarity 54.5%; Pred. No. 3.3e-81; Mismatches 87; Indels 62; Gaps 10;
 Matches 244; Conservative 55; Mismatches 87; Indels 62; Gaps 10;

Qy 3 LLARCLLVLVSSILVCGLACGPGRG-FGKRRPKK-LTPLAYKOFITVAEKTILGASG 60
 Db 7 LLPCLL---ALIALSAQSCGPGRGPGVGRRRVVKQLVPLPLYKQFVSMPEKTLGASG 61

Qy 61 RYEKTSRNSERKEELTPNYPDILFKDENTGADRMLTORCKKLNALAISVNQWPGV 120
 Db 62 PAEGRVTRGSESERFDLQDLPNYPDIFKDEENSGADRMLTERCKEIRNVALIAVNINWPGV 121

Qy 121 KLRTEGWDDEGHHSSEESLHVEGGAVDITTSDRRSKYGMLARAVEAGFDWVYIESKAH 180
 Db 122 RLRTYEGWDDEGHHAQDSLYEGGLYEGGALDTTSDRRNKYLAVRGEAFDWVYIESRNH 181

Qy 181 THCSVKAENSAVAKSGGCFFPSATVHLEQGKTLYKVDLSPGDRYLAADPGRLLSDFLT 240
 Db 182 IHVSKADNLAVRAGCFFGPNANVRLSGERKSKIRELHRGDWVLAADAGRIVPTPVLL 241

Qy 241 FLDRDGAKKVYVLTREPERRLLTAHLFLVAPHNDSATGCPREASSGSCP-PSGGAL 299
 Db 242 FLDRLDQLRRASFVAVETERPPRKLLTPHILVFLA-----RGPAPAGPDF 286

Qy 300 GPRALFAASRVRPGQRVYVAERDSDRRLIPAAVSVTLEAAAGAYAPITAQGTILNRY 359
 Db 287 AP-VFARRLRAGPSVLA---PGDQALQPARVARVA-HEEAQVEAPLTAHGTLVNDV 339

Qy 360 LASCVAVIEHSHWAIRAFRFLAHALLALAPARTDRGGDSSGGDRGGGGRVALTAGC 419
 Db 340 LASCVAVLESHQWAIRAFPLRLHLAGALL-----PG 372

Qy 420 AADPGAGATAGIHWYSQLIYQTCWLL 447
 Db 373 GAVQD----TGMMWISRLLYRLAELM 395

RESULT 8

C4925 Indian hedgehog protein - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000
 C;Accession: C49425
 R;Bchard, Y.; Epstein, D.J.; St-Jacques, B.; Shen, L.; Mohler, J.; McMahon, J.A.; McMahon, Cell 75, 1417-1430, 1993
 A;Title: Sonic hedgehog, a member of a family of putative signaling molecules, is implicated in the development of the nervous system
 A;Reference number: A49425; MUID:94094334; PMID:7916661
 A;Accession: C49425
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-336 <ECCH>
 A;Cross-references: GB:X76291
 A;Residues: 1-336 <ECCH>
 A;Cross-references: GB:X76291
 C;Superfamily: sonic hedgehog protein

Query Match 41.6%; Score 1027.5; DB 2; Length 336;
 Best Local Similarity 54.6%; Pred. No. 1.3e-69; Mismatches 77; Indels 65; Gaps 8;

Matches 218; Conservative 39; Mismatches 77; Indels 65; Gaps 8;

Qy 71 ERFELTPWNPDPDIFKDENTGADRMLQRCRDLNAISNMQWPGVLRTEGMD 130
 Db 1 ERFELTPWNPDPDIFKDENTGADRMLQRCRDLNAISNMQWPGVLRTEGMD 60

Qy 131 DGHISEESLHYEGRAVDTMTSDRURSKYGMARLAAVEGDFWVYYESKAHICVSVAENS 190
 Db 61 DGHISEESLHYEGRAVDTSDRURSKYGMARLAAVEGDFWVYYESKAHICVSVAENS 120

Qy 191 VAAASGGCPGSGATVHLSGGTQKVKDLSPGDVLAAQDQGRLLSDTFLDRDGAKK 250
 Db 59 RCL-----LTVLSSILVCGLACGPGRGKGRRPKLPLAKVQFIPVVAEKLG 57

RESULT 9

A46400 A;Cross-references: GB:S66384; NID:9435848; PID:9435849
 A;Experimental source: Oregon-R
 A;Residues: 1-471 <PTAS>
 A;Molecule type: mRNA
 A;Accession: A46400
 A;Status: preliminary
 A;Cross-references: GB:S66384; NID:9435848; PID:9435849
 A;Note: sequence extracted from NCBI backbone (NCBIN:138986, NCBIPI:138997)
 R;Tashiro, S.; Michie, T.; Higashijima, S.; Zenno, S.; Ishimaru, S.; Takahashi, F.;
 Gene 124, 183-189, 1993
 A;Title: Structure and expression of hedgehog, a Drosophila segment-polarity gene req
 A;Reference number: A46400; MUID:94094334; PMID:7916661
 A;Accession: C49425
 A;Molecule type: mRNA
 A;Residues: 1-471 <PTAS>
 A;Cross-references: GB:L05404
 A;Note: It is uncertain whether Met-1 or Met-51 is the initiator
 A;Note: intron positions were determined from partial DNA sequence
 R;Lee, J.J.; von Kessier, D.P.; Parks, S.; Beachy, P.A.
 Cell 71, 33-50, 1992
 A;Title: Secretion and localized transcription suggest a role in positional signaling
 A;Reference number: A43480; MUID:93008241; PMID:1394430
 A;Accession: A43480
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: DNA
 A;Residues: 1-471 <DEE>
 A;Cross-references: GB:L02793; NID:9157609; PID:9157610
 A;Note: sequence extracted from NCBI backbone (NCBIP:115418)
 C;Comment: This protein is required for cell-cell communication.
 C;Genetics:
 A;Gene: hh
 A;Cross-references: FB:FBgn0004644
 A;Introns: 160/3; 248/1
 C;Superfamily: sonic hedgehog protein
 C;Keywords: transmembrane protein
 F;62-82/Domain: transmembrane #status predicted <TM>
 Query Match 36.0%; Score 890; DB 2; Length 471;
 Best Local Similarity 44.3%; Pred. No. 4.3e-59; Mismatches 202; Conservative 65; Mismatches 137; Indels 52; Gaps 10;

Qy 6 RCL-----LTVLSSILVCGLACGPGRGKGRRPKLPLAKVQFIPVVAEKLG 57
 Db 59 RCLSLRLTSLVALLLIVLPWVFPAHSCGPGRGKGRRPKLPLAKVQFIPVVAEKLG 117

QY 58 ASGRVEKISKRSERKELTPIWNPDIKFDEENTGADRIMTQRCKDKLNALISANQW 117
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 118 ASCPLEGVIRRSPKFDLVPNRLFRFEGTGADRMLSKRCNEKLNLAYSTNW 177

QY 118 PGVLRVTEGWDDEGHSEESLHYEGRAVDTTSDRDRSKYGMALARAVEAGFDWYYES 177
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 178 PGIRLVITESWDEDYHNGQESLHYEGRAVITTSDRDOSKGYGMALARAVEAGFDWYVS 237

QY 178 KAHHCYCSKAENSVAAKSGGCPPGSAVHLPOGGTKLYKDLSPGDRVLAADDOGRILYSD 237
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 238 RRHLYCYSKSDDISSVHGCCTPESTALLSISGVRKELSIGDRYLSTMANGQAVYE 297

QY 238 FITFLRDGAKKVYVETREBERRERLLTAHHLFVAPHNDSATGEPERASSGGPPSGG 297
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 298 VIFLMDRNLEONKFNFVOLHT-DGGAVLTVTPAHLSV-----WOPESDKLT----- 342

QY 298 ALGPRALFAFSRVRPGQRYVVAERDGDRRLPAVHSVTLSBEAAGAYAPLTAQGTLLIN 357
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 343 ---FVAFDRFEKQVLYVRFETGLR- PQRVKVG-SVRSKGIVVAPLTEREGTIVN 394

QY 358 RYIASCYAVIEBHSWAHRAFPERLAHALLAALAPARDRGSGDGGDRGGGGRVALTA 417
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 395 SYVARSCAVINSQSLSLAWGLAPMRLLSTEALW-PANEQ-----LHSS 436

QY 418 PGADARGAGATAGIHYSQLIQIGTWLDSEALH 453
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 437 PKVVS--AQOONGIHNVANALYKVKBVDPQLRQSWRH 470

RESULT 10
 G02735
 desert hedgehog - human (fragment)
 C;Species: Homo sapiens (man)
 C;Accession: 21-hec-1996 #sequence_revision 06-Jun-1997 #text_change 11-Jan-2000
 C;Accession: G02735
 R;Drummond, I.A.
 submitted to the EMBL Data Library, June 1996
 A;Reference number: H01643

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: mRNA
 A;Residues: 1-94 <DRU>
 A;Cross-references: EMBL:U59748; NID:91401271; PID:91401272
 C;Genetics:
 A;Gene: hdhh
 C;Superfamily: sonic hedgehog protein

Query Match 18.2%; Score 449; DB 2; Length 94;
 Best Local Similarity 84.0%; Pred. No. 7e-27; Mismatches 79; Conservative 13; Indels 0; Gaps 0; Matches 79;

QY 84 TIPKDEENTGARRLMTGCKDKNIALATSYMMQPGCVKLRYEGWDDEGHSEESLHYEG 143
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 1 TIPKDEENSGADRMLTERCKERNALIAVMKMWPGVLRVTEGWDDEGHHAQDSLHYEG 60

QY 144 RADITTSDRDRSKYGMALARAVEAGDWYIES 177
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 61 RADITTSDRDRSKYGMALARAVEAGDWYIES 94

RESULT 11
 T29550
 hypothetical protein zk377.1 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 C;Accession: T29550
 R;Nhan, M.; Hawkins, J.
 submitted to the EMBL Data Library, February 1997
 A;Description: The sequence of C. elegans cosmid zk377.
 A;Accession number: Z26639
 A;Accession: T29550
 A;Status: preliminary; translated from GB/EMBL/DDJB

RESULT 12
 T23754
 hypothetical protein T05C12.10 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
 C;Accession: T23754; T24513
 R;Thomas, K.
 submitted to the EMBL Data Library, June 1995
 A;Reference number: Z19793

A;Accession: T23754
 A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: DNA
 A;Residues: 1-1207 <WT>
 A;Cross-references: EMBL:Z49968; PIDN:CAA90265.1; GSPDB:GN00020; CESP:T05C12.10
 A;Experimental source: clone MI10
 R;Burton, J.
 submitted to the EMBL Data Library, October 1995
 A;Reference number: Z19901
 A;Accession: T24513
 A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: DNA
 A;Residues: 1-1207 <WT>
 A;Cross-references: EMBL:Z66500; PIDN:CAA91313.1; GSPDB:GN00020; CESP:T05C12.10
 A;Experimental source: clone T05C12
 C;Genetics:
 A;Map position: 2
 A;Introns: 31/3; 87/2; 141/3; 180/2; 203/3; 267/1; 776/2; 794/2; 834/2; 1086/3; 1143/
 Query Match 6.0%; Score 149; DB 2; Length 1207;
 Best Local Similarity 26.5%; Pred. No. 0.0065; Mismatches 56; Conservative 37; Indels 36; Gaps 9; Matches 56;

QY 184 SVAENSAVSKGG-----CPGSATVHLEOGGTLKVLDSPGDRVLAADDOGRILYSD 238
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 942 AVIADTPGAGAGGGNSNCADSLS-TVYGQKRMDLQGDYVLPSSGNVLRKV 1000

QY 239 LTFLRDGAKKVYVETREBERRERLLTAHHLFVAPHNDSATGEPERASSGGPPSGG 298
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 1001 EMFYHREPRTRTFEVVLYTKSGR-KLSLTGHLPPWEC-----QVEOTMNPDGID 1052

QY 299 LGPR-ALEASRVRPQRYVVAERDGDRRLPAVHSVTLSSEA-----AGAYAPL 349
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

RESULT 13

T24045 hypothetical protein R08B4.1 - *Caenorhabditis elegans*
Qy 350 AQQGILINRVLASCAYAVIEBHSHWRAFAPP 380
Db 1101 VEGSLIVDGVLSLSSFSHLHS-AHKLIDFP 1130

Qy 191 VAAKSGGCPEGSATVHLEGGTKYKVDLSFGDRVLAADQGRLLYSDETFLDGGAKK 250
Db 283 VASGVpacFGNSKV-MTPAGEKSMDLSVGDMNTY-BYGMWTTTRVSWLHLRPDTKA 340

Qy 251 VFYVITREPERERLLTAAHLLFVAPHNDSATGEPEASSSSGPPSGGAFLASFV 310
Db 341 AFIKL-TTEGAIIDMTPOHFIYKA---NCVTERME-----LVAEDEMT 380

Qy 311 PGQRVVVAERDGDRRLPAVHSVTLSERA---AGAVAPLTAQGTLINRVLASCAY 366
Db 381 IGDCLMV---KENERLVM---TTSKESTFTETGVYAPMTEGDLIVDDVYASCHV 431

C;Accession: T24045
R;White, S
R;Reference number: Z19834
A;Accession: T24045
A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Map position: X
A;Molecule type: DNA
A;Residues: 1-1226 <WIL>
A;Cross-references: EMBL:Z68008; PIDN:CAA92000.1; GSDB:GN00028; CESP:R08B4.1
A;Experimental source: clone R08B4

C;Genetics:
A;Gene: CESP:R08B4.1

A;Map position: 53/2; 113/1; 204/3; 272/1; 354/1; 389/3; 714/3; 839/3; 877/1; 960/3; 1

Query Match 5.6%; Score 138.5; DB 2; Length 1226;
Best Local Similarity 24.4%; Pred. No. 0.041; **Mismatches** 50; **Conservative** 38; **Indels** 49; **Gaps** 8;

Db 1012 SALVAATGACFSLIDWW-**TTPTGKRMDOIDIGDVLTADLE-KTYFTPITLWHREPK** 1069

Qy 189 NSVVAKSGGCPEGSATVHLEGGTKVLDLSPGSRVLAADDQGRLLYSDETFLDLRDGA 248
Db 1070 VQEELTTI-EYGTILRITSRHEMYRNKGKSYPPQYIKMLPHD---GB----- 1113

Qy 296 GGALGPRALFAVRPGRQVYVVAVERGDRRLLPAVHSVTLSEBAAAGAYAPLTAQGTTL 355
Db 1114 -----AIFASDLEVGDCVVNLKGKRMQKETITRSV---RIGIYSPUNNRGII 1161

Qy 356 INRYVLASCYAVIEHS-----WAH 374
Db 1162 VNDMLASCYSEIQLQTFFWAY 1186

RESULT 14

T34504 hypothetical protein ZK1290.12 - *Caenorhabditis elegans*
Qy 313 QRVVVAERDGDRRLPAVHSVTLSE-----EAAGAYAPLTAQGTLINRVLASCY 365
Db 416 DCFYLAQSE-----ALTKYRUELEIDLKRVKKTGIVAPMISQGHLLVNLKHTSCHS 466

C;Accession: T34504
R;Rich, A
R;Submitted to the EMBL Data Library, July 1995
A;Description: The sequence of C. elegans cosmid ZK1290.
A;Reference number: 221535
A;Accession: T34504
A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA
A;Residues: 1-484 <TAT>
A;Cross-references: EMBL:U21308; PIDN:AAB93321.1; GSDB:GN00020; CESP:ZK1290.12
A;Experimental source: strain Bristol N2; clone ZK1290
C;Genetics:
A;Gene: CESP:ZK1290.12
A;Map position: 2
A;Introns: 66/3; 124/2; 181/2; 392/1

Query Match 5.5%; Score 135.5; DB 2; Length 484;
Best Local Similarity 24.5%; Pred. No. 0.021; **Mismatches** 46; **Conservative** 42; **Indels** 35; **Gaps** 8;

Search completed: February 20, 2003, 10:13:37
Job time : 18.632 secs

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OM protein - protein search, using sw model.

Run on:

February 20, 2003, 10:07:32 ; Search time 14.5662 Seconds

(without alignments)
1352.533 Million cell updates/secTitle:
Perfect score: US-09-827-110a-15

Sequence: 1 MLLARCLLVLVSSLLVCS..... GMAYKSSXSRGAGGGAREGA 475

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Swissprot,40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	2407	97.5	462	1 SHH_HUMAN	Q15465 homo sapien
2	2068	83.8	437	1 SHH_MOUSE	Q62266 mus musculus
3	2050	83.4	437	1 SHH_RAT	Q63673 rattus norvegicus
4	1807	73.2	425	1 SHH_CHICK	Q91035 gallus gallus
5	1539.5	62.4	432	1 SHH_CINPY	Q90385 cynops pyrrhura
6	1506	61.0	418	1 SHH_BRARE	Q92008 brachydanois
7	1498	60.7	444	1 SHH_XENLA	Q92000 xenopus laevis
8	1432	58.0	416	1 TWHH_BRARE	Q90419 brachydanois
9	1282.5	51.9	408	1 IHH_CHICK	Q98938 gallus gallus
10	1266	51.3	411	1 IHH_MOUSE	Q14623 homo sapiens
11	1252	51.1	411	1 IHH_XENLA	P97812 mus musculus
12	1248	50.5	409	1 IHH_BRARE	Q91612 xenopus laevis
13	1213	49.1	412	1 DHH_MOUSE	Q98862 brachydanois
14	1113	47.9	396	1 DHH_MOUSE	Q61488 mus musculus
15	1177	47.7	396	1 DHH_ROMAN	Q4323 homosapiens
16	1079.5	43.7	396	1 DHH_XENLA	Q91610 xenopus laevis
17	1077.5	43.6	398	1 HH_DROME	Q91611 xenopus laevis
18	890	36.0	471	1 HH_DROME	Q03936 drosophila melanogaster
19	854	34.6	481	1 HH_DROHY	P55674 drosophila melanogaster
20	602	24.4	121	1 SHH_RASEL	P78858 rasbora elegans
21	599	24.3	121	1 SHH_CARAU	P79691 carassius auratus
22	599	24.3	121	1 SHH_PUNTE	P79850 puntius tetrazona
23	598	24.2	121	1 SHH_RASHE	P79864 rasbora heteromorpha
24	598	24.2	121	1 SHH_RASPA	P79869 rasbora pavonia
25	597	24.2	121	1 SHH_TANAL	P79915 tanichthys tanichthys
26	595	24.1	121	1 SHH_AMBCH	P79682 ambylpharynx pseudoplatensis
27	594	24.1	121	1 SHH_DANAA	Q13235 danio rerio
28	594	24.1	121	1 SHH_DANAE	Q13234 danio aequipinnatus
29	594	24.1	121	1 SHH_DANAI	Q13235 danio affinis
30	594	24.1	121	1 SHH_DANER	Q13245 danio franklini
31	594	24.1	121	1 SHH_DANER	P79709 danio kerri
32	594	24.1	121	1 SHH_DANPP	P79717 danio pulchellus
33	594	24.1	121	1 SHH_DEVDE	Q13241 devario devadatta

ALIGNMENTS

34	594	24.1	121	1 SHH_DEVMA	Q13247 devario malabaricus
35	594	24.1	121	1 SHH_DEVPO	Q13250 devario patersoni
36	590	23.9	121	1 SHH_PUNCO	P79838 puntius conchophilus
37	396	16.0	88	1 DHH_BRARE	P79729 brachydanois
38	293	11.9	58	1 IHH_CARAU	P79693 carassius auroensis
39	293	11.9	58	1 IHH_DANAT	Q13240 danio affinis
40	293	11.9	58	1 IHH_DANKE	P79711 danio kerri
41	293	11.9	58	1 IHL_DANPU	P79719 danio pulchellus
42	293	11.9	58	1 IHH_DEVDE	Q13243 devario devadatta
43	293	11.9	58	1 IHH_PUNTE	P79852 puntius tetrazonatus
44	293	11.9	58	1 IHL_RASEL	P79860 rasbora elephas
45	289	11.7	58	1 SHH_PSEPR	P79839 pseudoraspis

"Mutations in the human Sonic hedgehog gene cause holoprosencephaly."

RL	Nat. Genet. 14:357-360(1996).	CC	OBLIGATE CARRIERS OF HPE GENE IN AD PEDIGREES ARE CLINICALLY UNAFFECTED.
RN	[7]	CC	- I - SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.
RP	VARIANTS HPE ARG-31; GLY-117; ARG-117; GLU-224; THR-226 AND THR-383.	CC	- I - DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
RX	MEDLINE=98027056; PubMed=9302262;	CC	WWW= http://www.inphobiogen.fr/services/chromancer/Genes/SHHID378.html ".
RA	Roessler E., Bellonci E., Gaudenz K., Vargas F., Scherer S.W., Tsui L.-C., Muenke M.;	CC	
RA	"Mutations in the C-terminal domain of Sonic hedgehog cause holoprosencephaly";	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
RA	Hum. Mol. Genet. 6:1847-1853(1997).	CC	-----
RN	[8]	CC	-----
RP	VARIANTS HPE HIS-100; GLN-188 AND ASN-222.	CC	-----
RX	"Expression of the Sonic hedgehog (SHH) gene during early human development and phenotypic expression of new mutations causing holoprosencephaly";	CC	-----
RT	Hum. Mol. Genet. 8:1683-1689(1999).	CC	-----
RL	[9]	CC	-----
RP	VARIANTS HPE V-88; K-115; R-236; 263-R-A-269 DEL; D-290; A-424 AND L-436.	DR	EMBL: L38518; AAA62179_1; -.
RX	MEDLINE=90025757; PubMed=1056295;	DR	EMBL: AC002484; AA667604_1; -.
RA	Nanni L., Ming J.E., Bocian M., Steinhaus K., Bianchi D.W., Die-Smulders C., Giannotti A., Imazumi K., Jones K.L., Campo M.D., Martin R.A., Meinecke P., Pierpont M.E.M., Robin N.H., Young I.D., Roessler E., Muenke M.;	DR	HSSP: Q62262; IVHH.
RA	"The mutational spectrum of the sonic hedgehog gene in holoprosencephaly: SHH mutations cause a significant proportion of autosomal dominant holoprosencephaly";	DR	MEROPS: C46_002; -.
RT	Hum. Mol. Genet. 8:2479-2488(1999).	DR	GeneW: HGNC:10848; SHH.
RL	- I - FUNCTION: BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH, PTC REPRESSIONS THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO. ALSO REGULATES ANOTHER TARGET, THE GLI ONCOGENE. INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT: SIGNAL PRODUCED BY THE NOTOCORD THAT INDUCES VENTRAL CELL FATE IN THE NEURAL TUBE AND SOMITES, AND THE POLARIZING SIGNAL FOR PATTERNING OF THE ANTERIOR-POSTERIOR AXIS OF THE DEVELOPING LIMB BUD. DISPLAYS BOTH FLOOR PLATE- AND MOTOR NEURON-INDUCING ACTIVITY. THE THRESHOLD CONCENTRATION OF N-PRODUCT REQUIRED FOR MOTOR NEURON INDUCTION IS 5 FOLD LOWER THAN THAT REQUIRED FOR FLOOR PLATE INDUCTION (BY SIMILARITY).	DR	DRIM: 600725; -.
CC	- I - SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURFACE. IT IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).	DR	DRIM: 142454; -.
CC	- I - TISSUE SPECIFICITY: EXPRESSED IN FETAL INTESTINE, LIVER, LUNG, AND KIDNEY. NOT EXPRESSED IN ADULT TISSUES.	DR	InterPro: IPRO00320; HH_signal.
CC	- I - PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N- TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).	DR	InterPro: IPRO01767; Hedgehog_hintC.
CC	- I - DISEASE: DEFECTS IN SHH ARE THE CAUSE OF HOLOPROSENCEPHALY (HPE). HPE IS A CLINICALLY VARIABLE AND GENETICALLY HETEROGENEOUS MALFORMATION IN WHICH THE DEVELOPING FOREBRAIN FAILS TO CORRECTLY SEPARATE INTO RIGHT AND LEFT HEMISPHERES. IN THE MOST SEVERE FORM (ALOAR HPE), THERE IS NO INTERHEMISPERIC FISSURE, A SINGLE BRAIN VENTRICLE IS PRESENT. HPE IS ASSOCIATED WITH SEVERAL DISTINCT FACTORS AND PHENOTYPIC VARIABILITY. IN THE MOST EXTREME CASES, ANOPHTHALMIA OR CYCLOPS IS EVIDENT ALONG WITH A CONGENITAL ABSENCE OF THE MATURE NOSE. THE LESS SEVERE FORM FEATURES FACIAL DYSMORPHIA CHARACTERIZED BY OCULAR HYPERTELORISM, DEFECTS OF THE UPPER LIP AND/OR NOSE, AND ABSENCE OF THE OLFACTORY NERVES OR CORPUS CALLOSUM. THE MAJORITY OF HPE CASES ARE APPARENTLY SPORADIC, ALTHOUGH CLEAR EXAMPLES OF AUTOSOMAL DOMINANT (AD) INHERITANCE HAVE BEEN DESCRIBED. INTERESTINGLY, UP TO 30% OF	DR	InterPro: IPRO03586; Hedgehog_hintN.
CC		DR	InterPro: IPRO02203; Intein.
CC		DR	InterPro: IPRO01657; SonichH.
CC		DR	Pfam: PF01079; Hint_1.
CC		DR	PRINTS: PR00632; HH_signal_1.
CC		DR	PRODOM: PD003042; HH_signal_1.
CC		DR	SMART: SM00306; HIntC_1.
CC		DR	Developmental protein: Autocatalytic cleavage; Hydrolase; Protease; Signal; Lipoprotein; Palmitate; Disease mutation; Holoprosencephaly.
CC		FT	FT SIGNAL_1
CC		FT	FT POTENTIAL_1
CC		FT	FT SONIC_HEDGEHOG_PROTEIN_N-PRODUCT.
CC		FT	FT SONIC_HEDGEHOG_PROTEIN_C-PRODUCT.
CC		FT	FT CLEAVAGE_(AUTO-)_(BY SIMILARITY).
CC		FT	FT INVOLVED_IN_CHOLESTEROL_TRANSFER_(BY SIMILARITY).
CC		FT	FT INVOLVED_IN_AUTO-CLEAVAGE_(BY SIMILARITY).
CC		FT	FT SEMANTICALLY_EQUIVALENT_FOR_AUTO-CLEAVAGE_(BY SIMILARITY).
CC		FT	FT CHOLESTEROL_(BY SIMILARITY).
CC		FT	FT POLY-GLY.
CC		FT	FT PALMITATE.
CC		FT	FT G->R_(IN HPE).
CC		FT	FT D->V_(IN HPE; FAMILIAL).
CC		FT	FT W->G_(IN HPE).
CC		FT	FT /FTId-Var_009163.
CC		FT	FT O->H_(IN HPE; SPORADIC).
CC		FT	FT /FTId-Var_009164.
CC		FT	FT N->K_(IN HPE; FAMILIAL).
CC		FT	FT /FTId-Var_009165.
CC		FT	FT W->G_(IN HPE).
CC		FT	FT /FTId-Var_009167.
CC		FT	FT W->R_(IN HPE).
CC		FT	FT /FTId-Var_009161.
CC		FT	FT E->Q_(IN HPE; FAMILIAL).
CC		FT	FT /FTId-Var_009168.
CC		FT	FT D->N_(IN HPE; FAMILIAL).
CC		FT	FT S->R_(IN HPE; FAMILIAL).
CC		FT	FT /FTId-Var_009170.
CC		FT	MISSING_(IN HPE; SPORADIC).
FT	VARIANT	263	269

Query Match 97.5%; Score 2407; DB 1; Length 462;
 Best Local Similarity 100.0%; Pred. No. 2.4e-10; Indels 0; Gaps 0;
 Matches 462; Conservative 0; Mismatches 0; RT
 QY 1 MULLARCLLIVNSSLVSLVCSGLACGPGPGKRRHPPKKLTPLAYKQFIPNVAEKTIGASG 60
 1 MULLARCLLIVNSSLVSLVCSGLACGPGPGKRRHPPKKLTPLAYKQFIPNVAEKTIGASG 60
 DR 61 RYVGKISRNRSERKELTPNYNPDIKFDEENGTGADRMLTQRCKDKLNLATSWMNQPGV 120
 61 RYVGKISRNRSERKELTPNYNPDIKFDEENGTGADRMLTQRCKDKLNLATSWMNQPGV 120
 DR 61 RYVGKISRNRSERKELTPNYNPDIKFDEENGTGADRMLTQRCKDKLNLATSWMNQPGV 120
 DR 121 KLRVTEGDEDGHSESELHYECRAVOLTSRDRSKYGMALARLAVEAGFDWYYESKAH 180
 121 KLRVTEGDEDGHSESELHYECRAVOLTSRDRSKYGMALARLAVEAGFDWYYESKAH 180
 DR 181 IHQSVKAENSAVAKSGGCFPGSATVHLREQGKTKLVKDLSPGDRVLAAADDQGRLLSDFL 240
 181 IHQSVKAENSAVAKSGGCFPGSATVHLREQGKTKLVKDLSPGDRVLAAADDQGRLLSDFL 240
 DR 241 FLRDDGAKKVYVIEPREPRLTAHLIFVAPHDSDATEPEASSGSPPSGALG 300
 241 FLRDDGAKKVYVIEPREPRLTAHLIFVAPHDSDATEPEASSGSPPSGALG 300
 DR 301 PRALFAVRVPGCORYVVAERDCRRLPAAVHSVTLSSEAAGAYAPLTQCTILINRLV 360
 301 PRALFAVRVPGCORYVVAERDCRRLPAAVHSVTLSSEAAGAYAPLTQCTILINRLV 360
 DR 361 ASCYAVIEEHSHWAHAFAPRFLAHALLAALAPARTDRGGDSGGDRGGGGRVALTAPGA 420
 361 ASCYAVIEEHSHWAHAFAPRFLAHALLAALAPARTDRGGDSGGDRGGGGRVALTAPGA 420
 DR 421 ADPGAGATAGIHWYSQQLYQITGTLWLDSEALPHLGMAVKSS 462
 421 ADPGAGATAGIHWYSQQLYQITGTLWLDSEALPHLGMAVKSS 462

RESULT 2

SHH_MOUSE	STANDARD;	PRT;	437 AA.
ID			
AC	062226;		
DT	15-JUL-1999 (Rel. 38, Created)		
DT	15-JUL-1999 (Rel. 38, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Sonic hedgehog protein precursor (SHH) (HHG-1).		
GN	SHH OR HHG-1.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX			
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-G57BL/6J; TISSUE-Embryo;		
RX	MEDLINE-9409334; PubMed-7916661;		
RA	Echelard Y., Epstein J.D., St. Jacques B., Shen L., Mohler J., McMahon J.A., McMahon A.P.;		
RA	"Sonic hedgehog, a member of a family of putative signaling molecules, is implicated in the regulation of CNS polarity.", Cell 75:1417-1430(1993).		
RN	[2]		
RP	REVISION TO 122.		
RC	STRAIN-G57BL/6J;		
RA	McMahon A.P.;		
RL	Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.		
RN	[3]		
RP	SEQUENCE FROM N.A., AND AUTOPROTEOLYTIC CLEAVAGE.		
RX	MEDLINE-9523697; PubMed-7720571;		
RA	Chang D.T., Lopez A., von Kessler D.P., Chiang C., Simandl B.K., Zhao R., Selain M.F., Fallon J.F., Beachy P.A.;		
RT	"Products, genetic linkage and limb patterning activity of a murine hedgehog gene.", Development 120:3339-3353(1994).		

RN

FUNCTION, AND AUTOPROTEOLYTIC CLEAVAGE.

RP FUNCTION, AND AUTOPROTEOLYTIC CLEAVAGE.

RX MEDLINE-9523697; PubMed-7720571;

RA Reelin H., Porter J.A., Chiang C., Chang D.T., Beachy P.A., Jessell T.M.;

RA "Floor plate and motor neuron induction by different concentrations of the amino-terminal cleavage product of sonic hedgehog autoproteolysis"; Cell 81:445-455(1995).

RN [5]

X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 34-195.

RX X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 34-195.

RN MEDLINE-96059744; PubMed-7477325;

RA Hall T.M.T., Porter J.A., Beachy P.A., Leahy D.J.;

RT "A potential catalytic site revealed by the 1.7-A crystal structure of the amino-terminal signalling domain of Sonic hedgehog.";

RL Nature 378:212-216(1995)

CC -1 FUNCTION: BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH, PTC REPRESSIONS THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO. ALSO REGULATES ANOTHER TARGET, THE GLI ONCOGENE. INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT: SIGNAL PRODUCED BY THE NOTOCHORD THAT INDUCES VENTRAL CELL FATE IN THE NEURAL TUBE AND SOMITES, AND THE POLARIZING SIGNAL FOR PATTERNING OF THE ANTERIOR-POSTERIOR AXIS OF THE DEVELOPING LIMB BUD. DISPLAYS BOTH FLOOR PLATE AND MOTOR NEURON-INDUCING ACTIVITY. THE THRESHOLD IS 5-FOLD LOWER THAN THAT REQUIRED FOR FLOOR PLATE INDUCTION (BY SIMILARITY).

CC -1 SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).

CC -1 TISSUE SPECIFICITY: EXPRESSED IN A NUMBER OF EMBRYONIC TISSUES INCLUDING THE NOTOCHORD, VENTRAL NEURAL TUBE, FLOOR PLATE, LUNG BUD, ZONE OF POLARIZING ACTIVITY AND POSTERIOR DISTAL MESENCHIME OF LIMBS. IN THE ADULT, EXPRESSED IN LUNG AND NEURAL RETINA.

CC -1 DEVELOPMENTAL STAGE: FIRST DETECTABLE DURING GASTRULATION.

CC -1 INDUCTION: BY RETINOIC ACID.

CC -1 PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N-TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE C-PRODUCT HAS NO SIGNALING ACTIVITY.

CC -1 SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.

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CC EMBL: X76290; CAM53922.1; .

DR PDB; 1VHH; 29-JAN-96.

DR MEROPS; C46:002; .

DR MGD; MGI: 98297; Shh.

DR InterPro; IPR000320; HH_signal.

DR InterPro; IPR00167; Hedgehog_hint.

DR InterPro; IPR0386; Hedgehog_hintc.

DR InterPro; IPR0387; Hedgehog_hints.

DR InterPro; IPR02203; Intein.

DR InterPro; IPR01657; sonicHH.

DR Pfam; PF01079; Hint; 1.

DR Pfam; PF01085; HH_signal; 1.

DR PRINTS; PRO0632; SONICHHOG.

DR PRODom; P003042; HH_signal; 1.

DR SMART; SM00305; HintC; 1.

DR	SMART; SM0306; HINN; 1.	RX	MEDLINE=94170375; PubMed=8124714;
KW	PROSTE; PS50817; INTEIN_N_TER; 1.	RA	Roelink H., Augsburger A., Heemskerk J., Korzh V., Norlin S.,
KW	Developmental protein; Autocatalytic cleavage; Hydrolase; Protease;	RA	Ruiz I., Attaba A., Tanabe Y., Placzek M., Edlund T., Jessell T.M.,
SIGNAL	Signal; Lipoprotein; Palmitate; 3D-structure.	RA	Dodd J.;
FT	"Floor plate and motor neuron induction by vhh-1, a vertebrate homolog	RT	of hedgehog expressed by the notochord.";
FT	CHAIN	RT	Cell 76:761-775(1994).
FT	CHAIN	RL	-1- FUNCTION: BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN
FT	25	CC	ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE TRANSCRIPTION
FT	198	CC	OF TARGET GENES. IN THE ABSENCE OF SHH, PTC REPRESSES THE
FT	437	CC	CONSTITUTIVE SIGNALING ACTIVITY OF SMO. ALSO REGULATES ANOTHER
FT	SITE	CC	TARGET, THE GLI ONCOGENE. INTERCELLULAR SIGNAL ESSENTIAL FOR A
FT	198	CC	VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT: SIGNAL PRODUCED
FT	199	CC	BY THE NOTOCHORD THAT INDUCES VENTRAL CELL FATE IN THE NEURAL TUBE
FT	387	CC	AND SOMITES, AND THE POLARIZING SIGNAL FOR PATTERNING OF THE
FT	244	CC	ANTERIOR-POSTERIOR AXIS OF THE DEVELOPING LIMB BUD. DISPLAYS BOTH
FT	25	CC	FLOOR PLATE AND MOTOR NEURON INDUCING ACTIVITY. THE THRESHOLD
FT	LIPID	CC	CONCENTRATION OF N-PRODUCT REQUIRED FOR MOTOR NEURON INDUCTION IS
FT	SITE	CC	5-FOLD LOWER THAN THAT REQUIRED FOR FLOOR PLATE INDUCTION (BY
FT	268	CC	SIMILARITY).
FT	437 AA;	CC	-1- SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE
ACT_SITE	47773 MW;	CC	CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE
ACT_SITE	83 88;	CC	CELL SURFACE. IS ALSO SECRETED IN EITHER CLEARED OR UNCLEAVED FORM
ACT_SITE	Score 2063; DB 1;	CC	TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).
ACT_SITE	Length 437;	CC	-1- TISSUE SPECIFICITY: EXPRESSED IN THE NODE, NOTOCHORD, FLOOR PLATE,
ACT_SITE	Best Local Similarity 87.4%;	CC	AND POSTERIOR LIMB BUD MESONEPHRINE.
ACT_SITE	Pred. No. 2.3e-145;	CC	-1- FTN: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY
ACT_SITE	Matches 404; Conservativeness 8;	CC	AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN
ACT_SITE	Mismatches 24; Indels 26; Gaps 3;	CC	THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF
ACT_SITE	62 RYEGKTRNNSERFELPNINPDLIKDEENTGADRMLTORCKLKLNALAISVNQWPGV	CC	A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N-
ACT_SITE	121 KLRVTEGWDGHSEEHSHVEGRADITSDRRSKYGMARLAAVEGDWTTYESKAH	CC	TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS
ACT_SITE	182 IHCSTYKAENSAVAAAGGCCPGSATVHLEGGTKYJVDLQRGDRVLADQGRLLYSDT	CC	TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION
ACT_SITE	122 KLRVTEGWDGHSEEHSHVEGRADITSDRRSKYGMARLAAVEGDWTTYESKAH	CC	OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE
ACT_SITE	181 IHCSTYKAENSAVAAAGGCCPGSATVHLEGGTKYJVDLQRGDRVLADQGRLLYSDT	CC	ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE
ACT_SITE	181 IHCSTYKAENSAVAAAGGCCPGSATVHLEGGTKYJVDLQRGDRVLADQGRLLYSDT	CC	C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).
ACT_SITE	240	CC	-1- SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.
ACT_SITE	240	CC	-----
ACT_SITE	241	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
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ACT_SITE	242	CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/) or send an email to license@isb-sib.ch .
ACT_SITE	286	CC	-----
ACT_SITE	301 PRAFAFSRYPRGQTYVWAEGRGRLPAAVISVTLEAAGAYAPLTAQSTLILNRL	CC	-----
ACT_SITE	360	CC	-----
ACT_SITE	287 PSALFASRYPRGQYVVAERGGRLPLPAVHSVTREEEAGAYAPLTAQHTLILNRL	CC	-----
ACT_SITE	346	CC	-----
ACT_SITE	351 ASCAVIEHSHWAHAFAPRLAHALLALAPARTDRGGDGGDRGGGGRALTARGA	CC	DR
ACT_SITE	420	CC	DR
ACT_SITE	347 ASCAVIEHSHWAHAFAPRLAHALLALAPARTDRGGDGGDRGGGGRALTARGA	CC	DR
ACT_SITE	395	CC	DR
ACT_SITE	421 ADAPAGATAGIHWYSLQYQIGTWLDSSEALHPLGMAYKSS	CC	DR
ACT_SITE	462	CC	DR
ACT_SITE	396 TEARGAEPPIAGIHWYSLQYQIGTWLDSSEALHPLGMAYKSS	CC	DR
ACT_SITE	437	CC	DR
SHL_RAT	SHL_RAT	DR	DR
ID	STANDARD;	DR	InterPro; IPR01320; HR_signal.
AC	PRT;	DR	InterPro; IPR0167; Hedgehog_hntC.
DT	437 AA.	DR	InterPro; IPR00506; Hedgehog_hntC.
DT	15-JUL-1999 (Rel. 38, Created)	DR	InterPro; IPR00358; Hedgehog_hntN.
DT	15-JUL-1999 (Rel. 38, last sequence update)	DR	InterPro; IPR002203; Intein.
DT	15-OCT-2001 (Rel. 40, last annotation update)	DR	InterPro; IPR001657; SonichH.
DE	Sonic hedgehog protein precursor (SHH).	DR	Pfam; PF01079; HntC; 1.
GN	SHH OR VHH-1.	DR	PRINTS; PR0532; SONICHHG.
OS	Rattus norvegicus (Rat).	DR	PRODOM; PD003042; HH_signal; 1.
OC	Eukaryota; Chordata; Craniata; Vertebrata; Buteleostomi;	DR	SMART; SM0306; HntN; 1.
OC	Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Rattus.	DR	PROSITE; PS50817; INTEIN_N_TER; 1.
NCBI_TAXID	10116;	DR	Developmental protein; Autocatalytic cleavage; Hydrolase; Protease;
RN	[1]	DR	KW Signal; Lipoprotein; Palmitate.
SEQUENCE	FROM N.A.	FT	FT SIGNAL 1 24 POTENTIAL.
STRAIN-Sprague-Dawley; TISSUE=Embryonic floor plate;	RC	FT	FT CHAIN 25 437 SONIC_HEDGEHOG PROTEIN.
		FT	FT CHAIN 25 198 SONIC_HEDGEHOG PROTEIN_N-PRODUCT.
		FT	FT CHAIN 199 437 SONIC_HEDGEHOG PROTEIN_C-PRODUCT.
		FT	FT SITE 198 437 CLEAVAGE (AUTO-).
		FT	FT SITE 244 437 INVOLVED IN CHOLESTEROL TRANSFER (BY
		FT	FT SITE 268 268 SIMILARITY).
		FT	FT SITE 271 271 ESSENTIAL FOR AUTO-CLEAVAGE (BY

FT BINDING 198 198 SIMILARITY).
 FT DOMAIN 383 387 CHOLESTEROL (BY SIMILARITY).
 FT LIPID 25 25 POLY-GIX.
 SQ SEQUENCE 437 AA; 47630 MW; ODBFC19F0D1662A0 CRC64;
 Query Match 83.4%; Score 2050; DB 1; Length 437;
 Best Local Similarity 87.5%; Pred. No. 9. 2e-145; Indels 28; Gaps 4;
 Matches 405; Conservative 8; Mismatches 22; Indels 28; Gaps 4;
 Qy 1 MILLARCILLLVLLSLVCSGLACGPGORGKRRHPLKPLAKQIPNVAEKTGASG 60
 :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
 2 LILLARGLFLVALASSLIVCPGLAGCGCGRGFRKRQPRKLTPLAYKQFIPNVAEKTGASG 61
 Db 61 RVEGKISRSERERKELTPTNYNFDIIFKDEENGTADRLMTQRCKDKMLATSWMNOPGV 120
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Qy 62 RVEGKIRNSEEKELETPNYNFDIIFKDEENGTADRLMTQRCKDKMLATSWMNOPGV 121
 RVEGKIRNSEEKELETPNYNFDIIFKDEENGTADRLMTQRCKDKMLATSWMNOPGV 121
 Qy 121 KARYTEGWDEDGHSESSHLHYSGRAVIDTSURDRSKYGMALARLAVAGEPKWYVYESKAH 180
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 122 KLVTEGWDDEGHSESSHLHYSGRAVIDTSURDRSKYGMALARLAVAGEPKWYVYESKAH 181
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Qy 181 IHCVKNAENSAVAKSGCCFPGSATVHLEQGGIKLKVKVLQDPLSPGDRVLAADDQGRILYDFLT 240
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 182 IHCVKNAENSAVAKSGCCFPGSATVHLEQGGIKLKVKVLQDPLSPGDRVLAADDQGRILYDFLT 241
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Qy 241 FLDRDGAKKVYVIETREPFLTLTAHLFLVAPINDSATGEGPEASSGSGPPSGALG 300
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 242 FLDRDGAKKVYVIETREPFLTLTAHLFLVAPIND-----SGPTPG 286
 |||||:|||||:|||||:|||||:|||||:|||||:
 Qy 301 PRFLFAVRVPSQGRVYVAERDCCRLLPAVHSVTUSEAAAYAHLTAGTILNRL 360
 |||||:|||||:|||||:|||||:|||||:|||||:
 Db 287 PSPLFAASRVRPGQRYVVAERGDRRLPAVHSVTUREAAAGAYAHLTAGTILNRL 346
 |||||:|||||:|||||:|||||:
 Qy 361 ASQYAVZEEHSHWRAFAPRLAHALLAALAPRTDGGDSCGGDRGGGGNVALAP-G 419
 |||||:|||||:|||||:|||||:|||||:
 Db 347 ASQYAVZEEHSHWRAFAPRLAHALLAALAPRTDGGDSCGGDRGGGGNVALAP-G 437
 |||||:|||||:|||||:|||||:
 Qy 420 AADPAGAGATAGTHWYSOLLYQGTWLDSEALHPLGMVKS 462
 |||||:|||||:
 Db 395 VAEARGAGPAPPAGHWHYSOLLYHTWLDSETHPLGMVKS 437
 |||||:|||||:
 RESULT 4
 SHH_CHICK STANDARD; PRT; 425 AA.
 ID SHH_CHICK STANDARD; PRT; 425 AA.
 AC 091035; DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Sonic hedgehog protein precursor (SHH).
 GN SHH.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauvia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OX NCBI_TAXID=9031;
 RN [1]
 SEQUENCE FROM N.A.
 RP TISSUE=limb bud;
 RX MEDLINE=94094333; PubMed=8269518;
 RA Roelke R.D., Johnson R.L., Laufer E., Tabin C.;
 RT "Sonic hedgehog mediates the polarizing activity of the ZPA.";
 RL Cell 75:1401-1416(1993).
 RN [2]
 RP FUNCTION AND AUTOPROTOLYTIC CLEAVAGE.
 RX MEDLINE=9525654; PubMed=7736596;
 RA Roelink H., Porter J.A., Chiang C., Tanabe Y., Chang D.T.,
 RA Beachy P.A., Jessell T.M.;
 RT "Floor plate and motor neuron induction by different concentrations of
 the amino-terminal cleavage product of sonic hedgehog
 autoproteolysis";
 RT Cell 81:445-455(1995).
 RL
 CC -1- FUNCTION: Binds to the patched (PTC) receptor, which functions in
 CC ASSOCIATION WITH SMOOTHED (SMO), to activate the transcription
 CC OF TARGET GENES. IN THE ABSENCE OF SHH, PTC REPRESES THE
 CC CONSTITUTIVE SIGNALING ACTIVITY OF SMO. ALSO REGULATES ANOTHER
 CC TARGET, THE GLI ONCOGENE. INTERCELLULAR SIGNAL ESSENTIAL FOR A
 CC VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT: SIGNAL PRODUCED
 CC BY THE NOTOCHORD THAT INDUCES VENTRAL CELL FATE IN THE NEURAL TUBE
 CC AND SOMITES, AND THE POLARIZING SIGNAL FOR PATTERNING OF THE
 CC ANTERIOR-POSTERIOR AXIS OF THE DEVELOPING LIMB BUD. DISPLAYS BOTH
 CC FLOOR PLATE- AND MOTOR NEURON-INDUCING ACTIVITY. THE THRESHOLD
 CC CONCENTRATION OF N-PRODUCT REQUIRED FOR MOTOR NEURON INDUCTION IS
 CC 5-FOLD LOWER THAN THAT REQUIRED FOR FLOOR PLATE INDUCTION.
 CC -1- SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE
 CC CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE
 CC CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM
 CC TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE POSTERIOR LIMB BUD
 CC MESENCHIME, THE HENSEN'S NODE, THE NOTOCHORD, AND THE FLOOR PLATE
 CC OF THE NEURAL TUBE.
 CC -1- DEVELOPMENTAL STAGE: FIRST DETECTABLE AT STAGE 17 DURING THE
 CC INITIATION OF LIMB BUD FORMATION. FROM THAT POINT ONWARDS, THE
 CC EXPRESSION PATTERN EXACTLY MATCHES THE LOCATION OF THE ZONE OF
 CC POLARIZING ACTIVITY (ZPA).
 CC -1- INDUCTION: BY RETINOID ACID.
 CC -1- PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY
 CC AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN
 CC THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF
 CC A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N-
 CC TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS
 CC TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION
 CC OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE
 CC BETWEEN THE SWISS INSTITUTE OF BIOINFORMATICS AND THE EMBL OUTSTATION -
 CC THE EUROPEAN BIOINFORMATICS INSTITUTE. THERE ARE NO RESTRICTIONS ON ITS
 CC USE BY NON-PROFIT INSTITUTIONS AS LONG AS ITS CONTENT IS IN NO WAY
 CC MODIFIED AND THIS STATEMENT IS NOT REMOVED. USAGE BY AND FOR COMMERCIAL
 CC ENTITIES REQUIRES A LICENSE AGREEMENT (SEE [HTTP://WWW.ISB-SIB.CH/ANNOUNCE/](http://www.isb-sib.ch/announce/))
 CC OR SEND AN EMAIL TO LICENSE@ISB-SIB.CH).
 CC -----
 DR EMBL; L28099; AAJ72428.1; -.
 DR EMBL; 062226; IVHH.
 DR MERSF; C46_001; -.
 DR InterPro; IPR00320; HH_signal.
 DR InterPro; IPR01767; Hedgehog_hint.
 DR InterPro; IPR03586; Hedgehog_hintc.
 DR InterPro; IPR03587; Hedgehog_hintn.
 DR InterPro; IPR02203; Intelin.
 DR InterPro; IPR001657; Sonichh.
 DR Pfam; PF01079; Hint; 1.
 DR Pfam; PF01085; HH_signal; 1.
 DR PRINTS; PRO0032; SONICHHOG.
 DR ProDom; PD003042; HH_signal; 1.
 DR SMART; SM0305; HintC; 1.
 DR SMART; SM0306; HintN; 1.
 DR PROSITE; PS00817; INTELIN_TER; 1.
 KW Developmental protein; Autocatalytic cleavage; Hydrolase; Protease;
 KW Signal; Lipoprotein; Palmitate.
 FT SIGNAL 1 26 POTENTIAL.
 FT CHAIN 27 425 SONIC_HEDGEHOG PROTEIN.
 FT CHAIN 27 200 SONIC_HEDGEHOG PROTEIN_N-PRODUCT.
 FT CHAIN 201 425 SONIC_HEDGEHOG PROTEIN_C-PRODUCT.
 FT SITE 200 201 CLEAVAGE (AUTO-) (PROBABLE).
 FT SITE 246 246 INVOLVED IN CHOLESTEROL TRANSFER (BY
 FT SITE 270 270 INVOLVED IN AUTO-CLEAVAGE (BY
 FT ACT_SITE 273 273 SIMILARITY).
 FT ACT_SITE 273 273 ESSENTIAL FOR AUTO-CLEAVAGE (BY
 FT ACT_SITE 273 273 SIMILARITY).
 FT BINDING 200 200 CHOLESTEROL (BY SIMILARITY).

FT	ACT_SITE	270	270	SIMILARITY'). SIMILARITY FOR AUTO-CLEAVAGE (BY ESSENTIAL).	RT	gene family of <i>Xenopus laevis</i> .";
FT	BINDING	197	197	SIMILARITY).	RL	Development 121:2337-2347(1995). [3]
FT	LIPID	24	24	CHOLESTEROL (BY SIMILARITY).	RN	SEQUENCE FROM N.A.
FT	SEQUENCE	418 AA:	46402 MN:	PALMITATE (BY SIMILARITY).	RC	TISSUE=notochord;
SQ				CY000AFFF2D2F5795 CRC64;	RX	MEDLINE-96028338; PUBMED-7551564;
QY	1	MILLIARCLLVLVLLYSLNLLVSGLACGGPGRGFGKRRHKKLTPLAKQFIPVAEKTGLGAG	61	Score 1506; DB 1; Length 418; Best Local Similarity 64.5%; Pred. No. 6.7e-104; Matches 300; Conservative 47; Mismatches 68; Indels 50; Gaps 5;	RT	Ruiz J, Altaba A, Jessell T.M., Roelink H.;
Db	1	MRLJTRVLVLLVLLTSLVSGLACGGPGRGFGKRRHKKLTPLAKQFIPVAEKTGLGAG	60	"Restrictions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";	RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";
QY	61	RYECKISRNSERERELTPWNPYNDPIKFDEENTGDRMLMORCKDKLNALISTYNQNQGV	120	Mol. Cell. Neurosci. 6:106-121(1995);	RT	Mol. Cell. Neurosci. 6:106-121(1995);
Db	61	RYECKISRNSERERELTPWNPYNDPIKFDEENTGDRMLMORCKDKLNALISTYNQNQGV	120	FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT AND METAMORPHOSIS. INVOLVED IN LIMB FORMATION. PATTERNING OF THE CENTRAL NERVOUS SYSTEM AND VENTRAL SOMITE DIFFERENTIATION. INDUCES ECTOPIC CEMENT GLAND FORMATION IN EMBRYOS. BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO) TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH, PTC REPRESSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO (BY SIMILARITY).	CC	PATTERNING EVENTS DURING DEVELOPMENT AND METAMORPHOSIS. INVOLVED IN LIMB FORMATION. PATTERNING OF THE CENTRAL NERVOUS SYSTEM AND VENTRAL SOMITE DIFFERENTIATION. INDUCES ECTOPIC CEMENT GLAND FORMATION IN EMBRYOS. BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO) TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH, PTC REPRESSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO (BY SIMILARITY).
QY	121	KLRVTEGMEDGHHSEESLHYEGRAVITTSRDRSKYMLRILAVEAGFDWVYESKAH	180	121 KLRVTEGMEDGHHSEESLHYEGRAVITTSRDRSKYMLRILAVEAGFDWVYESKAH	180	121 KLRVTEGMEDGHHSEESLHYEGRAVITTSRDRSKYMLRILAVEAGFDWVYESKAH
Db	181	IHESYKAENSAVAKSGGCPGSAVTHLEQGGTKLVKVDLSPGDRVLAADDQGRYLSDLT	240	181 IHESYKAENSAVAKSGGCPGSAVTHLEQGGTKLVKVDLSPGDRVLAADDQGRYLSDLT	240	181 IHESYKAENSAVAKSGGCPGSAVTHLEQGGTKLVKVDLSPGDRVLAADDQGRYLSDLT
QY	181	IHSQSYKAENSAVAKSGGCPGSAVSLQDGQRAVKDINGPKDRVLAADDQGRYLSDLT	240	181 IHSQSYKAENSAVAKSGGCPGSAVSLQDGQRAVKDINGPKDRVLAADDQGRYLSDLT	240	181 IHSQSYKAENSAVAKSGGCPGSAVSLQDGQRAVKDINGPKDRVLAADDQGRYLSDLT
Db	241	FLDODDGAKKVYVETREPRERLLTAHLFWAPHNDSATGEPEASSGGPPGSGAL	300	241 FLDODDGAKKVYVETREPRERLLTAHLFWAPHNDSATGEPEASSGGPPGSGAL	300	241 FLDODDGAKKVYVETREPRERLLTAHLFWAPHNDSATGEPEASSGGPPGSGAL
Db	341	341 ASCAVIVEDQGLAHAFAPRALLYVYVSSLFLR-----	375	341 ASCAVIVEDQGLAHAFAPRALLYVYVSSLFLR-----	375	341 ASCAVIVEDQGLAHAFAPRALLYVYVSSLFLR-----
QY	421	ADREGAGAT--AGHWIQLQQLQIGTMLDSEBALHPIGMAVKS	462	421 ADREGAGAT--AGHWIQLQQLQIGTMLDSEBALHPIGMAVKS	462	421 ADREGAGAT--AGHWIQLQQLQIGTMLDSEBALHPIGMAVKS
Db	376	--SSRSNATLQQGCVHWSRLLYQMGTMWLDNSMLHPIGMVNS	418	376 --SSRSNATLQQGCVHWSRLLYQMGTMWLDNSMLHPIGMVNS	418	376 --SSRSNATLQQGCVHWSRLLYQMGTMWLDNSMLHPIGMVNS
RESULT 7						
SHL_XENLA						
ID	SHL_XENLA	STANDARD:	PRT:	444 AA.	CC	
AC	Q92000; Q91894;				CC	
DT	15-JUL-1999 (Rel. 38, Created)				CC	
DT	16-OCT-2001 (Rel. 40, Last annotation update)				CC	
DE	Sonic hedgehog protein precursor (X-SHH) (VHH-1).				CC	
GN	SHH.				CC	
OS	Xenopus laevis (African clawed frog).				CC	
OC	Xenopus, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;				CC	
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;				CC	
OX	Xenopodaen; Xenopus.				CC	
NCB_TAXID=8355;					CC	
[1]	SEQUENCE FROM N.A.				CC	
RP	SEQUENCE FROM N.A.				CC	
RC	TISSUE=vertebrate;				CC	
RC	Medline:95357169; PubMed=7630736;				CC	
RC	Stolow M.A., Shi Y.-B.;				CC	
RT	"Xenopus sonic hedgehog as a potential morphogen during embryogenesis and thyroid hormone-dependent metamorphosis.";				CC	
RL	Nucleic Acids Res. 23:2555-2562(1995).				CC	
RN	{2}				CC	
RP	SEQUENCE FROM N.A.				CC	
RC	TISSUE=embryo;				CC	
RC	Medline:95401852; PubMed=7671800;				CC	
RA	Ekiert S.C., McGrew L.L., Lai C.-J., Lee J.J., von Kessler D.P.,				CC	
RA	Moon R.-T., Beachy P.A.;				CC	
RT	Distinct expression and shared activities of members of the hedgehog				CC	
RT	gene family of <i>Xenopus laevis</i> .";				CC	
RL	Development 121:2337-2347(1995). [3]				CC	
RN	SEQUENCE FROM N.A.				CC	
RC	TISSUE=notochord;				CC	
RC	MEDLINE-96028338; PUBMED-7551564;				CC	
RT	Ruiz J, Altaba A, Jessell T.M., Roelink H.;				CC	
RT	"Restrictions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Ruiz J, Altaba A, Jessell T.M., Roelink H.;				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";				CC	
RT	Mol. Cell. Neurosci. 6:106-121(1995);				CC	
RT	"Restricions to floor plate induction by hedgehog and winged-h					

FT	CHAIN	25	444	SONIC HEDGEHOG PROTEIN N-PRODUCT.
FT	CHAIN	199	444	SONIC HEDGEHOG PROTEIN C-PRODUCT.
FT	SITE	198	199	CLEAVAGE (AUTO-) (BY SIMILARITY).
FT	SITE	266	266	INVOLVED IN AUTO-CLEAVAGE (BY SIMILARITY).
FT	ACT-SITE	269	269	ESSENTIAL FOR AUTO-CLEAVAGE (BY SIMILARITY).
FT	DOMAIN	386	409	3 X 8 AA TANDEM REPEATS OF Q-V-D-L-Q-S-H-
FT	REPEAT	386	393	H.
FT	REPEAT	394	401	1.
FT	REPEAT	403	409	2.
FT	BINDING	198	198	CHOLESTEROL (BY SIMILARITY).
FT	LIPID	25	25	PALMITATE (BY SIMILARITY).
FT	CONFLICT	5	9	TOSLU > NSNCW (IN REF. 3).
FT	CONFLICT	302	319	DPTKMLKAVKVERDLE -> ESQDHLDLGRGKWRRLILR (IN REF. 3).
FT	CONFLICT	432	432	N->S (IN REF. 3).
SO	SEQUENCE	444 AA:	49453 MW:	73B4E932FA2EFF2 CRC64;
Query Match		60.7%	Score 1498;	DB 1;
Best Local Similarity		64.1%	Length 444;	Pred. No. 2.8e-103;
Matches		305;	Conservative	Mismatches 38;
				Indels 46;
				Gaps 7;
QY	1	MILLARCLLV-LVSSILVCSLLACGGGRGEKKRKRLTFLAYKOFIPNAAKTGAS	59	-1- SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).
QY	1	MIVATOSLLLSSFLCIFTVTTPGLAGFGRRGKRRHHKKLTFPLAYKOFIPNAAKTGAS	59	EYES
QY	60	GRYEKGKISRNSERFKELTPPNYAPDITPKDEENTGADLMLTORKDKNDKLNALASVMNQWP	119	-1- TISSUE SPECIFICITY: EXPRESSED IN THE VENTRAL MIDLINE OF THE NEURAL TUBE AND BRAIN. IN THE DEVELOPING BRAIN, EXPRESSION OCCURS IN DOMAINS THAT INCLUDE A DISCRETE REGION IN THE FLOOR OF THE Diencephalon. NOT DETECTED IN THE NOTOCHORD OR DEVELOPING FIN BUD.
Db	61	GRIEGKITRNSDCPKELTPNYAPDIMKDEESTGADLMLTORKDKNDKLNALASVMNQWP	120	CC -1- PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYTIC ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N- TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).
QY	120	VKLRYTEGWDPEOCHHSEESLHVEGRADITVSDRSKYMLARLAVEAGPFWVYSSKA	179	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
Db	121	VKLRYTEGWDPEOCHHLEESLHVEGRADITVSDRSKYMLGRLAVEAGPFWVYSSKA	180	CC
QY	180	HIHCSVWAENSAAKSGCGFPSSATVILEQDGSTKLVLQDSDPDRVLAADQQRLLYSDL	239	CC
Db	181	HIHCSVKAENSAAKSGCGFPAGARWAEFFGTAKVQLRPQDRVLSSDPQNLILYSDL	240	CC
QY	240	TFLDRDGAKKVYVETRPREPLRLLTAHHLFVAPHNDSATGEPEAASSSSGPPSGAL	299	CC
Db	241	MFIQERDVKKLFYVIENSQ-RKIRLTAHHLFVAQ-----TKVNGTR	282	CC
QY	300	GPRALERSRVRQGVVVAERGDRLRLLPAAVHSVTLSEEAGAKAPLTAQCTILINRV	359	CC
Db	283	SEFSKSVFATNPQPGDLITYTAQPK-TMFLKAVKVKVEKD-EEGTAVYAPLTAQTVWIDQ	339	CC
QY	360	LASCYAVTEENSWAHRAPPFELAHALALAPARTDRGGDSGGDKKGGG-----411	411	CC
Db	340	LASCYAVIEHTWAHLAFAPLRFGMSLSSYYIYPR-----DSSPPSLQPHHQDQ	388	CC
QY	412	-----RVALTAGAADDPGAGATAGTHWSQLYQIGTWTLOSEALHPLGMVKSS	462	CC
Db	389	LQSHHQVDLQSHHQVDLQSHHQLEGTHWSQLYQIGTWTLOSDNSLHPLGMATKSS	444	CC
RESULT	8			
TWHH_BRARE		STANDARD:	PRT:	416 AA.
TWHH_BRARE	ID			
AC	Q90419;			
DT	15-JUL-1999 (Rel. 38, Created)			
DT	15-JUL-1999 (Rel. 38, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	TIGGY-winkle hedgehog protein precursor (TWHH)			
GN	TWHH			
OS	Brachydanio rerio (Zebrafish) (Danio rerio).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.			
OC	NCBI_TaxID:7955;			
[1]				
Query Match		58.0%	Score 1432;	DB 1;
Best Local Similarity		62.6%	Length 416;	Pred. No. 1.9e-98;
Matches		288;	Conservative	Mismatches 39;
				Indels 56;
				Gaps 5;

QY	2	LILLARCLLVLVLLVSSLVCGSLACGPGRGKRRHKPKKLTPPLAYKQFIPNVAEKTIGASGR	61	CC
5	LHLKQFALLCFSILLIPCGLACGPGRGKRRHKPKKLTPPLAYKQFIPNVAEKTIGASGR	64	CC	
Db	62	YEKGTSNSRERKELETPNYNPNDIKEEENTGADRIMTORCKDKLNALATSMVNQPGVK	121	CC
OY	65	YEKGTSNSRERKELETPNYNPNDIKEEENTGADRIMTORCKDKLNALATSMVNQPGVK	124	CC
Db	122	LRTVEGDEDGHHSSEESILHVEGRANDITTSDRSKYGMARLAVEAGFDWVYESKAHI	181	CC
OY	125	LRTVEGDEDGHHLHLESHYVEGRADITTSDRDKSKYGMRLAVEAGFDWVYESKAHI	184	CC
Db	182	HCSVKAENSVAAKSGGCFFPGSATVHLEQGKLYKLDLSGDRVLAAADDQGRLLYSDFL	241	CC
OY	185	HCSVKAENSVAAKSGGCFFPGSATVHLEQGKLYKLDLSGDRVLAAADDQGRLLYSDFL	244	CC
Db	242	LDRDGAKKVFVVIETREPRLLTAAHLLVAPHDSDATGEPEASSSGCPSPGGALP	301	CC
OY	245	IDHDPTRRQFTVIEITERSEPTFLTTLTAHHLVEV-NSSA-----ASGI	286	CC
Db	302	RALFASRVPPGORYVVAERDGDRRLPAVHSVTL---SFEAAAGAYAPLTAQGTLLIN	357	CC
OY	287	TATFASNVKPGTVLWED-----TCESLKSVTYKRITYEEHEGSFAPVTAHGTLIV	339	CC
Db	358	RYLASCVAVTEHHWAIRAFRFLAHLLALAPARTDGDGGDRGSGGGVALTA	417	CC
OY	340	: : : : : : : : : : :	383	CC
Db	418	PGAADAPGAGATAGTHYSLQLYQIGWLOSEALRHGM	457	CC
OY	384	-----EDGIRHYSNMUFHIGSWLIDDSFHULGI	412	CC
RESULT 9				
IHH_CHICK	STANDARD;	PRT;	408 AA.	
ID	098938;			
AC				
DT	15-JUL-1999 (Rel. 38 Created)			
DT	15-JUL-1999 Rel. 38, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Indian hedgehog protein precursor (IHH).			
GN	IHH.			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archaeabacteria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OC	Gallus.			
OX	NCBI_TAXID=9031;			
RN	[1]			
RP	SEQUENCE FROM N_A.			
RX	MEDLINE=96125423; PubMed=662546;			
RA	Vortkamp A., Lee K., Lanske B., Segre G.V., Kronenberg H.M.,			
RA	Tabin C.J.,			
RT	"Regulation of rate of cartilage differentiation by Indian hedgehog			
RT	and pH-related protein".			
RL	Science 273:613-622(1996).			
-- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT. BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES, IMPLICATED IN ENDCHONDRAL OSSIFICATION. MAY REGULATE THE BALANCE BETWEEN GROWTH AND OSSIFICATION OF THE DEVELOPING BONES. INDUCES THE EXPRESSION OF PARATHYROID HORMONE-RELATED PROTEIN (PTHrP).				
-- SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL SURFACE, IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).				
-- TISSUE SPECIFICITY: EXPRESSED IN DEVELOPING MIDGUT, LUNG AND CARTILAGE OF DEVELOPING LONG BONES IN THE LIMB.				
-- PFM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N-TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS				
Query Match	51.9%	Score 1282.5;	DB 1;	Length 408;
Best Local Similarity	59.7%	Pred. No. 2e-87;		
Matches	271;	Conservative	34;	Mismatches 92;
				Indels 57; Gaps 8;
QY	5 ARCLLVLVSSLVCGSL-ACCGFGRGFG-KRRHPKLPPLAYKQFIPNVAEKTIGASRY	62		
Db	4 ARCLLVLVSSLVCGSL-ACCGFGRGFG-KRRHPKLPPLAYKQFIPNVAEKTIGASRY	63		
OY	63 EGKTSNSRERKELETPNPNPDIFKDEENTGADRIMTORCKDKLNALATSMVNQPGVK	122		
Db	64 EGKTSNSRERKELETPNPNPDIFKDEENTGADRIMTORCKDKLNALATSMVNQPGVK	123		
QY	123 RYVEGWDSDGHHSSEESILHVEGRADITTSDRDKSKYGMRLAVEAGFDWVYESKAHI	182		
Db	124 RYVEGWDSDGHHSSEESILHVEGRADITTSDRDKSKYGMRLAVEAGFDWVYESKAHI	183		
QY	183 HCSVKAENSVAAKSGGCFFPGSATVHLEQGKLYKLDLSGDRVLAAADDQGRLLYSDFL	242		
Db	184 HCSVKAENSVAAKSGGCFFPGSATVHLEQGKLYKLDLSGDRVLAAADDQGRLLYSDFL	243		
QY	243 DRDGAKKVFVVIETREPRLLTAAHLLVAPHDSDATGEPEASSSGCPSPGGALP	302		
Db	244 DKPRALTAHFVETRQPRRLAIPHTHLLFVA--DNA-----SAPAOFR	287		
OY	303 ALFASRVPPGORYVVAERDGDRRLPAVHSVTSEEAGAYAPLTAQGTLLINRIVAS	362		
Db	288 PTFASHVOPGFHVLAVALGSGGLQPAEVGVGR-GRTDVGVAYPLTRHGTVDWVAS	343		

Db 350 AVADHHLQALAFRLRLHSL----- AWGSWTPG 378
Oy 426 AGAVAGIHWYSQQLYQIGWVLLDSEALHPLGMVAKSSXSRGAG 468
Db 379 ---EGHWVPPOLLYRGRLLBEGSFHPLGMS----GAG 410

RESULT 11

IHH_MOUSE STANDARD; PRT; 411 AA.

ID IHH MOUSE STANDARD; PRT; 411 AA.

AC P97812; Q61724;

DT 15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)

DE Indian hedgehog protein precursor (IHH) (Hhg-2).

GN IHH.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Mus.

OX NCBI_TAXID=10090;

RN [1].

RP SEQUENCE FROM N.A., AND AUTOPROTEOLYTIC CLEAVAGE.

RC STRAIN=CDD-1; TISSUE=Kidney;

RX MEDLINE-97236802; PubMed-9079674;

RA Valentini R.P., Brookhiser W.T., Park J., Yang T., Briggs J., Dressler G., Holzman L.B.,

RA McMahon J.A., Epstein D.J., St Jacques B., Shen L., Mohler J., RT "post-translational processing and renal expression of mouse Indian hedgehog";

RL J. Biol. Chem. 272:8466-8473(1997).

RN [2].

RP SEQUENCE OF 76-411 FROM N.A.

RX MEDLINE-94094334; PubMed-7916661;

RA Echelard Y., Epstein D.J., St Jacques B., Shen L., Mohler J., RT "Sonic hedgehog, a member of a family of putative signaling molecules, is implicated in the regulation of CNS polarity.";

RL Cell 75:1417-1430(1993).

RN [3].

RP REVISIONS.

RC STRAIN=C57BL/6J;

RA St Jacques B.; RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.

RN [4].

RP SEQUENCE OF 124-172 FROM N.A.

RX MEDLINE-95236997; PubMed-7720571;

RA Chang D.T., Lopez A., von Kessler D.P., Chiang C., Simandl B.K., Zhao R., Seidin M.F., Fallon J.F., Beachy P.A.; RT "Products, genetic linkage and limb patterning activity of a murine hedgehog gene";

RL Development 120:3339-3353(1994).

-1- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT. BINDS TO THE PATCHED (PTC) RECEPTOR WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IMPLICATED IN ENDOCHONDRAL OSSIFICATION: MAY REGULATE THE BALANCE BETWEEN GROWTH AND OSSIFICATION OF THE DEVELOPING BONES. INDUCES THE EXPRESSION OF PARATHYROID HORMONE RELATED PROTEIN (PTHrP).

-1- SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).

-1- TISSUE SPECIFICITY: IN THE EMBRYO, DEFECTED IN THE DEVELOPING GUT, THE GROWTH ZONE OF CARTILAGE OF DEVELOPING LONG BONES, EPITHELIUM AND UROGENITAL SINUS. IN THE ADULT KIDNEY, FOUND IN PROXIMAL CONVOLUTED AND PROXIMAL STRAIGHT TUBULE.

-1- DEVELOPMENTAL STAGE: DEFECTED AT 10 DAYS POST COITUM (DPC) IN DEVELOPING GUT, AT 14.5 DAYS DPC IN THE CARTILAGE PRIMORDIUM AND IN THE DEVELOPING UROGENITAL SINUS. EXPRESSION INCREASES WITH GESTATIONAL AGE IN KIDNEY AND DUODENUM, BECOMING MAXIMAL IN ADULTHOOD.

-1- PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN

CC THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N- TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.

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CC DR EMBL; U05610; ABAB9592.1; ALT_INTR.

DR DR HSSP; Q62226; IVHH.

DR DR MEROPS; C46_003; -.

DR DR MGDB; MGII-96553; Ihh.

DR DR InterPro; IPR000320; HH_signal.

DR DR InterPro; IPR003587; Hedgehog_hhtC.

DR DR InterPro; IPR002203; Intein.

DR DR Pfam; PF01079; Hht; 1.

DR DR Pfam; PF01085; HH_signal; 1.

DR DR ProDom; PD003042; HH_signal; 1.

DR DR SMART; SMN0305; HntC; 1.

DR DR SMART; SMN006; HntN; 1.

DR DR PROSITE; PS50817; INTEIN_N_TER; 1.

KW Developmental protein; Autocatalytic cleavage; Hydrolase; Protease; Signal; Lipoprotein; Palmitate.

FT FT SIGNAL 1 27 POTENTIAL.

FT FT CHAIN 28 411 INDIAN HEDGEHOG PROTEIN.

FT FT CHAIN 28 202 INDIAN HEDGEHOG PROTEIN N-PRODUCT.

FT FT CHAIN 203 411 INDIAN HEDGEHOG PROTEIN C-PRODUCT.

FT FT SITE 202 203 CLEAVAGE (AUTO-).

FT FT SITE 248 248 INVOLVED IN CHOLESTEROL TRANSFER (BY SIMILARITY).

FT FT SITE 272 272 INVOLVED IN AUTO-CLEAVAGE (BY SIMILARITY).

FT FT ACT_SITE 275 275 ESSENTIAL FOR AUTO-CLEAVAGE (BY SIMILARITY).

FT FT BINDING 202 202 CHOLESTEROL (BY SIMILARITY).

FT FT LIPID 28 28 PALMITATE (BY SIMILARITY).

FT FT CONFLICT 383 383 W->S (IN REF. 2).

FT FT SEQUENCE 411 AA; 45485 MW; 0BEB7AD8507C0D9B CRC64;

Query Match Best Local Similarity 51.1%; Score 1262; DB 1; Length 411; Matches 264; Conservative 56.9%; Pred No. 6..6e-86; Mismatches 86; Indels 68; Gaps 10;

Qy 7 CLLVLVLSLVLVSGLACGGPGRFG-KRRHPKLTPLAYQFIPNVAEKTGASGRVEK 65

Db 13 CLEFLLL--LLVPAARGCGGPGRVGVGSRRRPPRKLVPLAKQFSNPVNPKTLGASGRVEK 70

Qy 66 ISRNSERKELTNYNPDPFKEENTGADRMLTQRCKDKLNALAIISMNQPGVKLRT 125

Db 71 IARSSERKELTNYNPDPFKEENTGADRMLTQRCKDKLNALAIISMNQPGVKLRT 130

Qy 126 EGMDEDGHHSSEESLHYEGRADVDTTSRDRSKYGLMARLAVAEFGDWYVYESKAHICSV 185

Db 131 EGMDEDGHHSSEESLHYEGRADVDTTSRDRSKYGLMARLAVAEFGDWYVYESKAHICSV 190

Qy 186 KAENSAVAKSGGCPGSGATVHLEQGGTKLKLDSLPGDRVLAQDQGRILYSPFLFELRD 245

Db 191 KSEHSAAKTGCGCPAGAQVRLENGERVALSAVKGPDGVLAQEDGTPtPSDFVLFDR 250

Qy 246 DGAKKVVFVIEPREPARELLTAHLLEVPHDSAGEPASSGSGPPGGALGPRLF 305

GN INH OR EHH.
 OS *Brachydanio rerio* (*Zebrafish*) (*Danio rerio*).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio;
 OC NCBL-TAXID=7955;
 RN [1] SEQUENCE FROM N.A.
 RP
 RX
 RC TISSUE=MUSCLE;
 RX MEDLINE=96310664; PubMed=8686485;
 RA Currie P.D., Ingham P.W.;
 RT "induction of a specific muscle cell type by a hedgehog-like protein
 in zebrafish.";
 RL Zardoya R., Abouheif E., Meyer A.;
 RT Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species
 closely related to the zebrafish";
 PROC. NATL. ACAD. SCI. U.S.A. 93:13036-13041(1996).
 CC -1 FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF
 PATTERNING EVENTS DURING DEVELOPMENT. SIGNAL PRODUCED BY THE
 NOTOCHORD THAT INDUCES SOMITE PATTERNING AND MUSCLE PIONEER
 DIFFERENTIATION.
 CC -1 SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE
 CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE
 CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM.
 CC -1 TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN THE NOTOCHORD.
 CC -1 DEVELOPMENTAL STAGE: FIRST DETECTABLE AT THE MID-GASTRULA STAGE.
 CC -1 PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY
 AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN
 THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF
 A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N-
 TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS
 TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION
 OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE
 ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE
 C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).
 CC -1 SIMILARITY: BELONGS TO THE HEDGEHOG FAMILI.
 CC
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 the European Bioinformatics Institute. There are no restrictions on its
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC
 CC
 DR EMBL; Y08426; CAA69702.1; -.
 DR HSSP; Q62226; 1VHH.
 DR MEROPS; C46_UPW; -.
 DR ZFIN; ZDB-GENE_980526-135; ehh.
 DR InterPro; IPR003320; HH_signal.
 DR InterPro; IPR01757; Hedgehog_hint.
 DR InterPro; IPR03586; Hedgehog_hintC.
 DR InterPro; IPR003587; Hedgehog_hintN.
 DR InterPro; IPR002203; Intein.
 DR InterPro; IPR001657; Sonichh.
 DR Pfam; PRO01079; Hint; 1.
 DR PRINTS; PR00632; SONICHHOG.
 DR SMART; SNN0305; HintC; 1.
 DR SMART; SNN0306; HintC; 1.
 DR PROSITE; PS00817; INTEIN_N_TER; 1.
 DR Developmental protein_Auto catalytic cleavage; Hydrolase; Protease;
 KW Signal; Lipoprotein; Palmitate.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 412 INDIAN HEDGEHOG PROTEIN.
 FT CHAIN 24 197 INDIAN HEDGEHOG PROTEIN N-PRODUCT.

FT CHAIN 198 412 INDIAN HEDGEHOG PROTEIN C-PRODUCT.
 FT SITE 197 198 CLEAVAGE (AUTO-) (BY SIMILARITY).
 FT SITE 246 246 INVOLVED IN CHOLESTEROL TRANSFER (BY
 FT SITE 269 269 INVOLVED IN AUTO-CLEAVAGE (BY
 FT SITE 269 269 INVOLVED IN AUTO-CLEAVAGE (BY
 FT ACT_SITE 272 272 ESSENTIAL FOR AUTO-CLEAVAGE (BY
 FT BINDING 197 197 SIMILARITY).
 FT LIPID 24 24 CHOLESTEROL (BY SIMILARITY).
 FT CONFLICT 121 121 PALMITATE (BY SIMILARITY).
 SQ 412 AA: 45746 MW: 21D43F052A278CA1 CRC64:
 Query Match 49.1%; Score 1213; DB 1; Length 412;
 Best Local Similarity 57.4%; Pred. No. 2.7e-82;
 Matches 251; Conservative 44; Mismatches 86; Idents 56; Gaps 7;
 Db 24 CGPGRGFGKRRHPPKKLTPLAYKQFIPNVAEKTGASGRVEKTTSRNSERFKELTTPNYPD 83
 QY 84 IIFDEEENGDADMATORCKDKUNALATSWMNQPGVHLRVTRGWDDEGHHSSESLAHEC 143
 Db 84 IIFDEEENGDADMATORCKDKUNALATSWMNQPGVHLRVTRGWDDEGHHSSESLAHEC 143
 QY 144 RAVITTSDRRSKGMLARRAVEGFDWWYYESKAHHCVKRAENSTAKSGCCFGPSA 203
 Db 144 RAVDITTSDRDRNRYMLRARLAVEGFDWWYYESKGHHCVSREHSAKTKGGCFGCR 203
 QY 204 TVHLEQQGTRKLVKDLSPGDRVLA---ADDQGRLLYSDFLTFDLDGAKKVFVIETREP 260
 Db 204 LVTMKGDSHQRQLQGLDVLIASEGSDGTGDLIYESEVLTFLDRRPQTQHFVTVRT-ED 262
 QY 261 RERLUTTAHLLFWAPHNDATRPEAASSGGSPGSGALFAFASVRPSORVYVAE 320
 Db 263 GASVSLTAHLLFWAVGNGNSNRGPKP-----GAV----RTFASDAAQVSQCLL--- 308
 QY 321 RDGDRLLPAAVHSVTLSEEAGAYVAPLTQGTLINRLASCVAVIEEHSHWAHRAFP 380
 Db 309 --GKLKRKFPSQITHVGVRD-QGLYPLPFLTAHGTVVNDVLTSCYAVNVRQRLAHWAFAPL 365
 QY 381 RLAAHLLAALAPARTDRGGDGGDRGGGGGRVLTARGAADPGAGATAGIHWYSQLY 440
 Db 366 RLLYVSW-----TGPDQVLEKNGLHWYSQVLI 390
 QY 441 QIGTWLLOSEAHPLGM 457
 Db 391 GLGKLLLDSELFHLAL 407

RESULT 14

ID	DHH_MOUSE	STANDARD;	PRT;	396 AA.
AC	061188;			
DT	15-JUL-1999	(Rel. 38, Created)		
DT	15-JUL-1999	(Rel. 38, Last sequence update)		
DT	16-OCT-2001	(Rel. 40, Last annotation update)		
DE		Dessert hedgehog protein precursor (DHH) (HHG-3).		
GN		DHH.		
OS		Mus musculus (Mouse).		
OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;		
OC		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
NCBL-TAXID		10090;		
RN		[1]		
		SEQUENCE FROM N.A.		
RC		STRAIN=129/Sv;		
RX		MEDLINE=94094334; PubMed=7916661;		
RA		Echelard Y., Epstein D.J., St Jacques B., Shen L., Mohler J.,		
RA		McMahon J.A., McMahon A.P.;		
RT		"Sonic hedgehog", a member of a family of putative signaling		
RT		molecules, is implicated in the regulation of CNS polarity.";		
RL		Cell 75:1417-1430(1993).		
RN		[2]		

search completed: February 20, 2003, 10:12:40
Job time : 15.5662 secs

Developmental protein; Autocatalytic cleavage; Hydrolase; Protease;
SIGNAL; Lipoprotein; Palmitate.
POTENTIAL.
CHAIN 23 395 DESERT HEDGEHOG PROTEIN.
CHAIN 23 198 DESERT HEDGEHOG PROTEIN N-PRODUCT.
CHAIN 199 396 DESERT HEDGEHOG PROTEIN C-PRODUCT.
SITE 198 199 CLEAVAGE (AUTO-) (BY SIMILARITY).
SITE 244 INVOLVED IN CHOLESTEROL TRANSFER (BY SIMILARITY).
SITE 268 268 INVOLVED IN AUTO-CLEAVAGE (BY SIMILARITY).
ACT_SITE 271 271 ESSENTIAL FOR AUTO-CLEAVAGE (BY SIMILARITY).
BINDING 198 198 CHOLESTEROL (BY SIMILARITY).
LIPID 23 23 PALMITATE (BY SIMILARITY).
CONFLICT 177 177 E -> G (IN REF. 2).
SEQUENCE 396 AA: 43577 MW: FCFEBB1972C3ADS CRC64:
Query Match 47-%; Score 1177; DB 1; Length 396;
Best Local Similarity 54.4%; Pred. No. 1. 2e-79; Mismatches 245; Conservative 54; Mismatches 93; Indels 58; Gap

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OM protein - protein search, using sw model
Run on: February 20, 2003, 10:06:28 ; Search time 30.5535 Seconds
(without alignments)
scoring table: BLOSUM62
GapOp 10.0 , Gapext 0.5

Title: US-09-827-110A-15
perfect score: 2469
Sequence: 1 MLLARCLLVLVSSLVCS..... GMAVKSSXSRGAGGAREGA 475
Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_21; *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_oranelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rabbit: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_virus: *
16: sp_bacteriaph: *
17: sp_archeap: *

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	1544.5	62.6	434 13	057404 Pleurodeles
2	1544.5	58.9	414 13	057404 Pleurodeles
3	1308.0	53.0	406 13	057567 paralichthys
4	1094.5	44.3	415 5	057567 notophthalmus
5	1084.5	43.9	415 5	057567 branchiosoma
6	1099.5	42.5	442 13	073803 fugu rubripinnis
7	1041.5	42.2	447 5	095288 gryllus bimaculatus
8	916.6	37.1	410 6	061676 lyttaeinus
9	850.0	34.4	161 11	091799 rattus norvegicus
10	733.7	29.7	159 13	091677 ambystoma maculatum
11	29.6	139 6	093166 bos taurinus	
12	70.9	28.7	138 13	098651 eleutherodactylus
13	28.4	177 11	098w29 rattus norvegicus	
14	61.9	25.1	185 5	096699 junonia coenia
15	53.1	21.5	99 13	089941 scylliorrhina
16	52.3	21.2	119 13	042128 oryzias latipes
17	51.1	20.7	129 11	09wup6 ratus norvegicus
18	476.5	19.3	137 13	042234 cornix cornix
19	392	15.9	80 13	042441 orophylax latipes
20	392	15.9	87 5	09tx30 anophelis gambiae
21	339	13.7	63 13	091814 rana catesbeiana
22	332	13.4	64 13	09prf5 oryzias latipes
23	298	12.1	60 5	095zdb hydra attenuata
24	289	11.7	56 13	0902r0 oryzias latipes
25	237	9.6	49 5	097x33 hirundo mediterranea
26	229	9.3	49 5	09px31 tribolium castaneum
27	188	7.6	54 13	042233 cornix cornix
28	187.5	7.6	125 11	09esh3 rattus norvegicus
29	175.5	7.1	48 5	09px32 strongylocephalus
30	163.5	6.6	557 5	094110 caenorhabditis elegans
31	163.5	6.6	557 5	094129 caenorhabditis briggsae
32	159.5	6.5	615 5	091573 caenorhabditis
33	149	6.0	1207 5	021535 caenorhabditis
34	138.5	5.6	790 5	022872 caenorhabditis
35	138.5	5.6	1203 5	021835 caenorhabditis
36	135.5	5.5	485 5	094128 caenorhabditis
37	134.5	5.4	481 5	045992 caenorhabditis
38	128	5.2	550 5	045273 caenorhabditis
39	125.5	5.1	1029 5	09xuv2 caenorhabditis
40	125	5.1	550 5	094130 caenorhabditis
41	123.5	5.0	2639 5	076786 antitheraea pectinifera
42	121	4.9	868 5	09xvi4 caenorhabditis
43	119	4.8	318 16	086703 streptomyces
44	119	4.8	2655 5	0964f4 antitheraea
45	118	4.8	1832 3	08tgh8 podospora

ALIGNMENTS

RESULT 1
ID 057404 PRELIMINARY PRT: 434 AA.
AC 057404;
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Sonic hedgehog-related protein.
GN TW-SHH.
TPW-SHH.
OS Pleurodeles waltlili (Iberian ribbed newt).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
OC Pleurodeles.
OX NCBI_TAXID=8319;
[1]
RP SEQUENCE FROM N.A.
RA Caubit X., Nicolas S., Le Parco Y.;
RT "Pleurodeles sonic hedgehog";
RL Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF003532; RAB94412.1; -.
DR HSSP; 062226; IVHH.
DR MEROPS; C46_002; -.
DR InterPro; IPR00167; Hedgehog_hintC.
DR InterPro; IPR003586; Hedgehog_hintC.
DR InterPro; IPR00587; Hedgehog_hintN.
DR InterPro; IPR000320; HH_signal.
DR InterPro; IPR002203; Intein.
DR InterPro; IPR001657; SonichH.
PFAM; PF0105; HH_signal; 1.
PRIM; PR01079; Hint; 1.
DR PRO0632; SONICHHOG.
DR PRODom; PD00342; HH_signal; 1.
DR SMART; SM00305; HintC; 1.
DR SMART; SM00306; HintN; 1.
SQ SEQUENCE 434 AA: 48421 MW: A9495B367151AE74 CRC64:
Query Match Score 1544.5; DB 13; Length 434;
Best Local Similarity 67.7%; Pred. No. 8.1e-108;
Matches 313; Conservative 41; Mismatches 77; Indels 31; Gaps 6;

Qy 1 MLLARCLLIVLVLSSLLVCGSLAGCPGPGFKRRHKKLPTPLAYKOFIPNVAEKTGLASG 60
 ||| | :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| |||
 4 MILLRDLGGFSTTLLVPLGLGCGPGKGIGQRQRPKLTPLAKOFTPNVBERTLGASG 63

Qy 61 RYEKISRNSEREFELTPWNPDTIKDENTGADRMLTORKDKLNALAISTMNQWGV 120
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 64 RYEKISRNSEREFELTPWNPDTIKDENTGADRMLTORKDKLNALAISTMNQWGV 123

Qy 121 KLRYTEGMDGDGHSEESLHYEGRAVDTTSDRRSKGMLARAVEAGFDWYYESKAH 180
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 124 KLRYTEGMDGDGHSEESLHYEGRAVDTTSDRRSKGMLARAVEAGFDWYYESKAH 183

Qy 181 IHCSYKAENSAVAKSGGCCEPGSATVHLEOGGTKLPGNRVLAVIDVEGRILYSDFL 240
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 184 IHCSYKAENSAVAKSGGCCEPGSATVHLEOGGTKLPGNRVLAVIDVEGRILYSDFL 243

Qy 241 FLDRGDAKKVYIETPRERILLTAHLLFVAPHNDSATGEPEASGGSPSGGAIG 300
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 244 FLDRGDAKKVYIETPRERILLTAHLLFVAPHNDSATGEPEASGGSPSGGAIG 300

Qy 301 PRALEASRVPGQVWVAAERDGDRRLPAAVHSVTLSSEAAAGYAPLTAQGTLINRVL 360
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 299 PRSFASFASSVRPGHV-LIEDREG-RGLREATVDVRL-EATGAYAPTAHGTVIDRL 355

Qy 361 ASCYAVIEEHSAWAFAPLRVGFGILSFFSP--QDYSSH----- 394

Db 421 ADPAGAGATAGIHWSQLXQIGTWWLDSSEALHPLGMAKSS 462
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 395 --PPAPSOAEGVHMYSELVYRIGHTWWLQADTIHLPLGMAKSS 434

RESULT 2

Q9W7Q9 PRELIMINARY; PRT; 414 AA.

ID Q9W7Q9; PRELIMINARY; PRT; 414 AA.

AC DT 01-NOV-1999 (TREMBUREL, 12, Created)
 DT 01-NOV-1999 (TREMBUREL, 12, Last sequence update)

DE Sonic hedgehog.

GN SHH.

OS Paralichthys olivaceus (Flounder).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorphi; Pleuronectiformes; Pleuronectoidea; Paralichthyidae; Paralichthys.

OC NCBI_TAXID=8255;

OX RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE:99230226; PubMed=10223710;

RA Suzuki T., Ichiro O., Kurokawa T.;

RT "Retinoic acid given at late embryonic stage depresses sonic hedgehog and Hoxd-4 expression in the pharyngeal area and induces skeletal malformation in flounder (Paralichthys olivaceus) embryos.";

RL Dev Growth Differ. 41:143-152(1999).

DR EMBP: Q62917; BAA82360.1; -.

DR MEROPS: C46.001; -.

DR InterPro: IPR001767; Hedgehog_hint.

DR InterPro: IPR003586; Hedgehog_hintC.

DR InterPro: IPR003587; Hedgehog_hintN.

DR InterPro: IPR000320; HH_signal.

DR InterPro: IPR002203; Intein.

DR InterPro: IPR001657; SonichH.

DR Pfam: PF01085; HH_signal; 1.

DR Pfam: PF01079; Hint; 1.

DR PRINTS; PRO0532; SONICHHOG.

DR PRODOM; PD003042; HH_signal; 1.

DR SMART; SM00305; HintC; 1.

DR SMART; SM00306; HintN; 1.

SEQUENCE 414 AA; 45945 MN; 50607BR3DB/CODA3 CRC64;

Query Match 58.9%; Score 1454; DB 13; Length 414;
 Best Local Similarity 62.4%; pred. No. 4.7e-101; Matches 289; Conservative 55; Mismatches 69; Indels 50; Gaps 7;

Qy 1 MLLARCLLIVLVLSSLLVCGSLAGCPGPGFKRRHKKLPTPLAYKOFIPNVAEKTGLASG 60
 ||| | :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| |||
 Db 61 RYEKISRNSEREFELTPWNPDTIKDENTGADRMLTORKDKLNALAISTMNQWGV 120
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 64 RYEKISRNSEREFELTPWNPDTIKDENTGADRMLTORKDKLNALAISTMNQWGV 123

Qy 121 KLRYTEGMDGDGHSEESLHYEGRAVDTTSDRRSKGMLARAVEAGFDWYYESKAH 180
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 124 KLRYTEGMDGDGHSEESLHYEGRAVDTTSDRRSKGMLARAVEAGFDWYYESKAH 183

Qy 181 IHCSYKAENSAVAKSGGCCEPGSATVHLEOGGTKLPGNRVLAVIDVEGRILYSDFL 240
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 184 IHCSYKAENSAVAKSGGCCEPGSATVHLEOGGTKLPGNRVLAVIDVEGRILYSDFL 243

Qy 241 FLDRGDAKKVYIETPRERILLTAHLLFVAPHNDSATGEPEASGGSPSGGAIG 300
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 244 FLDRGDAKKVYIETPRERILLTAHLLFVAPHNDSATGEPEASGGSPSGGAIG 300

Qy 301 PRALEASRVPGQVWVAAERDGDRRLPAAVHSVTLSSEAAAGYAPLTAQGTLINRVL 360
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 356 ASCYAVIEEHSAWAFAPLRVGFGILSFFSP--QDYSSH----- 394

Db 421 ADPAGAGATAGIHWSQLXQIGTWWLDSSEALHPLGMAKSS 462
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 395 --PPAPSOAEGVHMYSELVYRIGHTWWLQADTIHLPLGMAKSS 434

RESULT 3

Q9W7Q9 PRELIMINARY; PRT; 406 AA.

ID Q9W7Q9; PRELIMINARY; PRT; 406 AA.

AC DT 057567; PRELIMINARY; PRT; 406 AA.

DE 057567; PRELIMINARY; PRT; 406 AA.

DT 057567; PRELIMINARY; PRT; 406 AA.

DT 01-JUN-1998 (TREMBUREL, 06, Last sequence update)

DT 01-JUN-2002 (TREMBUREL, 21, Last annotation update)

DE Hedgehog segment polarity homolog.

OS Notophthalmus viridescens (Eastern newt) (*triturus viridescens*); Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Caudata; Salamandroidea; Salamandriidae; Notophthalmus.

OC NCBI_TAXID=8316;

OX RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE:99230226; PubMed=10223710;

RA Stack D.R., Gates P.B., Broches J.P., Ferretti P.; "Hedgehog homologue from *Notophthalmus viridescens*."; Dev Dyn. 0:0-0(1998).

CC -1- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE PHOSPHORIBOSYLTRANSFERASE FAMILY.

EMBL: AF047466; AAC03108.1; -.

DR HSSP; Q62226; 1VHH.

DR InterPro; IPR001767; Hedgehog_hint.

DR InterPro; IPR003586; Hedgehog_hintC.

DR InterPro; IPR003587; Hedgehog_hintN.

DR InterPro; IPR000320; HH_signal.

DR InterPro; IPR002375; PR_Py_RP_transf.

DR InterPro; IPR001657; SonichH.

DR Pfam: PF01085; HH_signal; 1.

DR Pfam: PF01079; Hint; 1.

DR PRINTS; PRO0532; SONICHHOG.

DR PRODOM; PD003042; HH_signal; 1.

DR SMART; SM00305; HintC; 1.

DR SMART; SM00306; HintN; 1.

PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.

KW	GLYCOSYLTRANSFERASE; transferase.
SQ	SEQUENCE 406 AA; 45072 MW; 584CCAD514D4D0 CRC64;
Query Match	53.0%; Score 1308; DB 13; Length 406;
Best Local Similarity	59.2%; Pred. No. 4.2e-90;
Matches	274; Conservative 41; Mismatches 111; Indels 61; Gaps 9;
QY	1 MLLARCLLVLVSSLLVCSG-LACGPGRGFGKRRPKKLTPLAYKOFIPNVAEKTIGAS 59
Db	1 MLLAALPLAVACALLGGPAGALCPGRVTRPRPLPSVQFLPVKEPLGAS 60
QY	60 GRYEGKTSRNSRERFKELTPTNNPDITFKDEENTGADRMLTORCKDKLNALAI SVMNQPG 119
Db	61 GRYEGKTSRNSRERFKELTPTNNPDITFKDEENTGADRMLTORCKDKLNALAI SVMNQPG 119
QY	120 VKLRTVEGWDGEGHSESLEAVGRADITTSDRDSKGMLARLAVEAGDWVYYESKA 179
Db	121 VKLRTVEGWDGEHGHSDESLEYEGRADITTSDRDKLNALAI SVMNQPG 180
QY	180 HIHCSVKAENSAKSGCFPOSATVHLEOGCTKLVKDLSPGDRLYSDFL 239
Db	181 HIHCSVKSEHSAKAKTGCFPARALATLESGEKIPADLPGHRCMDEGGRTVSDFL 240
QY	240 TFLDRDGAKKVYVITREPRERLITAHLFVA---PHNDSATGEPEASSSGPP 294
Db	241 TFLDRDGSTAVKEVYVETRDPPRLTAHLFVADNFVPLTDST----- 288
QY	295 SGAGLSPRALFRSFRVPGQRVYVVAERDGRDLPLPAVHSVTLSEERAAGAYAPLTAQTI 354
Db	289 -----VRAHSVQO-YILTE-GVIGLQPARKVST-TQFDGAVAPLTHGTL 334
Qy	355 LINRVLASCYAVIEEWSWAHRAFPFLAHALLAALAPARTDGGDSGGDRGGGRVA 414
Db	335 LVDVVWVSCFAVVKOHLAQAFWPLRLYHSV-----GRPE 370
Qy	415 LTPGAADAPGAGATAGIHWSQLLIQIGTWWILDSEALHPGM 457
Db	371 -TQP-----EGMHVSLLLYRLGKVUMLKEOFHPPGM 401
RESULT 4	
O9U5Z6	PRELIMINARY; PRT; 415 AA.
ID	09U5Z6
AC	09U5Z6;
DT	01-MAY-2000 (TREMBREL. 13, Created)
DT	01-DEC-2001 (TREMBREL. 19, Last sequence update)
DT	01-JUN-2002 (TREMBREL. 21, Last annotation update)
DE	hedgehog protein.
GN	HEDGEHOC.
OS	Branchiostoma belcheri (Amphioxus).
OC	Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OX	NCBI_TAXID=7741;
[1]	SEQUENCE FROM N. A.
RP	
RA	
RA	Mac B., Zhang Y., Zhang H.; "A preliminary study on Qingdao amphioxus hedgehog gene."; Submitted (SBB-2001) to the EMBL/GenBank/DDBJ databases.
RT	
RL	
EMBL	Alt245882; CAB5831.2; .
DR	HSSP; 062256, 1VHH.
DR	InterPro; IPR001767; Hedgehog_hint.
DR	InterPro; IPR003586; Hedgehog_hintC.
DR	InterPro; IPR003587; Hedgehog_hintN.
DR	InterPro; IPR000320; HH_signal.
DR	InterPro; IPR02203; Intein.
DR	InterPro; IPR001657; SonichH.
DR	InterPro; IPR001657; SonichH.
DR	Pfam; PF01059; HH_Signal; 2.
DR	PRINTS; PR00632; SONICHHOG.
DR	PRODOM; PDO03042; HH_Signal; 1.
DR	SMART; SM00305; HintC; 2.
DR	SMART; SM00306; HintN; 2.
SQ	SEQUENCE 415 AA; 46912 MW; BR864704752BD6A8 CRC64;
Query Match	43.9%; Score 1084.5; DB 5; Length 415;

RESULT 6		RESULT 7	
ID 073803	PRELIMINARY; PRT: 442 AA.	ID 09GRAB	PRELIMINARY; PRT: 447 AA.
AC 078803;		AC 09GRAB;	
DT 01-AUG-1998 (Tremblrel. 07, Created)		DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)	
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)		DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)	
DE Fugu hedgehog.		DE Hedgehog protein (Fragment).	
GN Fugu rubripes (Japanese pufferfish) (<i>Takifugu rubripes</i>).		OS <i>Gryllus bimaculatus</i> (Two-spotted cricket).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; tetraodontiformes; OC OX NCBI_TAXID=3103;		OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; OC OX NCBI_TAXID=6999;	
RN [1]		RN [1]	
SEQUENCE FROM N.A.		SEQUENCE FROM N.A.	
RP MEDLINE-99177347; PubMed=10077531;		RP MEDLINE-20461145; PubMed=11003837;	
RX		RX	
RA Geilner K., Brenner S.;		RA Niwa N., Inoue Y., Nozawa A., Saito M., Misumi Y., Ohuchi H., Yoshioka H., Nojji S.;	
RT "Analysis of 148 bp of genomic DNA around the wnt1 locus of Fugu rubripes". Genome Res. 9: 251-258(1999). -.		RT "Correlation of diversity of leg morphology in <i>Gryllus bimaculatus</i> (cricket) with divergence in dpp expression pattern during leg development." Development 127: 4373-4381(2000).	
RL EMBL: AF056116; AAC34384.1; -.		RL EMBL: AB044709; BAB19658.1; -.	
DR HSSP; Q62226; 1VHH		DR HSSP; Q62226; 1VHH	
DR InterPro: IPR01767; Hedgehog_hint.		DR InterPro: IPR01767; Hedgehog_hint.	
DR InterPro: IPR03580; Hedgehog_hintC.		DR InterPro: IPR03586; Hedgehog_hintC.	
DR InterPro: IPR03587; Hedgehog_hintN.		DR InterPro: IPR03587; Hedgehog_hintN.	
DR InterPro: IPR002203; Intein.		DR InterPro: IPR00320; HH_signal.	
DR Pfam: PF0105; HH_signal; 1.		DR Pfam: PF01085; HH_signal; 1.	
DR Pfam; PF01079; Hint; 1.		DR Pfam; PF01079; Hint; 1.	
DR ProDom; PD000342; HH_signal; 1.		DR ProDom; PD003042; SONICHHOG.	
DR SMART; SM00305; HintC; 1.		DR SMART; SM00305; HintC; 1.	
DR SMART; SM00306; HintN; 1.		DR SMART; SM00306; HintN; 1.	
SQ SEQUENCE 442 AA; 49286 MW; 1 ICB2B423B4B748E8 CRC64;		SQ SEQUENCE 447 AA; 48008 MW; 29AEFB061C3EE6F0 CRC64;	
Query Match. 42.5%; Score 1049.5; DB 13; Length 442;		Query Match. 42.5%; Score 1049.5; DB 13; Length 442;	

Best Local Similarity 50.0%; Pred. No. 2.7e-73;
Matches 229; Conservative 53; Mismatches 119; Indels 57; Gaps 8;

Best Local Similarity 48.5%; Pred. No. 1.2e-70;
Matches 224; Conservative 67; Mismatches 132; Indels 39; Gaps 9;

QY 3 LLRCLL-LVLSLLVGSG--LACGPGRGFGRRPKKLTPLAKYQIPNVAEKTIGAS 59
Db 4 VLAKWMMVLAVALAISALAGTHGPGSCACPGQRGRRRPKLTPVYQOOPAYNTREAS 63

QY 60 GRFEKGKISRNEERKEELTPNPYNDIIFKDEENGADRMLTORCKDKUNALATSMNMQPG 119
Db 64 GLEFRGTRDSEERHTLKFNFNDIIFDEEKYGADRENTQRCKDKUNALATSMNMQPG 123

QY 120 VKLIVTEGKEDDGHSEHSESLHYCRAVDITTSDDRSKYGMALARLAVEAGFDWVYYESKA 179
Db 124 VKLRVTEGKEDDGHTEESLHYCRAVDITTSDDRSKYGMALARLAVEAGFDWVYYESKA 183

QY 180 HIRSVKVAESEDTTATQGGCFSAESWTRDGNRTRMRDVRPGKVLMSMSGHHRVFSLEV 239
Db 184 HIRSVKVAESEDTTATQGGCFSAESWTRDGNRTRMRDVRPGKVLMSMSGHHRVFSLEV 243

QY 240 TFLRDGDGAKKVVFVETREPREPLLTAHLFVAPHNDSATGEGPEASSGCPGSGAL 299
Db 244 TEMDRESRGPWVYVTTIHDDRNTTATPSHLVFTVTESRDLSS----- 286

QY 300 GPR-ALFAASRVPRQGQRYVVAERGDRRLPAAVHSVTLSEEAGAYAPLTAQGTILNR 358
Db 287 -PRAKFMSDARCPGEFLTPDSGCGFR--KVVKVSVTMRREE-KGAYAPLTVGTVVVDN 342

QY 359 VLASCYAVTEEHSHWAHRAFAPRFLAHALLAALAPARTDRGGSDGGDRGGGGGRVALTAP 418
Db 343 VAMSCYALIESQAAHAWHFAPPRKLYQISSL----- 374

QY 419 GAADAPGAGAT- -AGIHWSQLYQITWLDSBALHP 454
Db 375 --WDGSPHDOTLQGQHVWYPSFFRYGQISLVEPTLHP 410

QY 64 GKSRSNRSEERKEELTPNPYNDIIFKDEENGADRMLTORCKDKUNALATSMNMQPGKL 123
Db 67 GKTRNSRSEERELVCVNYPDIFVDEENWNADEFTRKCKDCINRLAVMMQPGHL 126

QY 124 VTEDWDEDCHHSESESLHYCRAVDITTSDDRSKYGMALARLAVEAGFDWVYYESKA 183
Db 127 VTEWDEDGHHPGSLHYCRAVDITTDRETEKYGLAQALAVEAGFDWVYYESKAHIC 186

QY 184 SVKENSVAKSAGCFCPSATVILEOGGPKLVIDSPDRVLAADDGGRLLSDFLTLD 243
Db 187 SVKADSVAEKGCPGWSRVTAGGFIQKSLSLPDTGDRVMALSETCQVVISPVPLFLH 246

QY 244 RDGAKKVVFVETREPREPLLTAHLFVAPHNDSATGEGPEASSGCPGSGALPRA 303
Db 247 RDPSRWRFITSQDTEGR-RLATVPHHLVFSDAH-----CGPDSSQY--OA 289

QY 304 LFASVRVPQGQRYVVAERGDRRLPAAVHSVTLSEEAGAYAPLTAQGTILNRVASC 363
Db 290 QFASRAQICQTCVLY--HTAGGEWHPRSVIS-EESVGAAPLATEAGSVFVDGVLOSS 345

QY 364 YAVTEEHSHWAHRAFAPRFLAHALLAALAPARTDRGGSDG-----GGDRGGGGGRVA 414
Db 346 YALVBDHQIAHWAEGPVRLISSSQLWAEPEERSDGSKTPQPHALVRGDR----RVC 400

QY 415 L--TAPGAADAPGAGATAGIHWSQLYQITWLDSALHP 454
Db 401 ARNSTSVRSEAGPRGRTSEHWYQQLHLRGWIVLNPDLFHP 442

Query Match	Score	Length	Best Local Similarity	Pred.	No.	1e-50;	Matches	206;	Conservative	65;	Mismatches	128;	Indels	54;	Gaps	11;
Best Local Similarity	51.4%	Pred. No.	5e-70;	Matches	228;	Conservative	47;	Mismatches	118;	Indels	51;	Gaps	10;			
Qy	1	MILLARCLLVLVSSLLVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	60	Db	6	NYKWLWVQITPACLTQCHPGIS-KUTSHRPNRPIQYOKVNPNTSEDTGAGS	64									
Qy	15	MPLLRLWLLL--LMGAARRACGPGAGRGRKRRHKLTPLAYKOPINVAEKTIGASG	71	Db	6	YEGKISRNSERKELETPNYNPDLIFKDEENTGADRMTQROCKDKLNALASVMNQPGVK	121									
Qy	61	RVEGKISRNSERFELTPNYNPDLIFKDEENTGADRMTQROCKDKLNALATSMNQPGV	120	Db	65	PEGRIDDRERSKLSNNNDIVFDEEGADRMTQROCKDKLNALASVMNQPGV	124									
Qy	72	PAERRVARDPDPERDLPVNPNAIDIVFDEEGADRMTQROCKDKLNALASVMNQPGV	131	Db	6	LRVTEGMDDEGHSEESLHYEGRADITTSQRDSKGMLARLAVAEAGFDWVYYESKAH	181									
Qy	121	KLRTGEWDEGHSEESLHYEGRADITTSQRDSKGMLARLAVAEAGFDWVYYESKAH	180	Db	6	LRVTEGMDDEGHSEESLHYEGRADITTSQRDSKGMLARLAVAEAGFDWVYYESKAH	180									
Qy	132	RLRVIEGWDEGGHAADSLHYEGRADITTSQRDRSKYGMALARLAVAEGDWVYYESKAH	191	Db	6	LRVTEGMDDEGHSEESLHYEGRADITTSQRDSKGMLARLAVAEAGFDWVYYESKAH	181									
Qy	181	IHCVKSAENSAKSGCCFPGSATVHIEQGGTQLKLVDLSPGDR-VLAADDQGRLLSDFL	239	Db	6	LRVTEGMDDEGHSEESLHYEGRADITTSQRDSKGMLARLAVAEAGFDWVYYESKAH	181									
Qy	192	IHCVKSAENSAKSGCCFPGSATVHIEQGGTQLKLVDLSPGDR-VLAADDQGRLLSDFL	239	Db	6	LRVTEGMDDEGHSEESLHYEGRADITTSQRDSKGMLARLAVAEAGFDWVYYESKAH	181									
Qy	240	TFLDRDGAKKYFYVISTREPRERLITAHLLEVPHNDSATGEPEASSSGPPSGGAL	299	Db	6	LRVTEGMDDEGHSEESLHYEGRADITTSQRDSKGMLARLAVAEAGFDWVYYESKAH	181									
Qy	251	LFLDRDP-APRFLVRVTAASGR-TLAIPSHII-----PVAGCGE-----290	300	Db	6	LRVTEGMDDEGHSEESLHYEGRADITTSQRDSKGMLARLAVAEAGFDWVYYESKAH	181									
Qy	300	GPRALFASRVRPGQRYVVAERGDRRLPAAWHSTLSEEAGAYAPLTAQTLINRV	359	Db	6	LRVTEGMDDEGHSEESLHYEGRADITTSQRDSKGMLARLAVAEAGFDWVYYESKAH	181									
Qy	291	-PEARFADAVRPDGALLVAADAGAVR-PDVLHVDAEATRGVWVPLTAQTVVVDGV	347	Db	6	LRVTEGMDDEGHSEESLHYEGRADITTSQRDSKGMLARLAVAEAGFDWVYYESKAH	181									
Qy	360	LASCYAVIEEHWSWAHRAFAPFRALAHALLAALAPARTDRGGDSGGDRGGGGVALTAPG	419	Db	6	LRVTEGMDDEGHSEESLHYEGRADITTSQRDSKGMLARLAVAEAGFDWVYYESKAH	181									
Db	348	LASCYAVGHSLSLAHWSFAPVRAWH-WLTANGHAAPDY-----384	420	Db	6	LRVTEGMDDEGHSEESLHYEGRADITTSQRDSKGMLARLAVAEAGFDWVYYESKAH	181									
Qy	420	AAADAGAGATACTIHWYOLLYQG 443	385	Db	6	LRVTEGMDDEGHSEESLHYEGRADITTSQRDSKGMLARLAVAEAGFDWVYYESKAH	181									
RESULT 8																
OI676																
ID	011676	PRELIMINARY;	PRT;	410 AA.	Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
AC	011676;				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
DT	01-AUG-1998 (TREMBREL. 07, Created)				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
DT	01-JUN-2002 (TREMBREL. 21, Last annotation update)				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
DE	Hedgehog.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
OS	Lytechinus variegatus (Sea urchin).				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
OC	Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa; Echinoidea; Euechinoidea; Echinacea; Temnopleuroidea; Toxopneustidae; OX				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
NCBI_TaxID=7654;					Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
[1]	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RA	Hertzler P.L., McCay D.R.; RT				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RP	"A sea urchin hedgehog homolog."; RL Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RA	Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RP	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RA	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RP	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RA	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RP	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RA	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RP	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RA	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RP	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RA	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RP	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RA	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RP	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RA	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RP	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RA	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RP	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RA	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RP	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RA	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RP	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RA	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RP	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RA	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RP	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RA	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RP	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RA	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RP	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RA	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RP	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RA	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RP	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RA	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RP	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RA	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RP	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RA	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RP	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RA	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RP	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RA	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RP	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RA	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RP	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RA	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RP	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RA	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RP	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RA	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RP	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RA	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RP	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RA	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIGASG	61								
RP	SEQUENCE FROM N.A.				Qy	4	LARCLLVLVSSL-LVCSGLACGPGRGFGKRRH-RPKLTPLAYKOPINVAEKTIG									

Db	1	IFKDEENGADRLLTORCKDKNIALISMMQNPGLKLVTEGWDDEGHSEESLH EG	RP
Qy	144	RAVDITSDRSKYGMLARLAVEAGEDWWYVESKAHICSTKAENSAKSGCFGSA	RC
Db	61	RAVDITSDRSKYGMLARLAVEAGEDWWYVESKAHICSTKAENSAKSGCFGSA	RA
Qy	204	TVHLEQGTTKLUKDLSDGDRVLADDQGRLLSDFLTFLDR	RA
Db	121	TVHLEQGTTKLUKDLSDGDRVLADDQGRLLSDFLTFLDR	RA
RESULT 10			
Q9YGV7		PRELIMINARY;	PRT;
ID	Q9YGV7		150 AA.
AC	Q9YGV7;		
DT	01-MAY-1999 (TREMBLEL. 10, Created)		
DT	01-JUN-2002 (TREMBLEL. 21, Last annotation update)		
DE	Sonic hedgehog (Fragment).		
OS	Ambystoma mexicanum (Axolotl).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;		
OX	NCBIL-TAXID=8296;		
RN	SEQUENCE FROM N.A.		
RA	Torok M.A., Izquierdo-Belmonte J.C., Gardiner D.M., Bryant S.V.;		
RL	Submitted (Oct-1997) to the EMBL/GenBank/DDBJ databases.		
DR	EMBL: AF031480; AAD18128.1; -.		
DR	HSSP: 062226; IVHH.		
DR	InterPro: IPR001657; Hedgehog_hint.		
DR	InterPro: IPR000220; HH_signal.		
DR	InterPro: IPR0105; HH_signal; 1.		
DR	PRINTS: PRO00532; SONICHHOG.		
DR	PRODOM: PDD003042; HH_Signal; 1.		
FT	NON_TER 150 AA; 16599 MW; 986F65037A69ABAC CRC64;		
FT	NON_TER 150 AA; 16599 MW; 986F65037A69ABAC CRC64;		
SQ	SEQUENCE 150 AA:		
Query Match	Best Local Similarity 29.7%; Score 733; DB 13; Length 150; Matches 140; Conservative 2; Mismatches 8; Indels 0; Gaps 0;		
Qy	83 DIFKDSENTGADRLLTQRCKDKNIALISMMQNPGLKLVTEGWDDEGHSEESLH E 142		
Db	1 DIFKDSENTGADRLLTQRCKDKNIALISMMQNPGLKLVTEGWDDEGHSEESLH E 60		
RESULT 11			
Q9XSI6		PRELIMINARY;	PRT;
ID	Q9XSI6		139 AA.
AC	Q9XSI6;		
DT	01-NOV-1999 (TREMBLEL. 12, Created)		
DT	01-NOV-1999 (TREMBLEL. 12, Last sequence update)		
DT	01-JUN-2001 (TREMBLEL. 17, Last annotation update)		
DE	Sonic hedgehog (Fragment).		
OS	Bos taurus (Bovine).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Gekkota; Carnivora; Artiodactyla; Ruminantia; Pecora; Bovoidea;		
OC	Bovidae; Bovinae; Bos.		
NCBI_TAXID=9913;	[1]		
RESULT 11			
Q9XSI6		PRELIMINARY;	PRT;
ID	Q9XSI6		139 AA.
AC	Q9XSI6;		
DT	01-NOV-1999 (TREMBLEL. 12, Created)		
DT	01-NOV-1999 (TREMBLEL. 12, Last sequence update)		
DT	01-JUN-2001 (TREMBLEL. 17, Last annotation update)		
DE	Sonic hedgehog (Fragment).		
OS	Bos taurus (Bovine).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Gekkota; Carnivora; Artiodactyla; Ruminantia; Pecora; Bovoidea;		
OC	Bovidae; Bovinae; Bos.		
NCBI_TAXID=9913;	[1]		
RESULT 12			
Q9WC1		PRELIMINARY;	PRT;
ID	Q9WC1		138 AA.
AC	Q9WC1;		
DT	01-NOV-1999 (TREMBLEL. 12, Created)		
DT	01-NOV-1999 (TREMBLEL. 12, Last sequence update)		
DT	01-JUN-2001 (TREMBLEL. 17, Last annotation update)		
DE	Sonic hedgehog protein (Fragment).		
OS	SHH.		
OC	Eleutherodactylus coqui (Puerto Rican coqui).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Leptodactylidae;		
OX	NCBI_TAXID=57060;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Carl T.P., Richardson M.K., Olsson L., Schlosser G., Klymkowsky M.W., Hanken J.;		
RA	Submitted (Dec-1998) to the EMBL/GenBank/DDBJ databases.		
DR	EMBL: AF113403; AAD23436.1; -.		
DR	HSSP: Q6226; IVHH.		
DR	InterPro: IPR000320; HH_Signal.		
DR	InterPro: IPR001657; SonicHH.		
DR	PRINTS: PRO00532; SONICHHOG.		
DR	PRODOM: PDD003042; HH_Signal; 1.		
FT	NON_TER 138 AA; 15751 MW; FP4156A17F4681FO CRC64;		
FT	NON_TER 138 AA; 15751 MW; FP4156A17F4681FO CRC64;		
SQ	SEQUENCE 138 AA:		
Query Match	Best Local Similarity 28.7%; Score 709; DB 13; Length 138; Matches 133; Conservative 2; Mismatches 3; Indels 0; Gaps 0;		
Qy	48 IPNAWEAKTIGASGRYEGKTSRNSERRFKEITPNYNPDITFKDEENTGADRLLTQRCKDKLN 107		

Thu Feb 20 10:43:54 2003

us-09-827-110a-15.rspt

Page 8

||||||||||||||||||||||||||||||||||||
Db 61 SLHNEGRADITSDRDRKYGMLARLAVEAGEFDWVYE 99

Search completed: February 20, 2003, 10:11:53
Job time : 32.5535 secs

Gencore version 5.1.3
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OM protein - protein search, using sw model.

Run on: February 20, 2003, 10:10:28 ; Search time 8.52655 Seconds

(without alignments)
 1423.285 Million cell updates/sec

Title: US-09-827-110a-15
 Perfect score: 2469
 Sequence: 1 MLLARCLLVLVSSLVCS..... GMAVKSSXSRGAGGAREGA 475

Scoring table: BLOSUM2
 Gapop 10.0 , Gapext 0.5

Searched: 140259 seqs, 25548876 residues

Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Listing first 45 summaries

Database : Published_Applications_AAI *

- 1: /cgn2_6/ptodata/1/pubpaa/us08_NEWPUB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCN_NEWPUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEWPUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEWPUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/PC08_PUBCOMB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEWPUB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US10_NEWPUB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEWPUB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	2467	99.9	475	8	US-09-900-220C-15	Sequence 15, Appl
2	2457	99.9	475	9	US-09-883-848A-15	Sequence 15, Appl
3	2457	99.9	475	10	US-09-021-660A-39	Sequence 39, Appl
4	2457	99.9	475	10	US-09-151-999-15	Sequence 15, Appl
5	2407	97.5	462	9	US-09-733-634-14	Sequence 14, Appl
6	2058	83.8	437	9	US-09-969-520A-1	Sequence 1, Appl
7	2058	83.8	437	9	US-10-015-310-1	Sequence 1, Appl
8	2058	83.8	437	9	US-09-733-634-16	Sequence 16, Appl
9	2058	83.8	437	10	US-09-921-660A-37	Sequence 37, Appl
10	2055	83.6	437	8	US-09-900-220C-13	Sequence 13, Appl
11	2055	83.6	437	9	US-09-883-848A-13	Sequence 13, Appl
12	2055	83.6	437	10	US-09-151-999-13	Sequence 14, Appl
13	2052	83.5	437	9	US-09-969-046-14	Sequence 3, Appl
14	2052	83.5	437	9	US-09-969-520A-3	Sequence 10, Appl
15	2059	83.4	437	9	US-09-969-520A-10	Sequence 11, Appl
16	2059	83.4	437	9	US-09-969-520A-11	Sequence 2, Appl
17	2058	83.4	437	9	US-09-969-520A-2	Sequence 9, Appl
18	2054	83.2	437	9	US-09-969-520A-9	Sequence 4, Appl
19	63.1					

ALIGNMENTS

RESULT 1

US-08-900-220C-15

; sequence 15, Application US/08900220C

; Patent No. US20020045206A1

GENERAL INFORMATION:

APPLICANT: Miao, Ningning

Wang, Monica

Mananthappa, Nagesh K.

Pang, Kevin

Jin, Ping

TITLE OF INVENTION: Method of Treating Dopaminergic and

GABA-nergic Disorders

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY, HOAG & ELIOT LLP

STREET: ONE POST OFFICE SQUARE

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII (text)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/900,220C

FILING DATE: 24-Jul-1997

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Vincent, Matthew P.

REGISTRATION NUMBER: 36,709

REFERENCE/DOCKET NUMBER: ONY-044.01

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 832-1000

TELEFAX: (617) 832-7000

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 475 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 15:
us-08-900-220c-15

Query Match 99.9%; Score 2467; DB 8; length 475;
Best Local Similarity 100.0%; Pred. No. 1.4e-192; ;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLARCLLVLYVSSLLVCSGLACGPGRGFGKRRHKPKLTPLAYQFIPVAEKTIGASG 60
Db 1 MLLARCLLVLYVSSLLVCSGLACGPGRGFGKRRHKPKLTPLAYQFIPVAEKTIGASG 60
Qy 61 RYEGKISRNSRERKELTPTNPNPDIFKDEENTGADRMLTORCKDKLNALISMNQWPGV 120
Db 61 RYEGKISRNSRERKELTPTNPNPDIFKDEENTGADRMLTORCKDKLNALISMNQWPGV 120
Qy 121 KLRVTEGWDGDGHSEESLHYEGRADITTSDRDRSKYGMALARAVEAGFDWVYESKAH 180
Db 121 KLRVTEGWDGDGHSEESLHYEGRADITTSDRDRSKYGMALARAVEAGFDWVYESKAH 180
Qy 181 IHCSVKAENSAAKSGCCFGSATVHLEOGCTKLYKDLSPGDRVIAADDQGRLLYSDFLT 240
Db 181 IHCSVKAENSAAKSGCCFGSATVHLEOGCTKLYKDLSPGDRVIAADDQGRLLYSDFLT 240
Qy 241 FLDRDDGAKKYVYETREPRERLITAHLFLVAPHNDSATGEPEAASSGGPSSGALG 300
Db 241 FLDRDDGAKKYVYETREPRERLITAHLFLVAPHNDSATGEPEAASSGGPSSGALG 300
Qy 301 PRALFAASRVPGQRYVVAERDGRRLLPAVHSTLSEERAGAYAPLTAQGTILINRVL 360
Db 301 PRALFAASRVPGQRYVVAERDGRRLLPAVHSTLSEERAGAYAPLTAQGTILINRVL 360
Qy 361 ASCYAVIEEHSHWAHRAFAPPRLAHALLAALAPARTDRGGDGGDGRGGGRVALTAPGA 420
Db 361 ASCYAVIEEHSHWAHRAFAPPRLAHALLAALAPARTDRGGDGGDGRGGGRVALTAPGA 420
Qy 421 ADAPGAGATGAIHWSQLQIGWILDSEALHPGMAYKSSXSRGAGGAREGA 475
Db 421 ADAPGAGATGAIHWSQLQIGWILDSEALHPGMAYKSSXSRGAGGAREGA 475
Db 421 ADAPGAGATGAIHWSQLQIGWILDSEALHPGMAYKSSXSRGAGGAREGA 475

RESULT 2

us-09-883-848A-15

Sequence 15, Application US/09883848A
Publication No. US20030022819A1
GENERAL INFORMATION:

APPLICANT: Ling, L.
TITLE OF INVENTION: ANGIOGENESIS-MODULATING COMPOSITIONS AND USES
FILE REFERENCE: CIBT-P01-119
CURRENT APPLICATION NUMBER: US/09/883, 848A
PRIOR APPLICATION NUMBER: 60/211, 919
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 475
TYPE: PRT

ORGANISM: Homo sapiens
FEATURE: SITE
NAME/KEY: SITE
LOCATION: (463)
OTHER INFORMATION: xaa=unknown amino acid residue
US-09-883-848A-15

Query Match 99.9%; Score 2467; DB 9; length 475;
Best Local Similarity 100.0%; Pred. No. 1.4e-192; ;
Matches 475; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 MLLARCLLVLYVSSLLVCSGLACGPGRGFGKRRHKPKLTPLAYQFIPVAEKTIGASG 60
Db 1 MLLARCLLVLYVSSLLVCSGLACGPGRGFGKRRHKPKLTPLAYQFIPVAEKTIGASG 60
Qy 61 RYEGKISRNSRERKELTPTNPNPDIFKDEENTGADRMLTORCKDKLNALISMNQWPGV 120
Db 61 RYEGKISRNSRERKELTPTNPNPDIFKDEENTGADRMLTORCKDKLNALISMNQWPGV 120
Qy 121 KLRVTEGWDGDGHSEESLHYEGRADITTSDRDRSKYGMALARAVEAGFDWVYESKAH 180
Db 121 KLRVTEGWDGDGHSEESLHYEGRADITTSDRDRSKYGMALARAVEAGFDWVYESKAH 180

RESULT 3

us-09-021-660A-39

Sequence 39, Application US/09021660A
Patent No. US20010041668A1
GENERAL INFORMATION:

APPLICANT: Baron, M.
APPLICANT: Farrington, S.
APPLICANT: Belauhoff, M.

TITLE OF INVENTION: METHODS FOR MODULATING HEMATOPOIESIS AND VASCULAR
FILE REFERENCE: HU1P-P01-060
TITLE OF INVENTION: METHODS FOR MODULATING HEMATOPOIESIS AND VASCULAR
CURRENT APPLICATION NUMBER: US/09/021, 660A
FILE REFERENCE: HU1P-P01-060
CURRENT FILING DATE: 2001-08-27
PRIOR APPLICATION NUMBER: 60/037, 513
PRIOR FILING DATE: 1997-02-10
PRIOR APPLICATION NUMBER: 60/049, 763
PRIOR FILING DATE: 1997-06-16
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 39
LENGTH: 475
TYPE: PRT

ORGANISM: Homo sapiens
FEATURE: SITE
NAME/KEY: SITE
LOCATION: (463)
OTHER INFORMATION: xaa=unknown amino acid
US-09-021-660A-39

Query Match 99.9%; Score 2467; DB 10; length 475;
Best Local Similarity 100.0%; Pred. No. 1.4e-192; ;
Matches 475; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 MLLARCLLVLYVSSLLVCSGLACGPGRGFGKRRHKPKLTPLAYQFIPVAEKTIGASG 60
Db 1 MLLARCLLVLYVSSLLVCSGLACGPGRGFGKRRHKPKLTPLAYQFIPVAEKTIGASG 60

RESULT 4

us-09-021-660A-39

Sequence 39, Application US/09021660A
Patent No. US20010041668A1
GENERAL INFORMATION:

APPLICANT: Baron, M.
APPLICANT: Farrington, S.
APPLICANT: Belauhoff, M.

TITLE OF INVENTION: METHODS FOR MODULATING HEMATOPOIESIS AND VASCULAR
FILE REFERENCE: HU1P-P01-060
TITLE OF INVENTION: METHODS FOR MODULATING HEMATOPOIESIS AND VASCULAR
CURRENT APPLICATION NUMBER: US/09/021, 660A
FILE REFERENCE: HU1P-P01-060
CURRENT FILING DATE: 2001-08-27
PRIOR APPLICATION NUMBER: 60/037, 513
PRIOR FILING DATE: 1997-02-10
PRIOR APPLICATION NUMBER: 60/049, 763
PRIOR FILING DATE: 1997-06-16
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 39
LENGTH: 475
TYPE: PRT

ORGANISM: Homo sapiens
FEATURE: SITE
NAME/KEY: SITE
LOCATION: (463)
OTHER INFORMATION: xaa=unknown amino acid
US-09-021-660A-39

RESULT 5

us-09-021-660A-39

Sequence 39, Application US/09021660A
Patent No. US20010041668A1
GENERAL INFORMATION:

APPLICANT: Baron, M.
APPLICANT: Farrington, S.
APPLICANT: Belauhoff, M.

TITLE OF INVENTION: METHODS FOR MODULATING HEMATOPOIESIS AND VASCULAR
FILE REFERENCE: HU1P-P01-060
TITLE OF INVENTION: METHODS FOR MODULATING HEMATOPOIESIS AND VASCULAR
CURRENT APPLICATION NUMBER: US/09/021, 660A
FILE REFERENCE: HU1P-P01-060
CURRENT FILING DATE: 2001-08-27
PRIOR APPLICATION NUMBER: 60/037, 513
PRIOR FILING DATE: 1997-02-10
PRIOR APPLICATION NUMBER: 60/049, 763
PRIOR FILING DATE: 1997-06-16
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 39
LENGTH: 475
TYPE: PRT

ORGANISM: Homo sapiens
FEATURE: SITE
NAME/KEY: SITE
LOCATION: (463)
OTHER INFORMATION: xaa=unknown amino acid
US-09-021-660A-39

RESULT 4
US-09-151-99-15
; Sequence 15, Application US/09151999
; GENERAL INFORMATION:
; APPLICANT: Wang, Elizabeth
; TITLE OF INVENTION: REGULATION OF EPITHELIAL TISSUE BY HEDGEHOG-LIKE
; FILE REFERENCE: ONV-031.02
; CURRENT APPLICATION NUMBER: US/09/151,999
; CURRENT FILING DATE: 1998-08-11
; EARLIER APPLICATION NUMBER: 08/955,552
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.0
; SBO ID NO: 15
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Homo sapien Shh
; FEATURE:
; OTHER INFORMATION: Xaa at position 463 is any or unknown amino acid
; US-09-151-99-15

Query Match 99.9%; Score 2467; DB 10; Length 475;
Best Local Similarity 100.0%; Pred. No. 1-4e-192;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLIARCLLIVLVSLLVCSGLACGPGRGKRRHKPKLTPLAYKQFIPNVAEKTIGASG 60
Db 1 MLLIARCLLIVLVSLLVCSGLACGPGSGKGKRRHKPKLTPLAYKQFIPNVAEKTIGASG 60

Qy 61 RYEGKISRNSERKELTPTNPNPDIFKDENTGADRIMTQRCDKLNALISMNQPGV 120
Db 61 RYEGKISRNSERKELTPTNPNPDIFKDENTGADRIMTQRCDKLNALISMNQPGV 120

Qy 121 KLRVTEGWDGHISEESLHYEGRAVDTTSDDRSKYGMLARLAVEAGFDWVYESKAH 180
Db 121 KLRVTEGWDGHISEESLHYEGRAVDTTSDDRSKYGMLARLAVEAGFDWVYESKAH 180

Qy 181 IHCSVKAENSAVAKSGGCFFPSATVHLEGGTKLVKDLSPGDVLAADDQGRILYSDELT 240
Db 181 IHCSVKAENSAVAKSGGCFFPSATVHLEGGTKLVKDLSPGDVLAADDQGRILYSDELT 240

Qy 241 FLORDDGAKKVVFVETREPRELLTAHLLEVAPHNDSATGEPEASSGSPGGALG 300
Db 241 FLORDDGAKKVVFVETREPRELLTAHLLEVAPHNDSATGEPEASSGSPGGALG 300

Qy 301 PRALFAASRVRPGQRYVVAERDGRRLPAAVISVTLSBEAGAYAAPTQGTILINRVL 360
Db 301 PRALFAASRVRPGQRYVVAERDGRRLPAAVISVTLSBEAGAYAAPTQGTILINRVL 360

Qy 421 ADAPGAGATAGIHWYSOLQIQTWLIDSEALHPLGMAVKSSSRGAGGGAREGA 475
Db 421 ADAPGAGATAGIHWYSOLQIQTWLIDSEALHPLGMAVKSSSRGAGGGAREGA 475

RESULT 5
US-09-733-634-14
; Sequence 14, Application US/09733634
; GENERAL INFORMATION:
; APPLICANT: Massachusetts General Hospital
; TITLE OF INVENTION: Method to stimulate Insulin production by pancreatic b-cells
; FILE REFERENCE: 1763/1240
; CURRENT FILING DATE: 2000-12-08
; PRIORITY APPLICATION NUMBER: US/09/733,634
; PRIOR APPLICATION NUMBER: US 60/170,282
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin version 3.0
; SEQ ID NO: 14
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-733-634-14

Query Match 97.5%; Score 2407; DB 9; Length 462;
Best Local Similarity 100.0%; Pred. No. 1e-187;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLIARCLLIVLVSLLVCSGLACGPGRGKRRHKPKLTPLAYKQFIPNVAEKTIGASG 60
Db 1 MLLIARCLLIVLVSLLVCSGLACGPGSGKGKRRHKPKLTPLAYKQFIPNVAEKTIGASG 60

Qy 61 RYEGKISRNSERKELTPTNPNPDIFKDENTGADRIMTQRCDKLNALISMNQPGV 120
Db 61 RYEGKISRNSERKELTPTNPNPDIFKDENTGADRIMTQRCDKLNALISMNQPGV 120

Qy 121 KLRVTEGWDGHISEESLHYEGRAVDTTSDDRSKYGMLARLAVEAGFDWVYESKAH 180
Db 121 KLRVTEGWDGHISEESLHYEGRAVDTTSDDRSKYGMLARLAVEAGFDWVYESKAH 180

Qy 181 IHCSVKAENSAVAKSGGCFFPSATVHLEGGTKLVKDLSPGDVLAADDQGRILYSDELT 240
Db 181 IHCSVKAENSAVAKSGGCFFPSATVHLEGGTKLVKDLSPGDVLAADDQGRILYSDELT 240

Qy 241 FLORDDGAKKVVFVETREPRELLTAHLLEVAPHNDSATGEPEASSGSPGGALG 300
Db 241 FLORDDGAKKVVFVETREPRELLTAHLLEVAPHNDSATGEPEASSGSPGGALG 300

Qy 301 PRALFAASRVRPGQRYVVAERDGRRLPAAVISVTLSBEAGAYAAPTQGTILINRVL 360
Db 301 PRALFAASRVRPGQRYVVAERDGRRLPAAVISVTLSBEAGAYAAPTQGTILINRVL 360

Qy 361 ASCYAVIEEHSMWAHRAFAFRFLAHALLAALAPARTDGGDSGGDRGGGGVALTARGA 420
Db 361 ASCYAVIEEHSMWAHRAFAFRFLAHALLAALAPARTDGGDSGGDRGGGGVALTARGA 420

Qy 421 ADAPGAGATAGIHWYSOLQIQTWLIDSEALHPLGMAVKSSSRGAGGGAREGA 475
Db 421 ADAPGAGATAGIHWYSOLQIQTWLIDSEALHPLGMAVKSSSRGAGGGAREGA 475

RESULT 6
US-09-465-520A-1
; Sequence 1, Application US/09969520A
; Patent No. US2002017163A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: BEACHY, Philip A.

FILE REFERENCE: JHU1670-1 ; TYPE: PRT
 CURRENT APPLICATION NUMBER: US/09/969,520A ; ORGANISM: House Mouse
 PRIORITY FILING DATE: 2002-06-04 ; SEQ ID NO: 1
 NUMBER OF SEQ ID NOS: 17 ; LENGTH: 437
 SOFTWARE: PatentIn version 3.1 ; SEQ ID NO: 1
 LENGTH: 437 ; TYPE: PRT
 ORGANISM: Mus musculus ; SEQ ID NO: 1
 LENGTH: 437 ;
 US-09-969-520A-1

Query Match 83.8%; Score 2068; DB 9; Length 437;
 Best Local Similarity 87.4%; Pred. No. 3.1e-160;
 Matches 404; Conservative 8; Mismatches 24; Indels 26; Gaps 3;

Qy 1 MLLARCLLVLVSSLLVSGLAGCPGGRGGKRRHKPKLTPLAYKOFIPNVAEKTIGASG 60
 Db 2 LLLARCFVLILASSLLVCGPLACGPGRGKRRHKPKLTPLAYKOFIPNVAEKTIGASG 61

Qy 61 RYEKGKSRNSRERKELTPTNPNDLIFKDEENTGADRIMTORCKOKNLALISVNQWPGV 120
 Db 62 RYEKGKTRNSRERKELTPTNPNDLIFKDEENTGADRIMTORCKOKNLALISVNQWPGV 121

Qy 121 KLRVTEGWDGDGHSEESLHYEGRAVDITSDRDRSKYGMALARAVEAGEDDWVYESKAH 180
 Db 122 KLRVTEGWDGDGHSEESLHYEGRAVDITSDRDRSKYGMALARAVEAGEDDWVYESKAH 180

Qy 181 IHCSYKAENSAAKSGCCFFGSATVHLEOGGTKLVKDLRPGDRVLAADDOGRRLYSDFLT 240
 Db 182 IHCSYKAENSAAKSGCCFFGSATVHLEOGGTKLVKDLRPGDRVLAADDOGRRLYSDFLT 241

Qy 241 FLDRDGAKKYFYVETREERERLLTAAILFLWPHND-----SGPTPG 286
 Db 242 FLDRDGAKKYFYVETLEBLERLLTAAILFLWPHND-----SGPTPG 286

Qy 301 PRALAFSRVRPGQRYVVAERDGDRRLPRAVHSVTLSEEAGAYAPLTAQGTLINRVL 360
 Db 287 PSALFASRVRPGQRYVVAERDGDRRLPRAVHSVTLSEEAGAYAPLTAQGTLINRVL 346

Qy 361 ASCYAVIEEWSWAHRAPPRLAHLAAALAPARTDRGGDGGDRGGGGDRGGGGVALTAPGA 420
 Db 347 ASCYAVIEEWSWAHRAPPRLAHLAAALAPARTDRGGDGGDRGGGGDRGGGGVALTAPGA 420

Qy 421 ADAPGAGATGIGHWSOLQIWTMILDSEALPHGMAYKSS 462
 Db 396 TEARGAEPTAGIHWSOLQIWTMILDSETMHPLGMAYKSS 437

RESULT 7
 US-10-013-310-1
 ; Sequence 1, Application US/1001310
 ; Publication No. US20020192216A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lamb, Jonathon Robert
 ; APPLICANT: Hoyne, Gerard Francis
 ; APPLICANT: Dallman, Margaret Jane
 ; TITLE OF INVENTION: Therapeutic Use
 ; FILE REFERENCE: 674525-2003
 ; CURRENT APPLICATION NUMBER: US/10/013, 310
 ; PRIORITY FILING DATE: 2001-12-07
 ; PRIORITY APPLICATION NUMBER: PCT/GB00/02191
 ; PRIORITY FILING DATE: 2000-06-05
 ; PRIORITY APPLICATION NUMBER: UK 9913350.6
 ; PRIORITY FILING DATE: 1999-06-08
 ; PRIORITY APPLICATION NUMBER: UK 9921953.7
 ; PRIORITY FILING DATE: 1999-09-16
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 1
 ; LENGTH: 437
 ; TYPE: PRT
 ; ORGANISM: Mus musculus ; SEQ ID NO: 1
 ; LENGTH: 437 ;
 US-09-733-634-16

Query Match 83.8%; Score 2068; DB 9; Length 437;
 Best Local Similarity 87.4%; Pred. No. 3.1e-160;
 Matches 404; Conservative 8; Mismatches 24; Indels 26; Gaps 3;

Qy 1 MLLARCLLVLVSSLLVSGLAGCPGGRGGKRRHKPKLTPLAYKOFIPNVAEKTIGASG 60
 Db 2 LLLARCFVLILASSLLVCGPLACGPGRGKRRHKPKLTPLAYKOFIPNVAEKTIGASG 61

Qy 61 RYEKGKSRNSRERKELTPTNPNDLIFKDEENTGADRIMTORCKOKNLALISVNQWPGV 120
 Db 62 RYEKGKTRNSRERKELTPTNPNDLIFKDEENTGADRIMTORCKOKNLALISVNQWPGV 121

RESULT 8
 US-09-733-634-16
 ; Sequence 16, Application US/09733634
 ; Publication No. US20030013646A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Massachusetts General Hospital
 ; TITLE OF INVENTION: Method to stimulate insulin production by pancreatic b-cells
 ; FILE REFERENCE: 1763371240
 ; CURRENT APPLICATION NUMBER: US/09/733, 634
 ; PRIORITY FILING DATE: 2000-12-08
 ; PRIORITY APPLICATION NUMBER: US 60/170, 282
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 16
 ; LENGTH: 437
 ; TYPE: PRT
 ; ORGANISM: Mus musculus ; SEQ ID NO: 1
 ; LENGTH: 437 ;
 US-09-733-634-16

Query Match 83.8%; Score 2068; DB 9; Length 437;
 Best Local Similarity 87.4%; Pred. No. 3.1e-160;
 Matches 404; Conservative 8; Mismatches 24; Indels 26; Gaps 3;

Qy 1 MLLARCLLVLVSSLLVSGLAGCPGGRGGKRRHKPKLTPLAYKOFIPNVAEKTIGASG 60
 Db 2 LLLARCFVLILASSLLVCGPLACGPGRGKRRHKPKLTPLAYKOFIPNVAEKTIGASG 61

Qy 61 RYEKGKSRNSRERKELTPTNPNDLIFKDEENTGADRIMTORCKOKNLALISVNQWPGV 120
 Db 62 RYEKGKTRNSRERKELTPTNPNDLIFKDEENTGADRIMTORCKOKNLALISVNQWPGV 121

QY 121 KLRVTEGDEDGHISEESEHYSERAVDITTSDDRSKYGMLARLAVEAGEDDWYYESKAH 180
Db 122 KLRVTEGDEDGHISEESEHYSERAVDITTSDDRSKYGMLARLAVEAGEDDWYYESKAH 181
Qy 181 IHESVKAENSAVAKSGGGPPGSATVHLEOGGTPLKVLKDLSPGDRVLAADQGRILYSPLT 240
Db 182 IHESVKAENSAVAKSGGGPPGSATVHLEOGGTPLKVLKDLSPGDRVLAADQGRILYSPLT 241
Qy 241 FLORDGAKKVFTETREPRELLTAHLITVAPHNDSATGEPEASSGGSPGGALG 300
Db 242 FLRDEGAKKVFTETREPRELLTAHLITVAPHND-----SGPTPG 286
Qy 301 PRALFASRVPGORVYVAERDDRLIPAAVISVTULEEAGAYAPLTAQGTILINRL 360
Db 287 PSALFASRVPGORVYVAERGGDRRLIPAAVISVTULEEAGAYAPLTAQGTILINRL 346
Qy 361 ASCYAVIEBHSWAHRAFAPFLAHALLAALAPARTDRCGDGGDRGGGRVALTARGA 420
Db 347 ASCYAVIEBHSWAHRAFAPFLAHALLAALAPARTD-----GGGGSIP-AAQSA 395
Qy 421 ADPAGAGATGTHWSOLLYQIGTWLDEAHLPLGMANKSS 462
Db 396 TEARGAEPPIGINWSOLLYHICGTWLDSETWHLPLGMANKSS 437

RESULT 9
US-09-021-660A-37
; sequence 37, Application US/09021660A
; Patent No. US20010041668A1
; GENERAL INFORMATION:
; APPLICANT: Baron, M.
; APPLICANT: Farrington, S.
; APPLICANT: Belauhoff, M.
; TITLE OF INVENTION: METHODS FOR MODULATING HEMATOPOIESIS AND VASCULAR GROWTH
; FILE REFERENCE: HU1P-P01-060
; CURRENT APPLICATION NUMBER: US/09/021,660A
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 60/037,513
; PRIOR FILING DATE: 1997-02-10
; PRIOR APPLICATION NUMBER: 60/049,763
; PRIOR FILING DATE: 1997-06-16
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 37
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-021-660A-37

Query Match 83.8%; Score 2068; DB 10; Length 437;
Best Local Similarity 87.4%; Pred. No. 3.1e-160; Matches 404; Conservative 8; Mismatches 24; Indels 26; Gaps 3;

Qy 1 MULLARCLLVLVSSLVCSGLACGPGRGKGRRHKPKLTPLAYKQFIPNVAEKTGASG 60
Db 2 LLLIARCLFLVILLASLLVCPGLACGPGRGKGRRHKPKLTPLAYKQFIPNVAEKTGASG 61

Qy 61 RYEGKISRNSERKELTPTNPNPDKPENTGADRMTQCDKLNALAISMNQPGV 120
Db 62 RYEGKITRN SERKELTPTNPNPDKPENTGADRMTQCDKLNALAISMNQPGV 121

Qy 121 KLRVTEGDEDGHISEESEHYSERAVDITTSDDRSKYGMLARLAVEAGEDDWYYESKAH 180
Db 122 KLRVTEGDEDGHISEESEHYSERAVDITTSDDRSKYGMLARLAVEAGEDDWYYESKAH 181

Qy 181 IHESVKAENSAVAKSGGGPPGSATVHLEOGGTPLKVLKDLSPGDRVLAADQGRILYSPLT 240
Db 182 IHESVKAENSAVAKSGGGPPGSATVHLEOGGTPLKVLKDLSPGDRVLAADQGRILYSPLT 241

Qy 241 FLORDGAKKVFTETREPRELLTAHLITVAPHND-----SGPTPG 300
Db 242 FLRDEGAKKVFTETREPRELLTAHLITVAPHND-----SGPTPG 286

QY 301 PRALFASRVPGORVYVAERDDRLIPAAVISVTULEEAGAYAPLTAQGTILINRL 360
Db 287 PSALFASRVPGORVYVAERGGDRRLIPAAVISVTULEEAGAYAPLTAQGTILINRL 346
Qy 361 ASCYAVIEBHSWAHRAFAPFLAHALLAALAPARTDRCGDGGDRGGGRVALTARGA 420
Db 347 ASCYAVIEBHSWAHRAFAPFLAHALLAALAPARTD-----GGGGSIP-AAQSA 395
Qy 421 ADPAGAGATGTHWSOLLYQIGTWLDEAHLPLGMANKSS 462
Db 396 TEARGAEPPIGINWSOLLYHICGTWLDSETWHLPLGMANKSS 437

RESULT 10
US-08-900-220C-13
; Sequence 13, Application US/08900220C
; Patent No. US2002005206A1
; GENERAL INFORMATION:
; APPLICANT: Miao, Ningning
; Wang, Monica
; Mahanthappa, Nagesh K.
; Pang, Kevin
; Jin, Ping
; TITLE OF INVENTION: Method of Treating Dopaminergic and GABAergic Disorders
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: ONE POST OFFICE SQUARE
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/900,220C
; FILING DATE: 24-Jul-1997
; CLASSIFICATION: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: ONV-044.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1000
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 437 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
; US-08-900-220C-13

Query Match 83.6%; Score 2065; DB 8; Length 437;
Best Local Similarity 87.2%; Pred. No. 5.4e-160; Matches 403; Conservative 9; Mismatches 24; Indels 26; Gaps 3;

Qy 1 MULLARCLLVLVSSLVCSGLACGPGRGKGRRHKPKLTPLAYKQFIPNVAEKTGASG 60
Db 2 LLLIARCLFLVILLASLLVCPGLACGPGRGKGRRHKPKLTPLAYKQFIPNVAEKTGASG 61

Qy 61 RYEGKISRNSERKELTPTNPNPDKPENTGADRMTQCDKLNALAISMNQPGV 120
Db 62 RYEGKITRN SERKELTPTNPNPDKPENTGADRMTQCDKLNALAISMNQPGV 121

Qy 121 KLRVTEGDEDGHISEESEHYSERAVDITTSDDRSKYGMLARLAVEAGEDDWYYESKAH 180

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122 RLURTEGHDDEGHHSERSSLHVEGRADWITTSRDRSKYGMARLAVERAGFDWVYESKAH 1811
Qy IHCSVKAEVNSVAAKSGCCFGSATVILEEQGKLVKDLSPGDRLAADDQGRLYSDFL 240
Db 181 IHC SVKAEN SVAAK SGCC FG SATVIL E QG KLV KDL SPGD RL A ADD QGR LY SD FL 241
Qy 241 FLD R D GAK KV YVIE R P R R L L TTA HLL F VAP H ND S AT G E PE AS GS GPP SG AL G 300
Db 242 FLD R D E GAK KV YVIE R P R R L L TTA HLL F VAP H ND S AT G E PE AS GS GPP SG AL G 300
Qy 301 PRALFASRVPRGQRYVVAERDGDRLLPAVHSVTLSERAGAYPLTAQSTILNRLV 360
Db 287 PSALFASRVPRGQRYVVAERDGDRLLPAVHSVTLSERAGAYPLTAQSTILNRLV 346
Qy 361 ASCYAVTEEHWSKAHAFAPRLAHALLA LAPART DRGGDSGGDRGGGRVALTNGA 420
Db 347 ASCYAVTEEHWSKAHAFAPRLAHALLA LAPART DRGGDSGGDRGGGRVALTNGA 395
Qy 421 ADAPGAGATAGHWSOLLYQIGTWLIDSEALHPLGAVKSS 462
Db 396 TEARGAEPPTAGHWSOLLYQIGTWLIDSEALHPLGAVKSS 437

RESULT 11
US-09-883-848A-13
; Sequence 13, Application US/09883848A
; Publication No. US20030022819A1
; GENERAL INFORMATION:
; APPLICANT: Ling, L.
; APPLICANT: Sanicola-Nadel, M
; TITLE OF INVENTION: ANGIOGENESIS-MODULATING COMPOSITIONS AND USES
; FILE REFERENCE: C1M-P01-119
; CURRENT APPLICATION NUMBER: US/09/883, 848A
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/211, 919
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-883-848A-13

Query Match          83.6%: Score 2065; DB 9; Length 437;
Best Local Similarity 87.2%; Pred. No. 5.4e-160; Matches 403; Conservative 9; Mismatches 24; Indels 26; Gaps 0
Qy 1 MILLARCLLVLVSLVSGLAGCPRGFGKRRHPKLTLPLAYKQIPINVAEKTGAS 60
Db 2 LILLARCLFLVTLASSILYCPGLACPGRGFGKRRHPKLTLPLAYKQIPINVAEKTGAS 61
Qy 61 RVEGKTSRN SERFKELT PNYNDI FIKD E NTGADRLMTQRCKDKLNALATSVMNDPVG 120
Db 62 RVEGKTRNSERFKELT PNYNDI FIKD E NTGADRLMTQRCKDKLNALATSVMNDPVG 121
Qy 121 KLRVTEGWD E GHSEESLHYEGRAV D ITTSRDRSKYGMARLAVEAGFDWVYESKAH 180
Db 122 RL RVTEGWD E GHSEESLHYEGRAV D ITTSRDRSKYGMARLAVEAGFDWVYESKAH 181
Qy 181 IHCSVKAEVNSVAAKSGCCFGSATVILEEQGKLVKDLSPGDRLAADDQGRLYSDFL 240
Db 182 IHCSVKAEVNSVAAKSGCCFGSATVILEEQGKLVKDLSPGDRLAADDQGRLYSDFL 241
Qy 241 FLD R D GAK KV YVIE R P R R L L TTA HLL F VAP H ND S AT G E PE AS GS GPP SG AL G 300
Db 242 FLD R D E GAK KV YVIE R P R R L L TTA HLL F VAP H ND S AT G E PE AS GS GPP SG AL G 300
Qy 301 PRALFASRVPRGQRYVVAERDGDRLLPAVHSVTLSERAGAYPLTAQSTILNRLV 360
Db 287 PSALFASRVPRGQRYVVAERDGDRLLPAVHSVTLSERAGAYPLTAQSTILNRLV 346
Qy 361 ASCYAVTEEHWSKAHAFAPRLAHALLA LAPART DRGGDSGGDRGGGRVALTNGA 420

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RESULT 12
US-09-151-999-13
; Sequence 13, Application US/09151999
; Patent No. US20020151460A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Elizabeth
; TITLE OF INVENTION: REGULATION OF EPITHELIAL TISSUE BY HEDGEHOG-LIKE
; FILE REFERENCE: ONY-031_02
; CURRENT APPLICATION NUMBER: US/09/151, 999
; CURRENT FILING DATE: 1998-08-11
; EARLIER APPLICATION NUMBER: 08/955, 552
; EARLIER FILING DATE: 1997-10-20
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 437
; TYPE: PRT
; ORGANISM: murine Shh
; US-09-151-999-13

Query Match          83.6%; Score 2065; DB 10; Length 437;
Best Local Similarity 87.2%; Pred. No. 5. 4e-16;
Matches 403; Conservative 9; Mismatches 24; Indels 26; Gaps 3;
QY  1 MLLARCLLVLVLLSSLLVCCGLACGPGRGFGKRRRHPKKLPLAYQFIPWAETLGASS 60
Db  2 LLLLARCLFLVLLASSLLVCCPGLAGCFCRGFGKRRRHPKKLPLAYQFIPWAETLGASC 61
QY  61 RYEKTSRNSERPEKEPLTPYNPDITPRDEENGADILMTRCKDKNLNALISVMQWPGV 120
Db  62 RYEKTSRNSERPEKEPLTPYNPDITPRDEENGADILMTRCKDKNLNALISVMQWPGV 121
QY  121 KURVTEGKWDGEHHSESLHVGRADITTSDRRSKYGMARLAVEGAEDWVYESKAH 180
Db  122 RLRTVTEGWDGEHHSESLHVGRADITTSDRRSKYGMARLAVEGAEDWVYESKAH 181
QY  181 IHCSVKAENSAVAKSGCCPGSATVHLEQGGTKLVKDLSQPSDVRVLAADDGRLYSDFT 240
Db  182 IHCSVKAEVSAVAKSGCCPGSATVHLEQGGTKLVKDLSQPSDVRVLAADDGRLYSDFT 241
QY  241 FLDRDDGAKKVYVIEPREPRERLTTAAHILFVAPHNDSATGEPEBASSSGPPSGGAGL 300
Db  242 FLDRDEGAKKVYVIEPREPRERLTTAAHILFVAPHNDSATGEPEBASSSGPPSGGAGL 301
QY  301 PRALFAASRVPRPQRYVVAERGDRLLPAVHSVTLSEAGAVAPLTQGTTILNRU 360
Db  287 PSALFAASRVPRPQRYVVAERGDRLLPAVHSVTLREBEGAVAPLTQGTTILNRU 346
QY  361 ASCYAVIEEWSWAHRAATAPFRLLAHALLAALAPARTDORGGSGGDRGGGGRVALTAPGA 420
Db  347 ASCYAVIEEWSWAHRAAFPLRLAHALLAALAPARTD-----GGGGSIP-AAQSA 395
QY  421 AADPAGACATAGTHWYSOLLYKIGTWLDSALHPGMAVSS 462
Db  396 TEARGAEPPTAGIHWYSOLLYHGTWLDSETMHPGMAVKS 437

RESULT 13
US-09-990-046-14
; Sequence 14, Application US/09990046
; Patent No. US20020156245A1
; GENERAL INFORMATION:
; APPLICANT: de Savage, Frederic
; APPLICANT: Carpenter, David A.

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TITLE OF INVENTION: Patched-2
FILE REFERENCE: P105R1
CURRENT APPLICATION NUMBER: US/09/990, 046
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/293, 505
PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-15
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 14
LENGTH: 437
TYPE: PRT
ORGANISM: *Mus musculus*
US-09-990-046-14

Query Match 83.5%; Score 2062; DB 9; Length 437;
Best Local Similarity 87.0%; Pred. No. 9, 4e-160; Matches 403; Conservative 8; Mismatches 3; Indels 26; Gaps 3;

QY 1 MLLARCLLVLVSSLLVCSGLACPGPGRGFGKRRHPRKKLTPLAYKOPTIPNVAEKTIGASG 60
Db 2 LLLARCLFLVILLASSLLVCPGLACPGPGRGFGKRRHPRKKLTPLAYKOPTIPNVAEKTIGASG 61
QY 61 RVEGKTSRNSERFERKELTPNYNPDIIFKDEENTGADRIMTORCKDKLNALATSVMNOPGV 120
Db 62 RVEGKTRNSERFERKELTPNYNPDIIFKDEENTGADRIMTORCKDKLNALATSVMNOPGV 121

QY 121 KLRVTEGWDGDHHSEESLHYEGRAVDITSDRDRSKYGMALARLAVEAGFDWVYESKAH 180
Db 122 KLRVTEGWDGDHHSEESLHYEGRAVDITSDRDRSKYGMALARLAVEAGFDWVYESKAH 181

QY 181 IHCSVKAENSAVAKSGGCFPGSATVHLEQGGTKLVKOLSPGDRVLADDQGRLLSDFLT 240
Db 182 IHCSVKAENSAVAKSGGCFPGSATVHLEQGGTKLVKOLSPGDRVLADDQGRLLSDFLT 241

QY 241 FLDRDGAKKVYVIETREPREBLUITAHLFLVAPHDNSATGEPEAASSGGPPSGALG 300
Db 242 FLDRDGAKKVYVIETREPREBLUITAHLFLVAPHDNSATGEPEAASSGGPPSGALG 301

QY 301 PRALFASRVRPGQRVYVAERGDRRLPPAAYHSVTLSSEAGAYAPLTAQGTILNRVL 360
Db 287 PSALFASRVPRPGQRVYVAERGDRRLPPAAYHSVTLSREEEAGAYAPLTAQGTILNRVL 346

QY 361 ASCYAVEEHSHWAHRAFPLRHALLAALAAPARTDRGGDSSGGDRGGGGRVALTAPGA 420
Db 347 ASCYAVEEHSHWAHRAFPLRHALLAALAAPARTDRGGDSSGGDRGGGGRVALTAPGA 421

QY 421 ADAPGAGATAGTHWSQLYQIQTWLWSEALHPLGHMAVKSS 462
Db 396 TEARGAEPTAGTHWSQLYIHTGWLDSETMPLGHMAVKSS 437

RESULT 14
US-09-990-520A-3
Sequence 3, Application US/09969520A
Patent No. US2002017163A1

GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: BEACHY, PHILIP A.
TITLE OF INVENTION: METHOD OF USE OF SONIC HEDGEHOG PROTEIN AS A LIGAND FOR PATCHED
FILE REFERENCE: JHU1670-1
CURRENT APPLICATION NUMBER: US/09/969, 520A
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 60/435, 153
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 10
LENGTH: 437
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Altered sonic hedgehog protein

Query Match 83.4%; Score 2059; DB 9; Length 437;
Best Local Similarity 87.0%; Pred. No. 1, 6e-159; Matches 402; Conservative 9; Mismatches 25; Indels 26; Gaps 3;

QY 1 MLLARCLLVLVSSLLVCSGLACPGPGRGFGKRRHPRKKLTPLAYKOPTIPNVAEKTIGASG 60
Db 2 LLLARCLFLVILLASSLLVCPGLACPGPGRGFGKRRHPRKKLTPLAYKOPTIPNVAEKTIGASG 61
QY 61 RVEGKTSRNSERFERKELTPNYNPDIIFKDEENTGADRIMTORCKDKLNALATSVMNOPGV 120
Db 62 RVEGKTRNSERFERKELTPNYNPDIIFKDEENTGADRIMTORCKDKLNALATSVMNOPGV 121

QY 121 KLRVTEGWDGDHHSEESLHYEGRAVDITSDRDRSKYGMALARLAVEAGFDWVYESKAH 180
Db 122 KLRVTEGWDGDHHSEESLHYEGRAVDITSDRDRSKYGMALARLAVEAGFDWVYESKAH 181

QY 181 IHCSVKAENSAVAKSGGCFPGSATVHLEQGGTKLVKOLSPGDRVLADDQGRLLSDFLT 240
Db 182 IHCSVKAENSAVAKSGGCFPGSATVHLEQGGTKLVKOLSPGDRVLADDQGRLLSDFLT 241

QY 241 FLDRDGAKKVYVIETREPREBLUITAHLFLVAPHDNSATGEPEAASSGGPPSGALG 300
Db 242 FLDRDGAKKVYVIETREPREBLUITAHLFLVAPHDNSATGEPEAASSGGPPSGALG 301

QY 301 PRALFASRVRPGQRVYVAERGDRRLPPAAYHSVTLSSEAGAYAPLTAQGTILNRVL 360
Db 287 PSALFASRVPRPGQRVYVAERGDRRLPPAAYHSVTLSREEEAGAYAPLTAQGTILNRVL 346

QY 361 ASCYAVEEHSHWAHRAFPLRHALLAALAAPARTDRGGDSSGGDRGGGGRVALTAPGA 420
Db 347 ASCYAVEEHSHWAHRAFPLRHALLAALAAPARTDRGGDSSGGDRGGGGRVALTAPGA 421

QY 421 ADAPGAGATAGTHWSQLYQIQTWLWSEALHPLGHMAVKSS 462
Db 396 TEARGAEPTAGTHWSQLYIHTGWLDSETMPLGHMAVKSS 437

RESULT 15
US-09-969-520A-10
Sequence 10, Application US/09969520A
Patent No. US2002017163A1

GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: BEACHY, PHILIP A.
TITLE OF INVENTION: METHOD OF USE OF SONIC HEDGEHOG PROTEIN AS A LIGAND FOR PATCHED
FILE REFERENCE: JHU1670-1
CURRENT APPLICATION NUMBER: US/09/969, 520A
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: 2000-09-22
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 10
LENGTH: 437
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Altered sonic hedgehog protein

Query Match 83.4%; Score 2059; DB 9; Length 437;
Best Local Similarity 87.0%; Pred. No. 1, 6e-159; Matches 402; Conservative 9; Mismatches 25; Indels 26; Gaps 3;

QY 1 MLLARCLLVLVSSLLVCSGLACPGPGRGFGKRRHPRKKLTPLAYKOPTIPNVAEKTIGASG 60
Db 2 LLLARCLFLVILLASSLLVCPGLACPGPGRGFGKRRHPRKKLTPLAYKOPTIPNVAEKTIGASG 61
QY 61 RVEGKTSRNSERFERKELTPNYNPDIIFKDEENTGADRIMTORCKDKLNALATSVMNOPGV 120
Db 62 RVEGKTRNSERFERKELTPNYNPDIIFKDEENTGADRIMTORCKDKLNALATSVMNOPGV 121

QY 121 KLRVTEGWDGDHHSEESLHYEGRAVDITSDRDRSKYGMALARLAVEAGFDWVYESKAH 180
Db 122 KLRVTEGWDGDHHSEESLHYEGRAVDITSDRDRSKYGMALARLAVEAGFDWVYESKAH 181

QY 181 IHCSVKAENSAVAKSGGCFPGSATVHLEQGGTKLVKOLSPGDRVLADDQGRLLSDFLT 240
Db 182 IHCSVKAENSAVAKSGGCFPGSATVHLEQGGTKLVKOLSPGDRVLADDQGRLLSDFLT 241

QY 241 FLDRDGAKKVYVIETREPREBLUITAHLFLVAPHDNSATGEPEAASSGGPPSGALG 300
Db 242 FLDRDGAKKVYVIETREPREBLUITAHLFLVAPHDNSATGEPEAASSGGPPSGALG 301

QY 301 PRALFASRVRPGQRVYVAERGDRRLPPAAYHSVTLSSEAGAYAPLTAQGTILNRVL 360
Db 287 PSALFASRVPRPGQRVYVAERGDRRLPPAAYHSVTLSREEEAGAYAPLTAQGTILNRVL 346

QY 361 ASCYAVEEHSHWAHRAFPLRHALLAALAAPARTDRGGDSSGGDRGGGGRVALTAPGA 420
Db 347 ASCYAVEEHSHWAHRAFPLRHALLAALAAPARTDRGGDSSGGDRGGGGRVALTAPGA 421

QY 421 ADAPGAGATAGTHWSQLYQIQTWLWSEALHPLGHMAVKSS 462
Db 396 TEARGAEPTAGTHWSQLYIHTGWLDSETMPLGHMAVKSS 437

Db 122 |||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:
 KLRVYEGWDEGDGHISEESLHYEGRAVDITSDAARAKYGMALARAVEGFDWVYESKAH 181
 Qy 181 IHCSYKAENSAVAKSGCCFGSATVHLBQGCKTUVKDISPGDRYLAADDGGRILYSDFT 240
 Db 182 IHCSYKAENSAVAKSGCCFGSATVHLBQGCKTUVKDISPGDRYLAADDGGRILYSDFT 241
 Qy 241 FLDRDGAKKVYVLTREPRLLTAAHLFVAPHND-SGPTPG 300
 Db 242 FLDRDGAKKVYVLTREPRLLTAAHLFVAPHND-SGPTPG 286
 Qy 301 PRALFAASRVYRPQRYVVAERDGDRRLPAVHSVTLSBAAAGAYAPLTAQGTILINRVL 360
 Db 287 PSALLEASRVYRPQRYVVAERGGRRLPAVHSVTLSBAAAGAYAPLTAQGTILINRVL 346
 Qy 361 ASCYAVTEEHSWAHRKFAPPRLAHLALLAPARTDRGDDGGDRGGGRVALTARGA 420
 Db 347 ASCYAVTEEHSWAHRKFAPPRLAHLALLAPARTD-GGGGSTP-AAQSA 395
 Qy 421 ADACAGATAGIHMYSQQLYQIGTWLDSEALHPLGMAYKSS 462
 Qy :1 |||||||:|||||||:|||||||:|||||||:
 396 TEARGAEPTAGIHWSQQLYHIGTWLDSETMHPPLGMAYKSS 437

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 Job time : 9.52655 secs